

**The transcriptional landscape and small RNAs
in *Acinetobacter baumannii* AB5075 during
antibiotic and environmental stress**

**A thesis submitted to the University of Dublin in fulfilment
of the
requirements for the degree Doctor of Philosophy by**

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Declaration

I hereby declare that this thesis is my own, independent work that has never before been submitted for credit toward a degree at this or any other university, with the exception of instances where it is properly recognized in the text,

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Summary

Multi-drug resistant *Acinetobacter baumannii* is considered a major challenge because it causes a variety of serious infections. Studying these bacteria at the level of their genetic response could facilitate finding a way to treat them. Tracking gene expression throughout the growth phases or when affected by any environmental stresses can deepen our understanding of how genes work and how cells function. Here, we studied global gene expression of *A. baumannii* AB5075 using RNA-seq under the influence of 12 different stresses divided into three groups. The first group includes five growth stages in rich medium, the second group includes four environmental shocks (osmotic, iron limitation and two antibiotic shocks), and the third group contains temperatures shift experiments (between 22°C and 37°C). An important finding is the dramatic up-regulation of the phenyl-acetic acid (*paa*) pathway including *paaA*, *paaB*, *paaC*, *paaJ*, *paaK* and *paaZ* in late exponential and early stationary phase in rich medium which influences virulence, antibiotic resistance, and biofilm formation. In the environmental shock conditions, we reveal that the transcriptional responses were similar between osmotic shock and iron limiting conditions, and the effect of antibiotics (exposure to chloramphenicol and tetracycline), respectively, indicating that similar pathways are involved in these stress responses. These included genes encoding siderophore Acinetobactin encoding genes that were up-regulated in both osmotic shock and iron limiting conditions. The two antibiotic shocks showed gene expression changes to a much larger than osmotic shock and iron limiting conditions suggesting that protein synthesis stress require a much larger transcriptomic response to cope with the stress compared to the osmotic and iron limitation stress. A response to the antibiotic stress was observed to be a down-regulation of the NADH-quinone oxidoreductase complex, a central protein complex in the respiratory chain, indicating the antibiotics could influence the proton gradient across the membrane or that further growth and ATP synthesis should be immediately stopped. When growing at different temperatures, there were large changes to the transcriptome in all temperature comparisons. The virulence-associated *otsAB* operon and *paa* genes were strongly up-regulated upon temperature shift. Type IV pilus encoding genes were down-regulated genes when

cells were experiencing a temperature upshift (TS) which could mean that DNA uptake is at least transiently down-regulated when *A. baumannii* enters a warm-blooded host. In contrast, a temperature downshift induced expression of the Type 6 Secretion System and Csu pili.

We also provide a first expression landscape of sRNAs in the suite of 12 conditions. We observed dynamic expression of many small RNAs across the 12 conditions. The sRNAs sRNA99 and sRNA100 very quickly dropped in abundance when the cells experienced antibiotic shocks which was independently validated by Northern blotting for sRNA99 and sRNA100. Deletion of sRNA99 and sRNA100, resulted in large expression changes in MEP in the mutants compared to the WT, which will require further analysis. The sRNA44 was investigated mechanistically in more detail in this study because previous data in *A. baumannii* AB5075 suggested that sRNA44 was ligated to the mRNA of the biofilm-associated *bap* gene. We show that sRNA44 translationally represses *bap* translation in *E. coli* and that overexpression of sRNA44 reduces *bap* mRNA levels, likely induced by a base-pairing mechanism. Deletion of sRNA44 and *bap* showed that *bap* is required for full biofilm formation after 24h, while deletion of sRNA44 increased biofilm formation suggesting that sRNA44 is a regulator of *A. baumannii* biofilm formation.

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*(Shaibah A) and (Bakheet A) both names refer to me

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Chapter 1

General Introduction

1.1 An historical perspective

Acinetobacter baumannii is a Gram negative, obligate aerobe, coccobacillus, and one of the most prevalent causes of nosocomial infections (Martín-Aspas *et al.*, 2018). Due to the World Health Organization's designation of *A. baumannii* as a top priority pathogen for research and development of new medicines, the amount of investigation into this microorganism has expanded during the past few years (Tacconelli *et al.*, 2018). The origins of the *Acinetobacter* genus can be traced back to the early decades of the 20th century (Peleg *et al.*, 2008). In 1911, a pathogen dubbed *Micrococcus calcoaceticus* was isolated from soil by Beijerinck and cultured on a medium consisting of calcium acetate and minerals (Beijerinck, 1911). This finding led to the identification of the genus *Acinetobacter* (Doughari *et al.*, 2011), which was named as *Acinetobacter* in the 1950s (Munoz-Price and Weinstein, 2008). The name "Acinetobacter" comes from the Greek word "akinetos" which means "nonmotile". It was originally proposed in 1954 by Brisou and Prevot to differentiate the organisms based on their motility in the "Achromobactereae", which was composed of non-pigmented, oxidase-negative and oxidase-positive Gram-negative saprophytic bacteria (Brisou and Prevot, 1954; Jung and Park, 2015). In 1957, Brisou discovered a species which he named *Acinetobacter anitratum* (Brisou, 1957; Jung and Park, 2015). In 1968, the genus *Acinetobacter* was finally established and accepted (Baumann *et al.*, 1968).

1.1.1 Taxonomic classification of *Acinetobacter* species

Because of recent advances in our understanding of the genetic make-up of this group of microorganisms that can be studied using molecular techniques, in particular next-generation sequencing (NGS) based genome sequencing, the names of the species of *Acinetobacter* have undergone significant taxonomic modifications over the course of time (Jung and Park, 2015). In 1991, it was proposed that *Moraxella*, *Acinetobacter*, *Psychrobacter*, and other closely related organisms should form a new family under the order Gamma-proteobacteria called *Moraxellaceae*, which would contain the

members of the genus *Acinetobacter* (Rossau *et al.*, 1991). The taxonomic hierarchy of *A. baumannii*, which is the bacterium used in this thesis, is shown in (Table 1-1).

Table 1-1: Taxonomic classification of *Acinetobacter* species.

Domain	Bacteria
Phylum	Proteobacteria
Class	Gamma-proteobacteria
Order	Pseudomonadales
Family	Moraxellaceae
Genus	<i>Acinetobacter</i>
Species	<i>baumannii</i>

1.1.2 Importance of *Acinetobacter* species

Acinetobacter is a diverse genus of mostly free-living, saprophytic microorganisms that can be found practically anywhere. Yet, diverse members of the genus are typically linked to specific environments, such as dirt, water, sewage, people, food, and animals (Doughari *et al.*, 2011; Jung and Park, 2015; Kurcik-Trajkovska). *Acinetobacter baumannii* is one of the most challenging pathogens for hospitals and other healthcare facilities worldwide, mostly because of antimicrobial resistance (AMR) (Peleg *et al.*, 2008; Tacconelli *et al.*, 2018; Whiteway *et al.*, 2022; Cain and Hamidian, 2023). *A. baumannii* causes disease largely in severely sick patients who are confined to hospital environments and typically infects individuals by opportunistic means (Antunes *et al.*, 2014).

1.2 Clinical manifestations of infections caused by *A. baumannii*

Hospital-acquired infections (HAI), are illnesses that are not present at the time of admission in hospital but are acquired during hospitalization. Other names for these infections are nosocomial infections and healthcare-associated infections (Monegro *et al.*, 2023). Opportunistic pathogens like *A. baumannii* are responsible for a variety of infections, the majority of which are seen in intensive care unit (ICU) patients who are

critically unwell. *A. baumannii* is the causative agent of a variety of hospital-acquired illnesses, including ventilator-associated pneumonia (VAP), infections of the skin and soft tissues, infections of wounds, urinary tract infections (UTIs), secondary meningitis, and bloodstream infections (Dijkshoorn *et al.*, 2007; Morris *et al.*, 2019). Patients who have undergone craniocerebral surgeries in neurosurgery are at an increased risk of developing bacterial meningitis caused by *A. baumannii*, which could result in deadly complications for the patient. The majority of the meningitis cases that were reported were linked to head trauma, cerebrospinal fluid (CSF) leaks, or external ventricular drainage (EVD) (Cascio *et al.*, 2010; Karaiskos *et al.*, 2013). In neurosurgical wards, the surveillance of local infections should help guide the selection of appropriate therapy, together with an efficient infection control approach (Joly-Guillou, 2005).

1.2.1 Ventilator-associated pneumonia

One of the most frequent infections acquired in the intensive care unit (ICU) is ventilator-associated pneumonia (VAP), which is linked to high rates of mortality and healthcare expenses, as well as a prolonged course of antibacterial therapy, a lengthened hospital stay, and mechanical ventilation (MV) (Guidelines for the Management of Adults with Hospital-acquired, Ventilator-associated, and Healthcare-associated Pneumonia, 2005; Özgür *et al.*, 2014; Li *et al.*, 2017; Vazquez Guillamet and Kollef, 2018). *A. baumannii*, is one of the most common organisms that cause VAP (Niederman and Kollef, 2015; Koulenti *et al.*, 2017).

1.2.2 Urinary tract infections

Infections in the urinary tract (UT) can be brought on by *A. baumannii*, and these infections are typically brought on by the presence of urinary catheters or percutaneous nephrostomy tubes (Bagińska *et al.*, 2021). There is a modest risk of infection despite the ease with which *Acinetobacter* can colonize the urinary system, which is particularly relevant when considering the presence of indwelling urinary catheters (Gaynes *et al.*, 2005; Weinstein *et al.*, 2005). Only 1.6% of patients in intensive care units have urinary tract infections caused by *A. baumannii*, most of which are caused by catheter-associated UT infections (CAUTI) or colonization (Gaynes *et al.*, 2005). Despite this,

there has been a steady rise in the number of urinary tract infections caused by *A. baumannii* and of all *A. baumannii* infection, 20% are now UTIs (Weinstein *et al.*, 2005; Bagińska *et al.*, 2021; Jackson-Litteken *et al.*, 2022). As long as the source of the illness is dealt with, urinary tract infections are regarded as relatively minor infections compared to bloodstream infections or VAP (Superti *et al.*, 2009).

1.2.3 Bloodstream infections

In health care settings, *A. baumannii* has emerged as a prominent cause of bloodstream infections (BSI), despite the fact that the incidence of infection with carbapenem- and ampicillin-sulbactam-resistant (CASR) *A. baumannii* has grown (Chopra *et al.*, 2013). It is possible that a bloodstream infection caused by *A. baumannii* could have a crude fatality rate of up to 52% (Wisplinghoff *et al.*, 2000). It is noteworthy that between January 1, 2002 and August 31, 2004, 102 individuals who were being treated for injuries sustained by members of the United States military in Iraq or Afghanistan had *A. baumannii* bloodstream infections (Peleg *et al.*, 2008).

1.2.4 Hospital acquired infections

In the intensive care unit (ICU), *Acinetobacter* has become an infamous causative agent of healthcare-associated illnesses. Community-acquired diseases in Asia and Australia, as well as war and natural disaster-related infections, have also been linked to this organism (Weiner *et al.*, 2016). Worldwide, *A. baumannii* is a significant contributor to the development of hospital-acquired illnesses. The National Healthcare Safety Network (NHSN) in the United States published research in 2016 that analyzed the most common antimicrobial-resistant bacteria that are connected with healthcare-related illnesses and *A. baumannii* was the most common in these diseases (Weiner *et al.*, 2016).

1.2.5 Other infections

Colonization of the eye or infection of the eye can be caused by *A. baumannii*, colonization has been seen in people who wear contact lenses (Corrigan *et al.*, 2001). Infections in the eye can take many forms, such as corneal ulcers, endophthalmitis,

periorbital cellulitis, and infections caused by trauma that penetrates the skin (Wang *et al.*, 1998; Mathews *et al.*, 2005). According to the results of surveillance efforts, *A. baumannii* is only seldom associated with skin and soft tissue infections (SSTI) (Moet *et al.*, 2007).

1.3 Antibiotic resistance of *Acinetobacter*

Numerous studies have demonstrated that *A. baumannii* quickly acquires antimicrobial drug resistance, and multidrug-resistant strains have been discovered (McConnell *et al.*, 2013). According to the Infectious Diseases Society of America, *A. baumannii* is among the most dangerous ESKAPE organisms (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *A. baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter species*) that may successfully evade the effects of antibiotics (Rice, 2008; Boucher *et al.*, 2009). Moreover, the World Health Organization (WHO) has included carbapenem-resistant *A. baumannii* (CRAB) into its top category of bacteria that require research and development of antimicrobial therapy (Tacconelli *et al.*, 2018). The enzymatic degradation of medicines, target alterations, multidrug efflux pumps, and permeability deficiencies are some of the *A. baumannii* resistance mechanisms that have been identified (Gordon and Wareham, 2010; Kim *et al.*, 2012; Lin and Lan, 2014).

1.3.1 Resistance and Persistence of *A. baumannii*

A. baumannii owes a substantial part of its effectiveness as a nosocomial pathogen to a strategy known as "persist and resist". This strategy allows the bacterium to survive in hostile conditions and to withstand the effects of antimicrobial agents (Harding *et al.*, 2018). Infections caused by *A. baumannii* are most common in hospitalized patients who are already in a severe condition. Since this pathogen has the ability to acquire resistance to multiple drugs, these infections have become a major cause for concern. About 45% of *A. baumannii* clinical isolates discovered around the world are reported to be resistant to multiple drugs (Giammanco *et al.*, 2017) and the development of bacteria resistant to carbapenem *A. baumannii* is currently regarded as a risk to the health care systems of all countries across the world (Tacconelli *et al.*, 2018). Along

with antibiotic resistance, the ability of this organism to remain in the environment of health care facilities has been a major contributor to the emergence of *A. baumannii* as a nosocomial pathogen. These bacteria are able to live on dry surfaces, can survive for an extended period of time without food, and can quickly colonize susceptible hosts in hospitals (Jawad *et al.*, 1998; Corbella *et al.*, 2000). The ability of *A. baumannii* to survive in dry environments is one of the characteristics that contributes to the pathogen's success in spreading through healthcare institutions. The majority of *A. baumannii* strains have been demonstrated to be able to survive on dry surfaces for at least 20 days, with some strains having the ability to persist for over three months, according to an examination of clinical isolates (Jawad *et al.*, 1998; Giannouli *et al.*, 2013; Farrow *et al.*, 2018). In addition, *A. baumannii* has been discovered on a wide variety of surfaces in clinical contexts during outbreaks. These surfaces include bed rails, pillows, mattresses, tables, and ventilators (Fournier *et al.*, 2006). Bacteria can be protected from drying out with the assistance of extracellular polysaccharides (Chang *et al.*, 2007), additionally, *A. baumannii* mutants that do not generate a polysaccharide capsule are susceptible to drying to a certain extent (Tipton *et al.*, 2018).

1.3.2 Colonization and disease

Although infections caused by *A. baumannii* are most frequently acquired in intensive care units (ICUs), they are also increasingly common in wards that are not ICUs and in facilities that provide long-term care. There has not been a thorough differentiation made between infections that are acquired in intensive care units and those that are acquired in wards that are not intensive care units (Villar *et al.*, 2014). It is challenging to identify colonization from infection due to the characteristics of the patients from whom *A. baumannii* is isolated. Therefore, up to half of the instances in which *A. baumannii* is isolated are indicative of colonization (Tacconelli *et al.*, 2008; Villar *et al.*, 2014). Additionally, up to 36% cases of bacteraemia in which *A. baumannii* is isolated are polymicrobial (with additional isolation of other bacteria, such as coagulase-negative (*Staphylococcus*, *Enterococcus spp.* or *Pseudomonas spp.*), which suggests that some of the isolates are pollutants from the skin or the environment. Therefore, it

is essential to make a distinction between infections and pseudo-infections from a clinical standpoint (Wisplinghoff *et al.*, 2000; Cisneros and Rodríguez-Baño, 2002). This circumstance needs to be taken into consideration in order to prevent incorrect diagnostics and treatment with antibiotics that is not essential (Peleg *et al.*, 2008).

1.4 Virulence Factors

The development of bacterial disease is dependent on a variety of variables that facilitate the colonization of the bacterium, the progression of infection, and the bacteria's ability to stay on biotic or abiotic surfaces (Rumbo *et al.*, 2014). Virulence factors are the molecular properties of a bacteria that facilitate contact and subsequent colonization in the human host (Harding *et al.*, 2018). Below are descriptions of some important virulence factors.

1.4.1 Efflux pumps

Bacterial efflux systems are systems that penetrate membranes, may have a broad substrate specificity, and are responsible for the expulsion of potentially harmful chemicals into the extracellular environment. Efflux pumps play a significant part in the resistance of bacteria to the action of antibiotics and could therefore be classified as an indirect virulence factor, because it allows *A. baumannii* to prolong an infection by surviving drug treatment. However, there is growing evidence that efflux pumps are engaged in a wide variety of activities, including pathogenesis, toxin excretion, and the balancing of heavy metals. These functions include nutrient balancing, the alleviation of stressors on the cell, toxin excretion, and heavy metal balancing (Du *et al.*, 2018; Pérez-Varela *et al.*, 2019). A total of six distinct types of efflux pumps have been described, and it has been demonstrated that all six classes of multidrug efflux pumps are present in *Acinetobacter spp.* (Kornelsen and Kumar, 2021). These six classes are: the ATP binding cassette (ABC) family, the major facilitator superfamily (MFS), the resistance-nodulation-division (RND) family, the multidrug and toxin extrusion (MATE) family, the small multidrug resistance (SMR) family and the drug/metabolite transporter (DMT) superfamily, the presence of these pumps in *Acinetobacter spp.* contributes to the bacteria's decreased sensitivity to a wide variety of antibiotic classes. (Kornelsen and Kumar, 2021).

1.4.2 Hemolytic factors

Infectious bacteria have developed the ability to produce hemolysins in order to harvest resources from host cells, such as iron. Historically, *A. baumannii* was considered non-hemolytic (Bouvet and Grimont, 1986). However today, many *A. baumannii* strains have been demonstrated to lyse erythrocytes (Mortensen and Skaar, 2013). A potential cause of the classification of *A. baumannii* as non-hemolytic might have been that *A. baumannii* does not display lysis of sheep blood but is effectively lysing horse blood to a comparable level to *P. aeruginosa* (Antunes *et al.*, 2011). Another study on *Acinetobacter* has uncovered three forms of hemolytic activity, with α -hemolysis being the most prevalent form seen in the tested group of strains (Dahdouh *et al.*, 2016). Two phospholipases C have been implicated in the lysis of erythrocytes, but more hemolytic factors are likely to be involved.

1.4.3 Lipopolysaccharides

In Gram-negative bacteria, lipopolysaccharide (LPS) is typically thought of as an essential component for viability (Nagy *et al.*, 2019). Clinical strains of the pathogen *A. baumannii* that are resistant to colistin, an antibiotic that binds to lipid A of the LPS, were found to have mutations in genes that are early in the LPS biosynthesis pathway that cause loss of function (Moffatt *et al.*, 2010). These cells were completely devoid of LPS; nonetheless, they were able to survive not only in the circumstances of the laboratory but also in patients, although the fact that *A. baumannii* may live without LPS, the cells exhibit growth and morphological abnormalities when grown in the laboratory (Beceiro *et al.*, 2014; Bojkovic *et al.*, 2016; Boll *et al.*, 2016; Powers and Trent, 2018).

1.4.4 Outer Membrane Vesicles (OMVs)

Gram-negative bacteria release outer membrane vesicles (OMVs) that range in diameter from 20 to 300 nm. OMVs are essential for bacterial cell survival under harsh environmental circumstances (Jan, 2017). They are involved in the processes of nutrition uptake, pathogenicity, horizontal gene transfer, and quorum-sensing signalling (Zingl *et al.*, 2020). OMVs are produced by the vast majority of Gram-negative bacteria,

which includes those that infect host tissue and serum (Schwechheimer and Kuehn, 2015). By carrying out several cellular functions, OMVs aid in the survival of bacterial cells. They eliminate misfolded proteins, carry enzymes that produce carbon sources from intricate macromolecules, and carry out transport duties (Schwechheimer and Kuehn, 2015). OMVs also include signalling molecules, which have an effect on the communication between cells and the immunological response of the host (Jan, 2017). *A. baumannii* OMVs serve as a vehicle for the delivery of outer membrane protein OmpA, and OmpA that is packaged in OMVs is thus responsible for inducing cytotoxicity (Jin *et al.*, 2011). and deliver a number of proteins that are thought to be related with virulence to the host cells (Kwon *et al.*, 2009).

1.4.5 Quorum sensing

Cells of bacterial populations can communicate with each other and coordinate gene expression through the process of quorum sensing (QS), which enables groupings of cells to respond more effectively to shifting environmental conditions (Diggle *et al.*, 2007; Li and Tian, 2012). The QS system can regulate gene expression, biofilm formation, and extracellular polysaccharides by secreting and receiving signal molecules. This allows bacteria as a group to collectively respond to changes in their surrounding environment, which can have unfavourable effects such as drug resistance and virulence (Miller and Bassler, 2001; Dong *et al.*, 2001). The QS system is able to upregulate genes that are associated with infections, but QS interference can also downregulate pathogenicity, which assists the immune system in eliminating pathogens that have been infected (Chen *et al.*, 2019). Recent research has led scientists to believe that the QS system in *A. baumannii* is responsible for regulating the response to ROS (Heindorf *et al.*, 2014; Bhargava *et al.*, 2014).

1.4.6 Biofilm production

Many bacteria use biofilms as a common pathogenicity mechanism to withstand harsh environments such the use of antimicrobials or disinfectants, dry surfaces, and nutrient deprivation (Law and Tan, 2022). Bacteria can produce a biofilm by encasing them in an extracellular matrix. Biofilms serve as a cooperative consortium to provide a

protected mode for microorganisms and promote resistance to a variety of antibiotics. Biofilms can be found in a variety of environments (Flemming and Wingender, 2010). Biofilm development is dependent on changes in gene expression, whereby different genes are either up- or down-regulated in response to the development of biofilm phenotypes. Biofilm production is a multi-step process that starts with planktonic cells adhering to a surface, multiplies the cells to produce mature biofilm and protective exopolymer saccharides, and then disperses the planktonic cells (Toyofuku *et al.*, 2016; Law and Tan, 2022).

The creation of a biofilm is a complicated process that involves a wide variety of contributors, such as the aggregation substance, the expression of pili, and the acquisition of iron (Longo *et al.*, 2014). *A. baumannii* can adhere to biotic surfaces, such as eukaryotic cells that cause host infection, as well as abiotic surfaces, such as catheters, endotracheal tubes, or other medical surfaces that facilitate device-related infections (Longo *et al.*, 2014; Law and Tan, 2022). In contrast to other nosocomial infections, the genes and proteins responsible for *A. baumannii*'s biofilm development remain to be well understood and verified (Longo *et al.*, 2014; Yang *et al.*, 2019). The *bla_{PER-1}* gene's expression and presence have been linked to surface adhesion (Lee *et al.*, 2008; Longo *et al.*, 2014). Nevertheless, since many isolates that are capable of producing biofilms do not possess the gene, there is still disagreement in the field regarding the necessity and precise function of this gene in biofilm formation (Rao *et al.*, 2008; Longo *et al.*, 2014). Contact-Dependent Growth Inhibition (CDI) proteins might have several functions given their enormous sizes, as a result, their roles may be more varied than those caused by bacterial competition (Roussin *et al.*, 2019). They found that CDI1 system does not boost biofilm formation nor adhesion to Eukaryotic cells, but instead, its absence increases the adhesiveness of *A. baumannii*. The process by which the CDI1 system restricts cell-to-cell or surface adhesion is yet unknown and has to be explored (Roussin *et al.*, 2019). Outer membrane protein A (OmpA) has a contribution, albeit a minor one, in the formation of robust biofilms on the surface of plastic (Loehfelm *et al.*, 2008). Pili, which mediate adhesion and biofilm formation, are also a major factor in *A. baumannii*'s capacity to produce biofilms. The genes are grouped together to form a *csu* operon, and in *A. baumannii*, the operon's

products create a bundle structure that resembles a pilus (Cincarova et al., 2016). Biofilm adhesion, the accumulation of bacterial cells, and the formation of biofilm are all significantly influenced by the biofilm-associated protein that is expressed by the *bap* gene (Lasa and Penadés, 2006; Fattahian et al., 2011; Aliramezani et al., 2016). High-molecular-weight proteins known as Bap family members are found on the surface of bacteria, have a tandem repeat core domain, and enable bacteria to build biofilms (Lasa and Penadés, 2006). With 8,621 amino acids, Bap is one of the largest bacterial proteins ever identified, making it an amazing protein (Loehfelm et al., 2008). It is believed that the biofilm associated protein (Bap) mediates biofilm development and maturation and is involved in cell-cell adhesion (Loehfelm et al., 2008; Eze et al., 2018). Analysis revealed that affinity-purified antibodies may suppress the expression of Bap, which is expressed at the cell surface (Goh et al., 2013). Goh et al. (2013) found that 22 out of 24 clinical strains of *A. baumannii* ST92 that were resistant to carbapenem had a high frequency of the *bap* gene (Goh et al., 2013). On the other hand, a different investigation by Badmasti and colleagues only found that 30% of isolates had *bap*, although other biofilm-associated *ompA* and *bla_{PER-1}* genes had 100% and 44% prevalence, respectively (Badmasti et al., 2015).

1.5 Transcriptome of *Acinetobacter*

The study of transcriptomics focuses on the "transcriptome" which is currently generally used to refer to the entire collection of ribonucleic acid (RNA) molecules, or transcripts, that are expressed in a particular entity, such as a cell, tissue, or organism (Skerrett-Byrne Anthony et al., 2023). The complete collection of RNA transcripts, both coding and non-coding, found in a single organism or a population of cells is referred to as the transcriptome of that organism or population (Wang et al., 2009). Depending on the nature of the investigation being conducted, the phrase may also be used to refer to all types of RNA rather than mRNA alone (Wang et al., 2009). A key component of functional genomic research aimed at determining the genetic basis of biological functions is the characterization of the transcriptional landscape and concurrent genome-wide quantification of gene expression via RNA sequencing (RNA-seq) (Colgan et al., 2017). Researchers aim to find out when and where genes are turned

on or off in different kinds of cells and tissues by examining transcriptomes. To gauge the degree of gene expression or activity in a cell, one can count the number of transcripts. In Eukaryotes, transcript data could potentially provide light on which genes confer developmental plasticity. Furthermore, a complete picture of the genes that are active at different phases of development can be produced by taking the transcriptome into account (Adams, 2008). Transcriptomics and the development of high-throughput technologies have revealed the existence of an impressive number and wide distribution of non-coding RNAs in the bacterial genome (Papenfort and Vogel, 2009; Oliva *et al.*, 2015). At the post-transcriptional level, these regulatory RNAs regulate the physiology and virulence of bacteria; most of them do this by interacting with other RNAs to regulate gene expression (Papenfort and Vogel, 2009; Barquist and Vogel, 2015a). Several studies of the transcriptome have investigated the transcriptional alterations that occur in the *A. baumannii*. For example, an early transcriptomic studies using the historical reference strain ATCC17978 was carried out when it is cultured in harsh environmental circumstances, such as being treated with ethanol (Camarena *et al.*, 2010), high levels of salinity (Hood *et al.*, 2010), as well as a lack of iron (Eijkelkamp *et al.*, 2011a). These research studies drew particular attention to the fact that *A. baumannii* has a high level of survival potential under such conditions. Recent transcriptome research has also looked into how this species reacts to drugs and found some interesting results. For instance, one study in which the *A. baumannii* reference strain ATCC19606 was treated with colistin and doripenem revealed the key genes involved in the process by which colistin kills bacteria (Henry *et al.*, 2015). However, in a different investigation, the multidrug-resistant *A. baumannii* strain MDR-ZJ was given tigecycline, which led to the discovery of an efflux pump as well as many transcriptional regulators implicated in the drug resistance response (Hua *et al.*, 2014). With the model strain *A. baumannii* ATCC 17978, Kroger's group performed the first dRNA-seq analysis, identifying thousands of TSS at single nucleotide precision and producing a thorough transcriptome map with 110 sRNAs (Kröger *et al.*, 2018).

1.5.1 Small RNA regulation

Bacteria must overcome numerous obstacles in order to proliferate and endure in any environment. These difficulties include living and replicating in unfavourable environments, invading hosts successfully, eluding immunological reactions, and obtaining nutrients. All of these functions necessitate vast and intricate gene regulatory networks, which enable quick on/off switching of genes as well as up/down regulation of genes as needed. Numerous precise mechanisms are still unknown, and research is ongoing to determine how these comparatively small organisms manage to survive in the harshest environments and propagate across the globe (Hibbing *et al.*, 2010). A greater understanding of the intricate network of regulatory processes involved, helps us to get a more in-depth knowledge of their survival both inside and outside the human host. This in turn supports better design of antimicrobials and disinfectants to counter their unrelenting attacks. Although there are several phases at which a protein product is translated from the gene that encodes it, post-transcriptional regulation is one kind of gene regulation that has gained attention recently (Martínez and Vadyvaloo, 2014). Small non-coding RNAs have been identified as essential regulatory components in bacteria that demonstrate high structural diversity and mechanisms of molecular action (Bloch *et al.*, 2017). In bacteria, sRNA molecules perform a broad range of regulatory roles and modulate almost every aspect of cell metabolism (Gottesman and Storz, 2011). In all living systems, including bacteria, regulation by RNA molecules plays a crucial role in altering gene expression. The majority of bacterial regulatory RNAs are non-coding RNAs, which are more often known as small RNA (sRNA) due to their small size (50–500 nucleotides). Small RNAs are responsible for controlling gene expression because of their ability to form base pairing to their cognate target molecule, which is often mRNA, (Figure 1.1) which then allows them to modulate the translation and/or the stability of the mRNA. Small RNAs are important to a pathogens because of the role they play in regulating virulence (Koo *et al.*, 2011; Sonnleitner *et al.*, 2012; Caswell *et al.*, 2012; Coornaert *et al.*, 2013). Genome-wide annotations for sRNA-encoding genes have not been performed in the clinically relevant pathogen *Acinetobacter baumannii*, despite the fact that it is generally acknowledged that sRNAs are encoded by most if not all bacteria. Because of their regulatory significance, small regulatory

RNAs (sRNAs) may play crucial roles in *A. baumannii* drug resistance (Sharma *et al.*, 2014). The role of small RNAs (sRNAs) in bacteria as gene regulators for a variety of different cellular activities is now well-established (Storz *et al.*, 2011; Papenfort and Vanderpool, 2015; Oliva *et al.*, 2015; Fröhlich and Papenfort, 2016). The expression patterns and regulatory mechanisms used by small non-coding RNAs in *Enterobacteriaceae* bacteria like *E. coli* and *Salmonella* are the ones that are understood the best (Chao *et al.*, 2012; Kröger *et al.*, 2013; Papenfort and Vogel, 2014; Srikumar *et al.*, 2015; Colgan *et al.*, 2016). To this day, we do not have enough evidence to determine whether or not sRNA-mediated regulation in *A. baumannii* is comparable to these extensively researched systems (Sharma *et al.*, 2014).

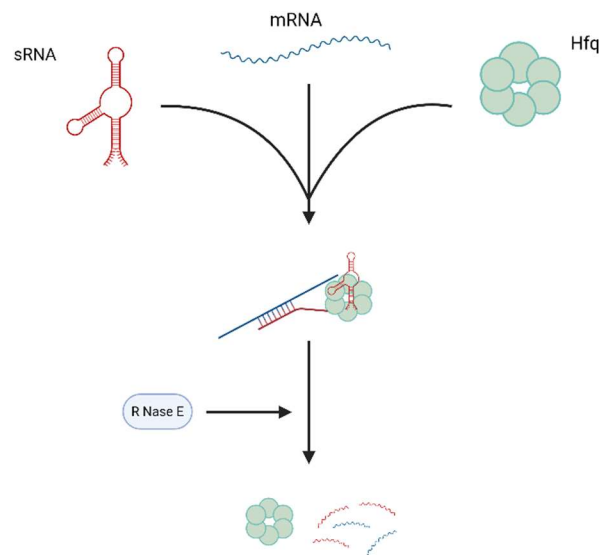


Figure 1.1: The most common mechanism of post-transcriptional regulation by an sRNA. The sRNA binds to an mRNA with help of chaperone (Hfq) that may induce the cleavage (often by RNase E) of some sRNAs and their target mRNAs.

1.5.2 Regulation of antimicrobial resistance

Despite the fact that the use of antibiotics to treat bacterial illnesses marks one of the most significant leaps forward in the field of medicine in the history of humanity, bacterial pathogens have not been eradicated, and a significant number of them have developed resistance to almost all of the therapeutically relevant antibiotics (Boucher *et al.*, 2009). The persistent and widespread rise of bacterial infections that possess multiple antibiotic resistances (also known as the multidrug-resistant [MDR] phenotype) poses a significant danger to the provision of efficient medical care (Hwang and Gums, 2016). *A. baumannii* is not an exception, as numerous clinical isolates have developed the MDR phenotype in recent years (Huttner *et al.*, 2013). The term "intrinsic antibiotic resistance" refers to the collection of resistance mechanisms that have not been acquired through recent instances of horizontal gene transfer (Gebhardt and Shuman, 2017). Because bacteria must carefully regulate gene expression to maintain proper spatiotemporal production, it is important to comprehend the processes that control the expression of virulence factors (Kröger *et al.*, 2016). Two-component systems (TCS), are one of the proteins and transcription factors that are known to govern the expression of virulence genes as well as antibiotic resistance in *A. baumannii* (Kröger *et al.*, 2016). (TCS) are found in virtually all bacteria and function as signal transduction systems (Groisman, 2016). The TCS is made up of a sensor kinase that is encased in the cytoplasmic membrane and a cognate response regulator. The sensor kinase is able to detect and react to external and/or intracellular characteristics, such as osmotic pressure or pH (Choi and Groisman, 2016) and activates the response regulator through phosphorylation. Annotations have been made on 10 sensor kinases and 17 response regulators found in *A. baumannii* AB5075-UW (Gallagher *et al.*, 2015b). This is an average number of response regulators for pathogenic bacteria, but it is significantly lower than the average of 40 in *Escherichia coli* and around 90 in the *Pseudomonas spp.* that is more closely related (Ashby, 2004). The regulatory system in *A. baumannii* with the best characterization is the *adeRS* TCS. Most remarkably, it regulates the expression of the AdeABC RND-type efflux pump (Magnet *et al.*, 2001; Marchand *et al.*, 2004). Aminoglycoside sensitivity increases upon deletion of *adeR* or *adeS* (Marchand *et al.*, 2004). Numerous studies have linked increased synthesis of

AdeABC to antibiotic resistance, including resistance to aminoglycosides, tigecycline, fluoroquinolones, and others (Ruzin *et al.*, 2007; Nemec *et al.*, 2007).

1.5.3 Adaptation to environmental conditions in *Acinetobacter baumannii*

Iron stress-related responses

Iron is necessary for the completion of a wide variety of biological functions, including the creation of DNA precursors and its role as a cofactor in redox enzymes. In order to successfully compete with their host for iron, bacteria have developed complex methods for iron uptake. One mechanism to secure free iron is to secrete iron-chelating molecules (siderophores) which may later be taken up again from the environment or to scavenge iron bound to host transferrin and lactoferrin (Yamamoto *et al.*, 1994). *A. baumannii* can grow in iron-limiting circumstances, such as those present in the human host and in aqueous solutions used in medicine, by actively acquiring iron. In the human host, ferritin, transferrin, lactoferrin, and heme bind iron, reducing the amount of free iron to concentrations as low as 10^{-18} M, which is below the threshold at which bacteria may survive in the environment and infect humans (Crosa JH, Mey AR, Payne SM, 2004). Iron acquisition mechanisms are crucial virulence factors that are exploited by bacterial pathogens in order to survive inside of a host (Cook-Libin *et al.*, n.d.). *Acinetobacter baumannii* is not an exception to this norm. In the electron transport chain, the production of energy cannot occur without iron and it is also necessary for DNA replication and repair, transcription, in addition to other metabolic processes such as the activation of enzyme reactions (Andrews *et al.*, 2003; Caza and Kronstad, 2013). Iron is generally an important cofactor for enzymes involved in these activities, such as cytochromes, succinate dehydrogenases, and catalases. Iron acquisition is essential for the course of the infection for *A. baumannii* and to receive iron from the iron-limited environment of the host, *A. baumannii* possesses a total of eight gene clusters (Antunes *et al.*, 2011b; Ramirez *et al.*, 2019). One of them is a conserved ferrous iron acquisition system (feoABC) that engaged in the process of iron acquisition (Álvarez-Fraga *et al.*, 2018; Runci *et al.*, 2019). Two heme uptake loci (heme uptake cluster 1,

and hemO cluster) are involved in the process of heme uptake, and the remaining five are involved in the production and usage of siderophores biosynthesis and utilization (Sheldon and Skaar, 2020). One of the siderophore biosynthetic clusters is made up of the two genes *entA* and *entB*, which are involved in the production of 2,3-dihydroxybenzoic acid, a weak iron chelator and siderophore precursor molecule (Eijkelkamp et al., 2011). Another cluster, exclusive to *A. baumannii* strain 8399, is engaged in the production of an unidentified catecholate siderophore (Echenique et al., 1992; Dorsey et al., 2003). After more thorough investigation, it was discovered that the remaining clusters encode up to 10 structurally different siderophores, including pre- and acinetobactin, which are expressed from three loci (Penwell et al., 2012; Shapiro and Wencewicz, 2016).

Growth-phase stress-related responses

Stress signals in bacteria are triggered not only by the presence of specific extracellular stressors, but also by changes in intracellular stressors as a result of nutrient consumption and waste generation during growth experiments typically used in laboratory-based studies. Proteome changes of *A. baumannii* ATCC 17978 cells during growth in rich medium such as Mueller-Hinton have been reported using a combination of 2D gel electrophoresis-MS and isobaric tags for relative and absolute quantitation (iTRAQ) liquid chromatography-MS/MS (Soares et al., 2010). This global study demonstrated that there are relevant protein changes as a result of oxidative-dependent protein modification processes that take place after proteins have been produced. Not only do significant changes occur in the production of 107 proteins as ATCC 17978 cells transition from the exponential into the late-stationary growth phase (Fiester and Actis, 2013).

Osmotic stress-related responses

Since most microbes lack active transport pathways for water itself, they must increase the concentration of osmotically active chemicals in their cytoplasm to prevent dehydration in a hyperosmotic environment (Kempf and Bremer, 1998). There are now two ways that bacteria can counteract the extracellular osmolarity. The "salt-in-

cytoplasm" method is used by organisms to build up KCl in molar concentrations (Epstein, 2003; Gunde-Cimerman *et al.*, 2018). Despite the fact that this is the less energy-intensive approach (Oren, 1999), few halophiles use it since all cellular processes need to be adjusted to this high salinity. Therefore, the organisms cannot thrive at low salinities and only slight or non-existent variations in the environmental osmolarity are tolerated (Galinski and Trüper, 1994; Epstein, 2003). The second way provide greater flexibility and well conserved, this is widely used in all three domains of life. *A. baumannii* does not have a salt tolerance that is much higher than that of other salt-tolerant bacteria; rather, it falls within the range of several other salt-tolerant bacteria (Zeidler *et al.*, 2017). The closely related non-pathogenic *Acinetobacter* halotolerance, which was recently isolated from soil and can thrive at NaCl concentrations higher than 1 M, is one of the species of the genus that exhibits a significantly more pronounced halotolerance (Dahal *et al.*, 2017). When grown in complex medium (LB), *A. baumannii* is able to thrive in an environment containing up to 700 mM of sodium chloride (Zeidler *et al.*, 2017). The same has been found with the non-pathogenic soil bacterium *A. baylyi*, which has been investigated extensively (Sand *et al.*, 2011).

Temperature stress-related responses

Temperature is a significant environmental shift that a pathogen like *A. baumannii* encounters while entering its host (De Silva *et al.*, 2017). Fortuitously, it is shown that *A. baumannii* ATCC 17978 exhibits lower levels of surface-associated motility at 28°C in comparison to 37°C. This implies that the phenotypic of *A. baumannii* ATCC 17978 may be influenced by the incubation temperature, potentially modulating its virulence (De Silva *et al.*, 2017). It has been demonstrated that numerous bacterial species can promote the production of virulence factors at 37°C. There are several possible underlying mechanisms for the thermoregulation of antibiotic resistance and/or the generation of virulence factors. For instance, it has been demonstrated that RNA thermometers in *Pseudomonas aeruginosa* influence this behavior, which leads to a rise in the virulence factors including elastase, pyocyanin, and rhamnolipids at 37°C (Grosso-Becerra *et al.*, 2014). De Silva *et al.* investigated the varying behaviors of *A.*

baumannii ATCC 17978 at various incubation temperatures. To comprehend the variations in the phenotypes at the molecular level, they compared the phenotypes of *A. baumannii* ATCC 17978, specifically focusing on antibiotic resistance and virulence. This was done in conjunction with proteome analysis. They found that the initial growth of *A. baumannii* ATCC 17978 was slower at 28°C than at 37°C, as the absorbance at 600 nm (A_{600}) of *A. baumannii* ATCC 17978 at 28°C was only about 40% of that at 37°C after 4 h of incubation. This difference became less pronounced after 12 h of incubation, with the growth rate at 28°C being about 92% of that at 37°C. This suggests that *A. baumannii* grows faster at 37°C than at 28°C, at least during the early log phase of the growth cycle (De Silva *et al.*, 2017). *A. baumannii* ATCC 17978's antibiotic susceptibility was evaluated at 28 and 37°C. At 28°C, *A. baumannii* ATCC 17978's susceptibility to aztreonam was 4-fold lower than at 37°C, but its susceptibility to trimethoprim-sulfamethoxazole was 8-fold higher. Additionally, there were minute but consistent alterations in the susceptibility to a few other antibiotics (De Silva *et al.*, 2017). Proteomic analysis was used to help understand the molecular basis of phenotypic differences displayed by *A. baumannii* at different growth temperatures. Of 2,446 proteins identified, 629 proteins were differentially expressed, with 366 proteins being upregulated and 263 being downregulated at 28°C, compared to 37°C. The largest subset of proteins that could be classified whose expression was upregulated or downregulated was those involved in metabolic and enzymatic processes. Proteins involved in RNA binding, processing, and translation were found to be largely upregulated at 28°C (De Silva *et al.*, 2017).

1.6 Project Aims.

The Aims of this project are:

- Transcriptomic analysis of *A. baumannii* AB5075 in different environmental and stress conditions
- To identify and characterize the expression and function of small RNAs in different environmental conditions.

Chapter 2

Material & Methods

2.1 Chemicals and Reagents

2.1.1 Media

Recipes for media are shown in (Table 2.1). All media were prepared with deionized water of analytical grade (Analar, BDH). Autoclaving or filtration with 0.2 µm polyether sulfone (PES) membrane filters (Fisher Scientific) was used to sterilize media. To make agar plates, Lennox agar (LA, L-agar) was melted at 95°C, cooled to 50°C, and then antibiotics were added (if required) prior to pouring. Before use, agar dishes were stored at 4°C. Antibiotic-containing L-agar plates were made by adding the necessary antibiotics to cooled molten L-agar and then pouring the mixture into petri dishes.

Table 2.1 Media recipes

Medium	Reagent	Concentration	Reference
Lysogeny broth (Lennox, L-)	Bacto-Tryptone NaCl Bacto-Yeast extract	10 g/L 5 g/L 5 g/L	(Lennox, 1955)
Lennox Agar	Lennox broth Bacto-Agar	L-broth+ 1.5% (w/v) agar	(Lennox, 1955)
Mueller Hinton Broth	Dehydrated infusion Casein hydrolysate Starch	300 g/L 17.5 g/L 1.5 g/L	
Mueller Hinton Agar	Dehydrated infusion Casein hydrolysate Starch Agar	300 g/L 17.5 g/L 1.5 g/L 17 g/L	
Brain Heart Infusion Broth (BHI)	Beef Heart Calf brains Disodium hydrogen phosphate D(+)-glucose Peptone Sodium chloride	5 g/L 12.5 g/L 2.5 g/L 2 g/L 10 g/L 5 g/L	

Motility Media	Agarose – D3 Tryptone Sodium chloride	20 g/L 5 g/L 2.5 g/L	

2.1.2 Bacterial strains and maintenance of bacterial stocks

In Table 2.2, all the bacterial strains utilized in this study are listed. Bacterial strains for long-term storage were prepared by combining overnight cultures in L-broth (Table 2.1) with 30% (v/v) sterile glycerol and freezing at -80°C. Strains were streaked for single colonies onto LA plates with the appropriate antibiotics and cultivated at 30°C or 37°C when necessary. Plates were stored at 4°C for no more than one week.

Table 2.2 Bacterial strains used in this study.

Species	Strain	Genotype	Resistance	Source/References
<i>A. baumannii</i>	AB5075	wild-type	-	S. Salcedo lab (Lyon) (Jacobs <i>et al.</i> , 2014a)
<i>E. coli</i>	TOP10	F- <i>mcrA</i> $\Delta(mrr-hsdRMS-mcrBC)$ $\phi80/lacZ\Delta M15$ $\Delta lacX74 nupG$ <i>recA1 araD139</i> $\Delta(ara-leu)7697$ <i>galE15 galK16</i> <i>rpsL(Str^R) endA1</i> λ^-	-	Invitrogen
<i>A. baumannii</i>	AB5075	$\Delta sRNA44$	-	This study
<i>A. baumannii</i>	AB5075	$\Delta sRNA65$	-	This study
<i>A. baumannii</i>	AB5075	$\Delta sRNA75$	-	This study
<i>A. baumannii</i>	AB5075	$\Delta sRNA76$	-	This study
<i>A. baumannii</i>	AB5075	$\Delta sRNA99$	-	This study
<i>A. baumannii</i>	AB5075	$\Delta sRNA100$	-	This study
<i>A. baumannii</i>	AB5075	Δbap	-	This study

2.1.3 plasmids

All plasmids' strains used in this study are listed in **Tables 2.3**

Table 2.3 Plasmids used in this study.

Plasmid	Description	Resistance	Source/References
pVRL2Z	Plasmid for overexpression using arabinose	Zeocin	(Lucidi <i>et al.</i> , 2018)
pPL-sRNA44	Plasmid for constitutive expression of sRNA44 from P _L promoter	Ampicillin	J. White
pPL-sRNA65	Plasmid for constitutive expression of sRNA65 from P _L promoter	Ampicillin	This study
pPL-sRNA75	Plasmid for constitutive expression of sRNA75 from P _L promoter	Ampicillin	This study
pPL-sRNA76	Plasmid for constitutive expression of sRNA76 from P _L promoter	Ampicillin	This study
pPL-sRNA99	Plasmid for constitutive expression of sRNA99 from P _L promoter	Ampicillin	This study
pPL-sRNA100	Plasmid for constitutive expression of sRNA100 from P _L promoter	Ampicillin	This study
pVRL2Z- sRNA44	Plasmid for overexpression of	Zeocin	This study

	sRNA44 from P _{ara} promoter		
pMHL-2	Template for amplification of <i>aacC4</i> and <i>sacB</i> genes	Apramycin	X. Charpentier (Lyon) (Godeux <i>et al.</i> , 2020)
pJV300		Ampicillin	J. Vogel (Würzburg) (Urban <i>et al.</i> , 1993)
pP _L -RybB	Template for construction of pP _L -based plasmids	Ampicillin	K. Papenfort (Jena) (Papenfort <i>et al.</i> , 2006)
pXG10sf-bap		Chloramphenicol	J. White
pXG10sf		Chloramphenicol	J. Vogel (Würzburg) (Corcoran <i>et al.</i> , 2012)

2.1.4 Culture Conditions

In this study, L-broth and L-agar plates were incubated at 37°C for 16-18 hours. Overnight cultures were inoculated with 5 ml of L-broth and cultivated in an environmental incubator shaker. For further growth in L-broth, bacterial cultures were sub-inoculated 1:1000 in 25 mL of L-broth in a 250 mL Erlenmeyer flask containing the appropriate antibiotics (if required) and cultivated either without agitation or with agitation at 200 rpm at 37°C in an Innova 3100 water-bath shaker (New Brunswick Scientific). A Memmert INB200 Incubator Oven was used to incubate agar plates at 37°C.

2.1.5 Monitoring Bacterial Growth

Using a Biomate 3S spectrophotometer (Thermo Scientific), the optical density at a wavelength of 600 nm (OD₆₀₀) was measured to track the growth of bacterial cultures. Before obtaining a measurement, cultures with an OD₆₀₀ greater than approximately 0.5 were diluted 10-fold in the appropriate medium.

2.1.6 Antibiotics

Antibiotic stocks were made at 1000× concentration and stored in aliquots at -20°C. Stocks were made in dH₂O and filter sterilized with 0.2 µm PES membrane filters

(Fisher Scientific), or in 70% ethanol. The following antibiotics were used in this study; Tetracycline (Tet, 12 µg/mL), Chloramphenicol (Chl, 25 µg/mL, EtOH) and Zeocin (25 µg/mL (*E. coli*) and 250 µg/mL (*A. baumannii*)).

2.1.7 Growth curves

Growth curves were used to measure growth rate of bacterial strains. Bacterial cultures for growth curves were inoculated as previously described in L-broth. Absorbance measurements (OD600) were taken every 1 – 2 h depending on the growth rate of the culture with a Biomate 3S spectrophotometer (Thermo Scientific).

2.2 General molecular techniques

2.2.1 Isolation of chromosomal *Acinetobacter baumannii* AB5075 DNA for use in PCR

Overnight cultures were prepared as previously described. 400 µL of the culture was harvested by centrifugation at 8,000 × g for 1 min at room temperature. The cell pellet was resuspended in 200 µL of sterile nuclease free H₂O and boiled at 100°C for 5 min, and subsequently vortexed for 30 s to ensure complete lysis. Cell debris was pelleted by centrifugation at 8,000 × g for 5 min, and supernatants were added to 1 volume chloroform and vortexed for 30 s. Organic and aqueous phases of the solution were separated by centrifugation at 8,000 × g for 10 min at 4°C. 75% of the aqueous layer was transferred to a new 1.5 mL tube to eliminate chloroform contamination. DNA contained in the aqueous phase was measured with the NanoDrop ND-1000 Spectrophotometer (Thermo Scientific) and the concentration was adjusted to 100 ng/mL.

2.2.2 Plasmid preparations

All plasmids were extracted from plasmid-containing *E. coli* using the E.Z.N.A. Plasmid DNA Mini Kit (Omega Bio-Tek). Plasmids were isolated from overnight L-broth cultures supplemented with an antibiotic if required. Cultures were then pelleted by centrifugation (13,000 × g) and plasmids were isolated and purified following

manufacturer's description (Omega Bio Tek). Plasmid concentration and isolation was quantified using the NanoDrop ND-1000 Spectrophotometer (Thermo Scientific).

2.2.3 Polymerase chain reaction (PCR)

PCR was used to amplify genomic and plasmid DNA in this study, the primers used are shown in Table 2.4. This study used MangoTaq™ DNA polymerase (Meridian Bioscience) for products less than 1kbp and VeriFi™ polymerase (PCRBIO Systems) was used for products larger than 1 kbp according to the manufacturers' specifications. As a template for PCR, 100 ng chromosomal DNA, 1-10 ng of plasmid DNA, or single colony resuspended in 200 µL of H₂O was used. The ingredients and conditions used in these reactions are shown in **Table 2.5, 2.6 and 2.7**. The MangoTaq™ DNA polymerase (Meridian Bioscience) master mix was made by combining 10× Standard Taq (Mg free) Reaction Buffer (5 µL), 10 mM deoxynucleotides (dNTP) solution mix (1 µL) and 25 mM Magnesium chloride (MgCl₂) solution (3 µL).

Table 2.4 primers used in this study.

Primer Name	Primer Sequence (5'→3')	Description	Source
sRNA44ribopr obe_ F	GCAGGTTATTACTACCCAG	Forward primer for sRNA44 Ripoprobe	Jessica White (Kröger Lab)
sRNA44ribopr obe_ R2	GAATTAATACGACTCACTATAAGC ACATAAAAAAAGGCC	Revers primer for sRNA44 Ripoprobe	Jessica White (Kröger Lab)
P1_RP_sRNA 65	GAATTAATACGACTCACTATATTAATCATTTATT TTGAATCATTGGC	Forward primer for sRNA65 Ripoprobe	This study
P1_RP_sRNA 65	TCCTTTTAAATCATGTGTAGG	Revers primer for sRNA65 Ripoprobe	This study

P1_RP_sRNA 75	GAATTAATACGACTCACTATAATACAGAAAAAG CACCCGTG	Forward primer for sRNA75 Ripoprobe	This study
P1_RP_sRNA 75	AGGCAAATTATCAGTGTGAAC	Revers primer for sRNA75 Ripoprobe	This study
P1_RP_sRNA 76	GAATTAATACGACTCACTATAATAAAAAAACC CGCATCTTG	Forward primer for sRNA76 Ripoprobe	This study
P1_RP_sRNA 76	TATACAGACTATTCTGTATTGC	Revers primer for sRNA76 Ripoprobe	This study
P1_RP_sRNA 99	GAATTAATACGACTCACTATAGTTTATAGTGTT TATCGC	Forward primer for sRNA99 Ripoprobe	This study
P2_RP_sRNA 99	GAAATAGAACTAAAACAACG	Revers primer for sRNA99 Ripoprobe	This study
P1_RP_sRNA 100	GAATTAATACGACTCACTATATCTCTCCCAAAA CTACAAGGC	Forward primer for sRNA100 Ripoprobe	This study
P1_RP_sRNA 100	AACGAGCTTGGCAAGGAATGTC	Revers primer for sRNA100 Ripoprobe	This study
P1_sRNA44_ Up_F	GTTGCAACCAACTTTAGCTGG	2Kb up forward for sRNA44 deletion	This study
P2_sRNA44_ Up_R	GGCCCAATTCGCCCTATAGTGAGTCGCCGAC CATTCTATCTTAATGC	2Kb up reverse for sRNA44 deletion	This study
P3_sRNA44_ down_F	GGGTTTGCTCGGGTCGGTGGCATATGGTGCT TTATATTTTAATTTTCTTG	2Kb down forward for sRNA44 deletion	This study
P4_sRNA44_ Down_R	CCGGATATTGATAATTTGATG	2Kb down reverse for sRNA44 deletion	This study
P7_sRNA44	GTGCTTTATATTTTAATTTTCTTG	For sRNA44 clean deletion	This study

P8_sRNA44	CAAGAAAATTAAAATATAAAGCACCCGACCATT CTATCTTAATGC	For sRNA44 clean deletion	This study
P1_sRNA65_ Up_F	CTTTCTATTGTCAAAAAAATGC	2Kb up forward for sRNA65 deletion	This study
P2_sRNA65_ Up_R	GGCCCAATTCGCCCTATAGTGAGTCGCTTAAA ACTTAACACCTATG	2Kb up reverse for sRNA65 deletion	This study
P3_sRNA65_ Down_F	GGGTTTGCTCGGGTCGGTGGCATATGGCCTG CTTCTTGAGTAGGC	2Kb down forward for sRNA65 deletion	This study
P4_sRNA65_ Down_R	CATAGTCACCAACATCAAGGG	2Kb down reverse for sRNA65 deletion	This study
P7_sRNA65	GCCTGCTTCTTGAGTAGGC	For sRNA65 clean deletion	This study
P8_sRNA65	GCCTACTCAAGAAGCAGGCCTTAAACTTAAC ACCTATG	For sRNA65 clean deletion	This study
P1_sRNA75_ Up_F	GGTATTTCGGCGAAAATGATTC	2Kb up forward for sRNA75 deletion	This study
P2_sRNA75_ Up_R	GGCCCAATTCGCCCTATAGTGAGTCGCTCTTC TTAAGGTTTTACTGTC	2Kb up reverse for sRNA75 deletion	This study
P3_sRNA75_ Down_F	GGGTTTGCTCGGGTCGGTGGCATATGGGGTG GATTAAATTAAGAACC	2Kb down forward for sRNA75 deletion	This study
P4_sRNA75_ Down_R	CCGGATATTGATAATTTGATG	2Kb down reverse for sRNA75 deletion	This study
P7_sRNA75	GGGTGGATTAAATTAAGAACC	For sRNA75 clean deletion	This study
P8_sRNA75	GGTTCTTAATTTAATCCACCCCTCTTCTTAAGG TTTTACTGTC	For sRNA75 clean deletion	This study
P1_sRNA76_ Up_F	GTTCAGGTATTGAAGCGGAAG	2Kb up forward for sRNA76 deletion	This study
P2_sRNA76_ Up_R	GGCCCAATTCGCCCTATAGTGAGTCGCATAAG CTATCCCACACTTAG	2Kb up reverse for sRNA76 deletion	This study

P3_sRNA76_ Down_F	GGGTTTGCTCGGGTCGGTGGCATATGCCTAC GAACGTAATAGACCGTAG	2Kb down forward for sRNA76 deletion	This study
P4_sRNA76_ Down_R	CTTCAGACGATGTCATCCAG	2Kb down reverse for sRNA76 deletion	This study
P7_sRNA76	CCTACGAACGTAATAGACCGTAG	For sRNA76 clean deletion	This study
P8_sRNA76	CTACGGTCTATTACGTTCTAGGCATAAGCTA TCCCACACTTAG	For sRNA76 clean deletion	This study
P1_sRNA99_ Up_F	CTAGCTGAGCAAATTCGCC	2Kb up forward for sRNA99 deletion	This study
P2_sRNA99_ Up_R	GGCCCAATTCGCCCTATAGTGAGTCGGGGAT GTATTTTGTCTATAACC	2Kb up reverse for sRNA99 deletion	This study
P3_sRNA99_ Down_F	GGGTTTGCTCGGGTCGGTGGCATATGGAGTT AATTTTAGCTATAACCAG	2Kb down forward for sRNA99 deletion	This study
P4_sRNA99_ Down_R	CTACAACTATCGGTAGGTAAATG	2Kb down reverse for sRNA99 deletion	This study
P7_sRNA99	GAGTTAATTTTAGCTATAACCAG	For sRNA99 clean deletion	This study
P8_sRNA99	CTGGTATAGCTAAAATTAAGTCGGGATGTATTT TGTCTATAACC	For sRNA99 clean deletion	This study
P1_sRNA100 _Up_F	GATGCTATTTTAGGGTACTTTG	2Kb up forward for sRNA100 deletion	This study
P2_sRNA100 _Up_R	GGCCCAATTCGCCCTATAGTGAGTCGGCGTTT ATAATCTCAAAAACAG	2Kb up reverse for sRNA100 deletion	This study
P3_sRNA100 _Down_F	GGGTTTGCTCGGGTCGGTGGCATATGGCATA AATCTTTAGATGGCTCAC	2Kb down forward for sRNA100 deletion	This study
P4_sRNA100 _Down_R	GCCATTCGATTTCTCCGAGATG	2Kb down reverse for sRNA100 deletion	This study
P7_sRNA100	GCATAAATCTTTAGATGGCTCAC	For sRNA100 clean deletion	This study

P8_sRNA100	GTGAGCCATCTAAAGATTTATGCGCGTTTATA ATCTCAAAAACAG	For sRNA100 clean deletion	This study
sRNA44_500 bp_Up	CTAAAACAGGTAAACAATATGTTG	For Sanger sequencing	This study
sRNA44_500 bp_Down	CTGTACCATTGGGTTGAATCC	For Sanger sequencing	This study
sRNA65_500 bp_Up	GCTAGTCAATATTGCGTTGAAC	For Sanger sequencing	This study
sRNA65_500 bp_Down	GTTAATCCATCTCAAAAAGTTATG	For Sanger sequencing	This study
sRNA75_500 bp_Up	GTTGACATGCATTAGCACATAAC	For Sanger sequencing	This study
sRNA75_500 bp_Down	CACAAAAAGAAAAATTACAGAGC	For Sanger sequencing	This study
sRNA76_500 bp_Up	GAACGTTTAGATAAACCTGATG	For Sanger sequencing	This study
sRNA76_500 bp_Down	GTTTTTTTAATAATAGCCTTTC	For Sanger sequencing	This study
sRNA99_500 bp_Up	GATTCGAGATATTTGCTGCTAG	For Sanger sequencing	This study
sRNA99_500 bp_Down	GCCGTTTTATGGATACCATCTG	For Sanger sequencing	This study
sRNA100_50 0bp_Up	GTAGGCCGTCCGTTATGATG	For Sanger sequencing	This study
sRNA100_50 0bp_Down	CATGAAACCGATCTGGTATAGC	For Sanger sequencing	This study
pVRL2Z_sRN A_44_F	GCAACTCTCTACTGTTTCTCCATGCAGGTTATT ACTACCCAG	For creating sRNA44pVRL2Z plasmid	This study
pVRL2Z_sRN A_44_R	CCGTCGACCTCGAGATTCCAAATTGTCATTAA AGACTC	For creating sRNA44pVRL2Z plasmid	This study
BAP_del_up_ F	ACTTTTTAATTGCTTGGGC	2Kb up forward for Bab deletion	This study
BAP_del_up_ R	GGCCCAATTCGCCCTATAGTGAGTCGTGTTTT CGAGTTTTTGACC	2Kb up reverse for Bap deletion	This study

BAP_del_d_F	GGGTTTGCTCGGGTCGGTGGCATATGTATAAA AAGAGAACCCTAGGG	2Kb down forward for Bap deletion	This study
BAP_del_d_R	TAAGAATTGTAAGAGCTCGGC	2Kb down reverse for Bap deletion	This study
BAP_P7	TGTTTTCGAGTTTTTGACC	For Sanger sequencing	This study
BAP_P8	GGTCAAAAACCTCGAAAACATATAAAAAGAGAA CCCTAGGG	For Sanger sequencing	This study
pWH1266_BA P_GFP_F	AATATTGAAAAAGGAAGAGTGTAATAATGATC ACATTAC	For translation fusion of <i>bap</i> gene	This study
pWH1266_BA P_GFP_R	GAGTAACTTGGTCTGACAG TTATTTGTAGAGCTCATCCATGC	For translation fusion of <i>bap</i> gene	This study
qPCR_bap_F	GCTCCACAAGAGTTGGTATCT	For running qPCR	This study
qPCR_bap_R	TAGTGGAATAGCAGCCCATAAAC	For running qPCR	This study
qPCR_lptB_F	GTCGATCTTAGAGACGCGTAAAG	For internal control	This study
qPCR_lptB_R	CACCACCAGATACACTCATTCC	For internal control	This study

Table 2.5 master mix (Verifi or Mango Taq) polymerase PCR reactants.

Components	Standard PCR	Control
Master mix (VeriFi or Mango Taq)	25 µl	25 µl
Forward primer (10 µM)	1 µl	1 µl
Reverse primer (10 µM)	1 µl	1 µl
Template DNA (100 ng/µL)	1 µl	0 µl
dH ₂ O	22 µl	23 µl
Total Volume	50 µl	50 µl

All PCR reactions were prepared in PCR tubes and placed in the SimpliAmp™ Thermal Cycler for amplification using the cycles listed in **Table 2.6**. The annealing temperature and extension time are variable depending on primer sequence and the amplicon fragment sizes.

Table 2.6 PCR cycling conditions.

Step	Temperature	Time	Cycles
Denaturation	95°C	2 min	1
Denaturation	95°C	15 s	35
Annealing	Variable	30 s	
Extension	72°C	Variable	
Extension	72°C	2 min	1

Colony PCR was used to identify the presence of specific DNA sequences in bacterial colonies. These assays used Taq DNA polymerase for amplification, a single bacterial colony was selected and added to the Taq DNA polymerase reaction mixture. The cycling conditions primers used for colony PCR are shown in **Table 2.7**.

Table 2.7 Colony PCR cycling conditions.

Step	Temperature	Time	Cycles
Denaturation	95°C	10 min	1
Denaturation	95°C	15 s	35
Annealing	Variable	30 s	
Extension	72°C	Variable	
Extension	72°C	2 min	1

2.2.4 Agarose gel electrophoresis

Agarose gel electrophoresis was used for size separation of DNA and RNA molecules. DNA samples were mixed with DNA loading dye (40% (v/v) glycerol, 60 mM EDTA, 10 mM Tris HCl pH 7.6, 0.25% (w/v) bromophenol blue pH 8.0, 0.25% (w/v) xylene cyanol FF, 0.25% (w/v) orange G) to a final concentration of 1× DNA loading dye and routinely electrophoresed in a 1% to 2.5% (w/v) agarose gel in 1× Tris Acetate Ethylenediaminetetraacetic acid (TAE) buffer at 90 V. RNA samples were mixed with RNA loading dye (0.025% (w/v) xylene cyanol FF, 0.025% (w/v) bromophenol blue, 18 mM EDTA pH 8.0, 0.025% (w/v) SDS, 95% (v/v) formamide) to a final concentration of 1× RNA loading dye and heat denatured at 65°C for 5 min. RNA was routinely

electrophoresed in a 2.5% (w/v) agarose gel in 1× Tris Borate EDTA (TBE) buffer at 90 V. Gels were stained with SafeView Nucleic Acid Stain (NBS Biologicals) prior to visualization under ultra violet light in the ImageQuant™ LAS 4000 (GE Healthcare Life Sciences) or on a safeVIEW-MINI2 Blue Light Transilluminator (Cleaver Scientific). The molecular size of electrophoresed DNA fragments was estimated by comparison with HyperLadder™ I (Bioline) or O'GeneRuler™ 1 kb DNA Ladder (Thermo Scientific).

2.2.5 DpnI restriction digestion

Restriction enzymes were purchased from Thermo Scientific and used according to the manufacturers' specifications. DpnI is used to digest the methylated parental DNA template. Restriction digestions were carried out in a SimpliAmp Thermal Cycler (Applied Biosystems, Thermo Scientific) by taking purified PCR products (5 µl) with DpnI (1 µl), 10×CutSmart Buffer (5 µl) and water (39 µl) at 37°C for 5 min.

2.2.6 Purification of PCR products

PCR products were purified to remove primers, enzymes, and other impurities using E.Z.N.A. purification Kit (Omega Bio-Tek) according to the manufacturers' specifications. In order to concentrate samples, multiple PCR reaction products were combined and spun through a single spin column.

2.2.7 SLiCE cloning procedure

The SLiCE cloning procedure uses recombination to integrate DNA inserts into linearized plasmid vectors (Zhang *et al.*, 2014). This was made possible due to ~20 base-pairs homology of sequences at both ends of the insert to the ends of their target plasmid. The volumes and concentrations of reactants for this procedure is depicted in **Table 2.8** These mixtures were then incubated at 37°C for 1h. The SLiCE extract was prepared prior to the start of this project. This was accomplished by lysing *E. coli* cells that are overexpressing λ prophage protein Redα system.

Table 2.8 SLiCE reaction components

Component	SLiCE Reaction	SLiCE Control
T4 DNA Ligase buffer (10×)	1 µl	1 µl
SLiC extract	1 µl	1 µl
Linearised plasmid	100 ng	100 ng
Insert DNA	100 ng	0
Water	Variable	Variable
Total Volume	10 µl	10 µl

2.2.8 Preparation and transformation of competent *E. coli*

To prepare strains competent for transformation with plasmid DNA, overnight cultures were inoculated with the required *E. coli* strains. This (50 µL) was used to inoculate a larger culture (50 mL) which was grown at 37°C until it reached exponential phase (OD 0.4-0.8). This culture was then centrifuged (3220 × g, 10 min, 4°C), resuspended in ice-cold CaCl₂ (30 mM, 40 mL). It was then centrifuged again, resuspended and incubated on ice for 20 min. It was centrifuged again and resuspended in 10 mL CaCl₂ with 87% glycerol (1.25 mL). This was aliquoted in microcentrifuge tubes and stored at -80°C. To transform competent cells by heat shock, aliquots removed from the freezer, defrosted on ice and mixed with DNA (100 ng plasmids or 5 µL SLiCE products). Following this, cells were incubated on ice for 20 min, placed at 42°C for 2 min and re-incubated on ice for 2 min. Cells were then mixed with L-broth (800 µL) and incubated at 37°C for 90 min. 100 µL of the transformation mixture was then plated on L-agar plates with the required antibiotics and incubated at 37°C.

2.2.9 Measurement of fluorescence in 96-well plates

Cells grown in 96-well plates were used to identify posttranscriptional regulation by measuring fluorescence (GFP). A 1:100 dilution of overnight cultures was prepared by diluting the overnight culture (10 µL) in an L-broth containing Eppendorf (1 mL). Aliquots (200 µL) were transferred to individual wells as required. Fluorescence was measured (arbitrary units) for 24 hours in a Synergy H1TM Hybrid Multi-Mode

microplate fluorometer at 37°C with continuous orbital shaking and excitation at 485 nm and emission at 508 nm.

2.2.10 Sanger sequencing

PCR amplicons spanning the deleted region of Δ sRNA44, Δ sRNA65, Δ sRNA75, Δ sRNA76, Δ sRNA99, Δ sRNA100 and Δ bap mutants and plasmids pPL-sRNA44, pPL-sRNA65, pPL-sRNA75, pPL-sRNA76, pPL-sRNA99, and pPL-sRNA100 were sent as templates for Sanger sequencing with appropriate primers to Eurofins Genomics. The results were analyzed using a local alignment program (Madeira *et al.*, 2022).

2.3 RNA Isolation

Total RNA was isolated using TRIzol from cells grown aerobically to growth stages early exponential phase (EEP) (OD600 = 0.1), mid-exponential phase (MEP) (OD600 = 0.3), late exponential phase (LEP) (OD600 = 1), early stationary phase (ESP) (OD600 = 2), late stationary phase (LSP) (16 hours incubation) and also isolated from cells grown aerobically until (MEP) in L-broth, then different stresses were added: Iron limitation (LowFe) (L-broth, Growth until OD600 = 0.3, then addition Dipyrldyl 0.22 mM), osmotic shock (NaCl) (L-broth, Growth until OD600 = 0.3, then addition of NaCl (final concentration 0.3 M), antibiotic shock with chloramphenicol (Chl) (L-broth, Growth until OD600 = 0.3, then addition chloramphenicol 32 µg/ml), antibiotic shock with tetracycline (Tet) (L-broth, Growth until OD600 = 0.3, then addition tetracycline 1 µg/ml), ambient temperature (22°C) L-broth, Growth until OD600 = 0.3 + 15min., temperature shift (TS) from ambient (22°C) to (37°C) L-broth, Growth until OD600 = 0.3 at 22°C, then shift it to 37°C for 15 min. and cold shock (CS) L-broth, Growth until OD600 = 0.3 at 37°C, then shift it to 22°C for 15 min (Kröger *et al.*, 2012). Four ODs of *A. baumannii* cells were harvested, mixed with 2/5 vol. of the cell suspension of ice-cold “stop solution” [19% ethanol, 1% acidic phenol (pH 4.3)], and incubated on ice for 30 min to prevent RNA degradation (Tedin and Bläsi, 1996). The cells were then pelleted by centrifugation for 10 min (3,220 × g, 4°C). The major part of the supernatant was discarded, and the cell pellet was resuspended in the remaining liquid and transferred into a 2 mL Eppendorf tube. Subsequently, the cell suspension was

centrifuged for 1 min at 20,000 × g and 4°C and the supernatant was discarded. The cell pellet was resuspended in 1 mL TRIzol and transferred into a 2 mL heavy phase-lock tube, and 400 µL chloroform was added and immediately mixed for 10 s. After incubation for 2 min at room temperature, the suspension was centrifuged for 15 min at 20,000 × g. The upper phase containing the RNA (~500 µL) was then transferred into a 1.5 mL Eppendorf tube, 450 µL isopropanol was added, and the suspension was mixed by inverting and then incubated at room temperature for 30 min. The precipitated RNA was pelleted by centrifugation for 30 min at 20,000 × g and the supernatant discarded. The pellet was then washed in 350 µL ethanol (70 %) and the suspension was again centrifuged for 10 min at 20,000 × g. The supernatant was discarded, and the pellet was air-dried, resuspended in RNase-free water by shaking (900 rpm) for 5 min in a heat block (65°C), and then stored at –80°C until further use. The RNA quality was analysed using an Agilent Bioanalyzer 2100 or by agarose gel electrophoresis and RNA concentration was measured on a NanoDrop™.

2.4 Transcriptomic analysis (RNA-seq)

Library preparation for RNA-seq, sequencing and preliminary processing of reads was conducted at the Core Unit Systemmedizin (SysMed), University of Würzburg (Germany). Read trimming and Illumina universal adapter removal were performed by Trimmomatic v.0.39 (Bolger *et al.*, 2014) (4 bp sliding window; the quality threshold of 15; removing sequences shorter than 36 bp after trimming). Small RNAs for *A. baumannii* strain AB5075-UW (RefSeq ID GCF_000963815.1) were predicted by sequence identity (>80 sequence identity) to sRNAs from *A. baumannii* ATCC17978 (Kröger *et al.*, 2018). The 88 sRNA nucleotide sequences obtained were added to the *A. baumannii* strain AB5075-UW annotation. Trimmed reads were aligned to the *A. baumannii* genome and quantified using FeatureCounts (parameters "-t gene -O", reference (Liao *et al.*, 2014)). These counts were used for the calculation of transcripts per million (TPM) by custom script and DESeq2 gene expression analysis (v.1.30.0, (Love *et al.*, 2016). Transcripts with adjusted P-values < 0.01 and log2 (fold-change) > 1 were considered as differentially expressed. Regularised logarithm transformation (rlog) of counts was used for data visualization and clustering (Love *et al.*, 2016).

Mapped reads were visualized in AcinetoCom 2.0 and Jbrowse (Skinner *et al.*, 2009), which were set up by Dr Karsten Hokamp (Genetics Department, Trinity College Dublin).

2.5 Generation of Digoxigenin-labelled riboprobes

Digoxigenin (DIG)-labelled single-strand RNA molecules (“riboprobes”) were generated for Northern Blotting by *in vitro* transcription using T7 RNA polymerase and the DIG Northern Starter Kit (Roche). A linear DNA template including the T7 promoter sequence (GAATTAATACGACTCACTATA) was generated through PCR with MangoTaq™ DNA Polymerase (Meridian Bioscience) and primers found in **Table 2.4**. DNA templates were purified using E.Z.N.A. purification kit, 200 ng of DNA was used as template in each 20 µL reaction (1× labelling mix, 1× transcription buffer, 40 U T7 RNA polymerase (Roche)). Labelling transcription reactions were incubated at 42°C for 1 h in a SimpliAmp Thermal Cycler (Applied Biosystems, Thermo Scientific). Template DNA was removed by incubation with DNase I at 37°C for 15 min, and reactions were stopped by addition of 400 mM EDTA pH 8.0. Riboprobes were stored at -20°C. Labelling efficiency of labelled riboprobes was tested by a dot-blot of 10-fold serial dilutions of riboprobes on a positively charged nylon membrane. Membranes were UV-crosslinked at 120 mJ (PeqLab crosslinker), rinsed with washing buffer, incubated at room temperature in 1× blocking buffer for 30 min, and subsequently incubated with a 1:10,000 dilution of the Anti-digoxigenin-AP Fab fragments (Roche) in 1× blocking buffer for 30 min. The membrane was washed two times in washing buffer, equilibrated in detection buffer for 5 min, then covered with CDP-star (Applied Biosystems). CDP-star acts as the chemiluminescent substrate, where enzymatic dephosphorylation of CDP-star by the alkaline phosphatase conjugated anti-DIG produces light which was detected using the ImageQuant™ LAS 4000 (GE Healthcare Life Sciences).

2.6 Northern blotting

Total RNA was electrophoresed through 7% acrylamide, 8.3 M urea, 1× TBE gels. 5 µg of RNA was mixed with 2× RNA loading dye and heat denatured at 65°C for 10 min

prior to loading into gels. Gels were electrophoresed at 100 V in 1× TBE for 2 hours. RNA-containing gels, positively charged nylon membranes (Roche), and filter paper were equilibrated in ice-cold 1× TBE. RNA was transferred to the membrane using the Biometra Fastblot B43 semi-dry blotting apparatus at 125 mA for 30 min at 10°C. RNA was UV-crosslinked to membrane at 120 mJ (Peqlab crosslinker). The membrane was then pre-hybridized in pre-warmed DIG Easy Hyb buffer (Roche) in a rotating oven at 62°C for 1 h. Approximately 1.25 µg (5 µL) of riboprobe was boiled at 95°C for 5 min, then incubated on ice for 5 min before being added to pre-hybridization buffer. Hybridization of RNA with the riboprobe of interest was incubated in a rotating oven at 62°C overnight. Membranes were washed twice for 10 min in Stringency Wash Buffer I pre-warmed to 62°C, then washed twice for 30 min in Stringency Wash Buffer II at room temperature on a rocker. The membranes were blocked for non-specific sites with 1× blocking buffer at room temperature for 30 min, and subsequently incubated with a 1:10,000 dilution of the Anti-digoxigenin-AP Fab fragments in 1× blocking buffer for 30 min. The membrane was washed two times in washing buffer for a total of 10 min, equilibrated in detection buffer for 5 min, then covered with CDP-star (Applied Biosystems). Chemiluminescence was detected using the ImageQuant™ LAS 4000 (GE Healthcare Life Sciences). To determine if RNA samples were equally loaded onto gels, membranes were re-probed with a 1:1000 diluted 5S riboprobe. All buffer and solution recipes are listed in **Table 2.9**.

Table 2.9 Buffers and solutions for Northern blotting

Name	Reagent	Concentration
RNA loading dye	Xylene cyanol FF	0.025% (w/v)
	Bromophenol blue	0.025% (w/v)
	EDTA pH 8.0	18 mM
	SDS 0.025% (w/v)	0.025% (w/v)
	Formamide	95% (v/v)
20× SSC	NaCl	3 M
	Sodium Citrate	0.3 M
Stringency wash I	SSC	2×

	SDS H ₂ O	0.1% (w/v)
Stringency wash II	SSC SDS H ₂ O	0.5× 0.1% (w/v)
Maleic acid buffer pH 7.5	Maleic acid NaCl	0.1 M 0.15 M
Washing buffer	Maleic acid buffer Tween-20	1× 0.3% (v/v)
1× Blocking buffer	Casein Blocking Solution (Roche) Maleic acid buffer	1× 1×
Detection buffer pH 9.5	Tris-HCl NaCl	0.1 M 0.1 M

2.7 Creating deletion mutants in *A. baumannii* AB5075

Deletion mutants were created using the gene replacement strategy as published by (Godeux *et al.*, 2020), a PCR-based genome editing method of naturally transformable *A. baumannii*. 2 kbp upstream and downstream of the deleted region of sRNA were amplified then correct DNA size was confirmed by running an agarose gel (1%). After confirming DNA fragments of the correct size, the samples were purified using a PCR clean-up kit to be ready for the overlap-extension PCR to create the full-length deletion cassette. Overlap-extension PCR was performed with laboratory plasmid pMHL-2 that bears the counter selectable cassette with a *sacB* gene conferring sucrose sensitivity and the *aacC4* gene encoding resistance to apramycin. The chimeric product bears the *sacB_aacC4* cassette surrounded by two 2-kbp-long regions of homology with the recipient cell's genome, these homologous regions allow the recombination of the chimeric PCR product into the recipient cell's genome. Insertion mutants were selected by apramycin resistance and sucrose sensitivity. A clean deletion was constructed after two-step assembly PCR of products bearing the homologous regions surrounding the deleted gene. These cells were resistant to sucrose and sensitive to apramycin.

2.8 Real-time quantitative PCR

Real-time quantitative PCR (RT-qPCR) was used to quantify gene expression of three strains: *A. baumannii* wild-type with pVRL2Z plasmid (WT+pVRL2Z), the Δ sRNA44 mutant strains with pVRL2Z plasmid (Δ sRNA44 + pVRL2Z) and Δ sRNA44 mutant strain with pVRL2Z- sRNA44 plasmid (Δ sRNA44 + pVRL2Z-sRNA44). Expression was induced in all strains induced by addition of 100 mM arabinose for 30 min. RNA was isolated from all samples using GeneJET RNA Purification Kit (Thermo Scientific) according to manufacturer's instruction. cDNA synthesis was carried out using GoScript™ Reverse Transcription System (Promega). Luna® Universal qPCR Master Mix (New England Bio labs) was used for all RT-qPCR reactions in 20 μ L volumes including 8 μ L of cDNA, "No Reverse Transcriptase" RNA or genomic DNA as template. cDNA and "No Reverse Transcriptase" templates were diluted 5-fold to a final concentration of 0.67 ng/ μ L. Standard curves were generated with nine 10-fold serial dilutions of wild-type *A. baumannii* genomic DNA. RT-qPCR reactions were set up in duplicate in MicroAmp Fast Optical 96-well reaction plates (Applied Biosystems) and run on the ABI StepOnePlus™ Real-Time PCR System (Applied Biosystems). Default RT-qPCR settings were used for each run as well as for melt curves for each new primer set. All primers used for RT-qPCR are listed in **Table 2.4**.

2.9 Biofilm assay

Biofilm assay was carried out according to (Geoghegan *et al.*, 2010). Aliquots (995 μ L) of Brain Heart Infusion (BHI) broth with sterile 1% glucose were transferred to Eppendorf tubes. These were incubated overnight at 37°C to check for contamination. Overnight cultures of four strains: wild-type *A. baumannii* with pVRL2Z plasmid (w.t+pVRL2Z), Δ sRNA44 with pVRL2Z plasmid (Δ sRNA44 + pVRL2Z), complementation strain Δ sRNA44 with sRNA44 pVRL2Z plasmid (comp. Δ sRNA44 + sRNA44 pVRL2Z) and Δ bap were set up in LB Broth with 250 μ g/mL zeocin except Δ bap (with no zeocin). The following day, 1 mL of each overnight culture was transferred to sterile Eppendorf tubes. Using the Eppendorf tubes from the previous day, 5 μ L of culture was added to each and mixed well. Aliquots (200 μ L) were then added in quadruplicate to a 96-well plate (Costar). This was sealed with parafilm and

incubated static at 37°C for 24, 48 and 72 hours. The day next culture was decanted from the plate and the wells were washed 3 times with PBS and fixed with 100 µL of 100% EtOH. Once the plate was dry, 100 µL of crystal violet was added to stain the cells. After 15 minutes, the cells were washed 3× with PBS. 100 µL of 100% EtOH was added, and the plate was shaken gently to solubilize the crystal violet. The absorbance was read at 570 nm in a Synergy H1 TM Hybrid MultiMode microplate reader (BioTek).

Chapter 3

Global gene expression patterns of *A. baumannii* AB5075 in 12 different conditions

3.1 Introduction

Understanding the virulence mechanisms, antibiotic resistance, and adaptation of *A. baumannii* depends on gene expression patterns (Kröger *et al.*, 2016). Studying global gene expression patterns enables researchers to identify genes that are upregulated or downregulated under specific conditions, thereby shedding light on the microorganism's behavior and response to environmental changes (Kim *et al.*, 2008; Kröger *et al.*, 2013; Colgan *et al.*, 2017). The ability of *A. baumannii* to adapt and respond to changing environmental conditions through global gene expression patterns is a significant factor in its success as an opportunistic pathogen (Antunes *et al.*, 2014). Global gene expression patterns refer to the overall pattern of gene expression in an organism under particular conditions or at various periods of development and growth (Wilson and Daly, 2018).

3.1.1 Aim of this Chapter and Experimental Strategy

The aim of this chapter is to identify and characterise global transcriptional response and patterns of coding genes from different environmental and stress conditions using transcriptomic analysis of *A. baumannii* AB5075. Cells were grown in L-broth in different environmental conditions and total RNA was isolated. RNA quality and integrity were analysed using RNA bioanalyzer, libraries were prepared for RNA-seq then gene expression profiling was carried out using RNA-seq (Figure 3.1). The data were analysed by comparing different conditions and grouping them into functional pathways to understand what is the physiological and biological response to these different stresses.

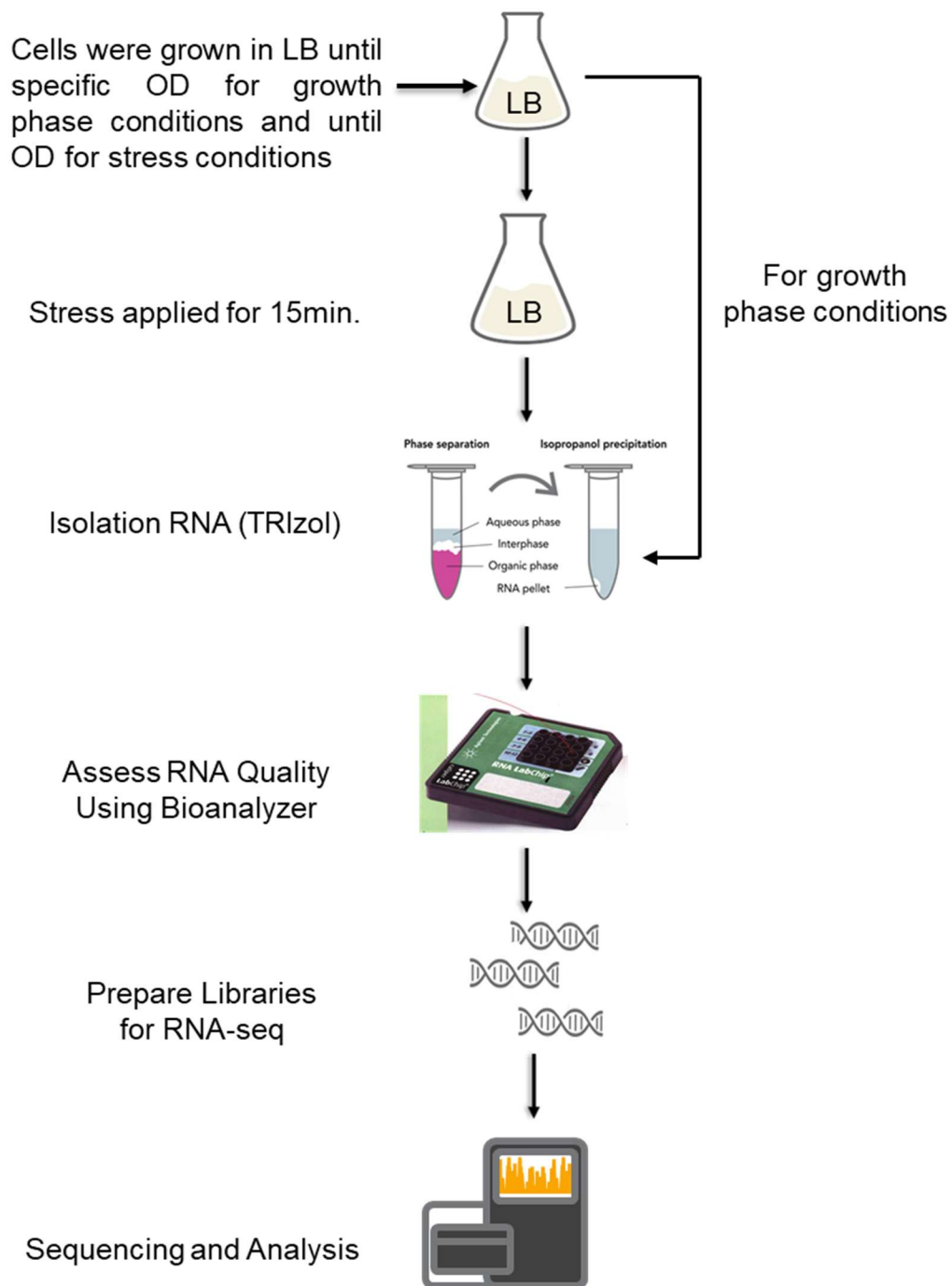


Figure 3.1: Strategy for experimental design. Cells grown at 37°C until a specific OD₆₀₀ then a stress applied for 15 min before isolating RNA using TRIzol. RNA quality and integrity was assessed using the Agilent bioanalyzer before libraries were commercially prepared for RNA-seq. The obtained sequencing reads were then bioinformatically analyzed.

3.2. Selection of growth conditions

To identify global gene expression patterns of *A. baumannii*, total RNA was isolated from 12 environmental conditions (Table 3.1, biological replicates n=3). We devised environmental conditions to induce transcriptional responses in *A. baumannii* but also monitored *A. baumannii* growth phases in L-broth. Total RNA was isolated from different optical densities in L-broth covering growth stages from early exponential to late stationary phase: OD₆₀₀ 0.1 (Early Exponential Phase, EEP), OD₆₀₀ 0.3 (Mid Exponential Phase, MEP), OD₆₀₀ 1 (Late Exponential Phase, LEP), OD₆₀₀ 2 (Early Stationary Phase, ESP) and 16 hours of growth (Late Stationary Phase, LSP). The MEP condition was used as a comparator for the growth and environmental stress conditions (see below). We designed a suite of infection-relevant stress conditions that are aimed to mimic different stresses that *A. baumannii* may encounter in their lifestyle:

Iron Limitation (Low Fe): Iron is an essential supplement for bacterial growth and during infection (Runci *et al.*, 2019). Siderophore-based iron uptake systems, in particular the siderophore Acinetobactin, have been shown to be important in *A. baumannii* to cause disease (Sheldon and Skaar, 2020). To induce iron limitation for the cells, we have added the iron chelator 2,2'-dipyridyl to the growth medium during exponential growth phase (MEP, OD 0.3) before isolating RNA.

Acinetobacter spp. Are non-flagellated but move on surfaces using surface-associated or twitching motility. During surface-motility, DNA uptake systems are upregulated (Wilharm *et al.*, 2013). Because the high concentration of NaCl severely hampers the motility and transformability of *A. baumannii* (De Silva and Kumar, 2018) and to study the response to osmotic stress, 0.3 M NaCl was added to the growth medium during exponential growth (NaCl).

Temperature shift: In other bacterial pathogens such as *Salmonella enterica*, virulence genes are up-regulated when shifted from ambient to body temperature (Ono *et al.*, 2005). Because *A. baumannii* is a problem in hospitals, we aimed to mimic the

transition from ambient (environmental) to body temperature by growing cells at 22°C and then shifting to 37°C (body temperature) for 15 minutes before isolating RNA (temperature shift, TS). As a control and comparator, we also isolated RNA from cells at OD₆₀₀ 0.3 and 22°C (ambient temperature, AT).

Antibiotic Stress: Multidrug resistance of *A. baumannii* is attributed to its ability to acquire and overexpress genes coding for a broad variety of functions mediating antibiotic resistance, as well as its intrinsic resistance due to specific properties of membrane permeability. Because antibiotics are very important stressors for *A. baumannii* during infection, we isolated RNA after addition sub-MIC levels from two antibiotics that target the ribosome and protein biosynthesis (Table 3.2): tetracycline (which *A. baumannii* AB5075 is sensitive to, Tet) and chloramphenicol (which *A. baumannii* AB5075 is resistant to, Chl) (Jacobs *et al.*, 2014; Karalewitz and Miller, 2018; Kröger *et al.*, 2018).

Cold Shock: The cold shock response has not been as extensively studied as the heat shock response and seems to be less conserved across organisms (Yamanaka, 1999) and not studied in *A. baumannii* at all. We isolated RNA under temperature downshift (Cold Shock, CS) by growing cells at 37°C and then shifting to 22°C for 15 min during MEP (OD₆₀₀ 0.3) mimicking return to the environment after being associated with a warm-blooded host.

3.3 Determination of MICs

To determine the concentration of antibiotics to elicit a transcriptomic response of *A. baumannii* to sub-inhibitory concentrations of different antibiotics (“Antibiotic Shock”, Table 3.2), we first determined the MICs using the broth microdilution method for two antibiotics (Table 3.2). The antibiotics are chloramphenicol, which *A. baumannii* is resistant to, and tetracycline which *A. baumannii* is sensitive to. The MIC for chloramphenicol was determined as 64 µg/ml and sub-MIC was 32 µg/ml and the MIC for tetracycline was 2 µg/ml and the sub-MIC 1 µg/ml (Table 3.2). Surprisingly, the MIC for chloramphenicol was lower than in a published report (Karalewitz and Miller, 2018),

which was reported as 128 µg/ml. Perhaps differences in expression of efflux pumps could account for this difference (Kröger *et al.*, 2018). In the antibiotic shock experiment, antibiotics were then used below the minimal inhibitory concentrations (MIC) such that growth rate was lowered compared to growth without antibiotics (Figure 3.2).

Table 3.1: Different environmental conditions the RNA was isolated from. Conditions of which RNA has been isolated.

Name	Sample Abbreviation	Growth Conditions
Early Exponential Phase	EEP	L-broth, OD = 0.1
Mid Exponential Phase	MEP	L-broth, OD = 0.3
Late Exponential Phase)	LEP	L-broth, OD = 1
Early Stationary Phase	ESP	L-broth, OD = 2
Over-night culture	LSP	L-broth, 16h of growth (o/n)
Ambient Temp	AT	L-broth, Ambient temperature (22°C) OD 0.3 + 15min
Temperature Shift	TS	L-broth, Temperature shift Growth at 22°C until OD 0.3, then shift to 37°C for 15 minutes
Cold Shock	CS	L-broth, Temperature shift Growth at 37°C until OD 0.3, then shift to 22°C for 15 minutes
Iron Limitation	Low Fe	L-broth, Growth until OD 0.3, then addition of 0.22 mM 2,2'-dipyridyl
Osmotic Shock	NaCl	L-broth, Growth until OD 0.3 + then addition of NaCl (final concentration 0.3M)
Antibiotic Shock	Chl	L-broth, Growth until OD 0.3 + then addition of chloramphenicol (32 µg/ml)
Antibiotic Shock	Tet	L-broth, Growth until OD 0.3 + then addition of Tetracycline (1 µg/ml)

Table 3.2: Minimum inhibition and sub-inhibition concentration of antibiotics.

Antibiotic	MIC	Sub-IC
Chloramphenicol	64 µg/ml	32 µg/ml
Tetracycline	2 µg/ml	1 µg/ml

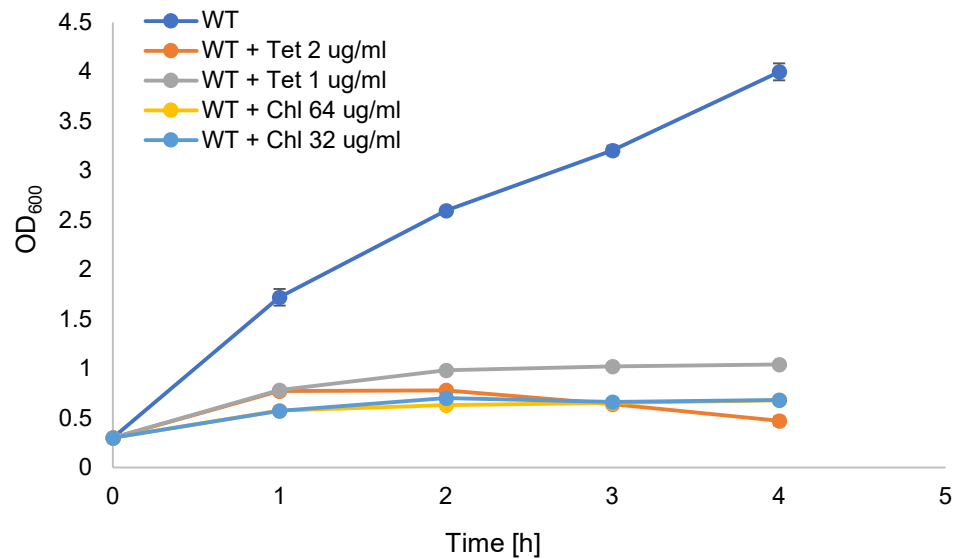


Figure 3.2: Growth curve of *A. baumannii* in absence (control) and presence of antibiotics (tetracycline and chloramphenicol). The time refers to hours after cells reached OD₆₀₀ 0.3. Mean values are plotted (n=3).

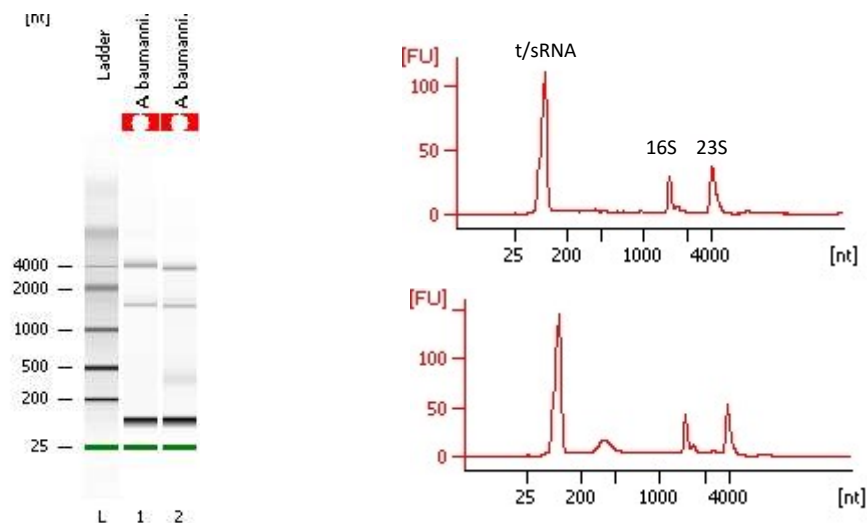


Figure 3.3: Assessment of total RNA quality for *A. baumannii* cells grown to MEP condition (OD₆₀₀ = 0.3) using the Agilent Bioanalyzer. Two replicates of RNA are shown next to the RNA ladder (left panel). Line graphs of total RNA from left panel are shown (right panels). Peaks for tRNA, sRNAs (including 5S rRNA), 16S and 23S rRNA are indicated.

3.4 Quality control of RNA and RNA-seq

Because we need high-quality RNA for RNA-seq, we analysed the integrity of RNA using the Agilent Bioanalyzer (Figure 3.3) shows examples of two biological replicates were isolated from the MEP condition. Sharp peaks at higher molecular weight correspond to the 16S and 23S rRNA and no peaks at lower molecular weight indicate highly intact RNA. RNA from three biological replicates based on their quality were subjected for all environmental condition to RNA-seq.

3.5 RNA-seq

RNA was isolated from environmental conditions as shown in Table 3.1 and subjected to RNA-seq at the Core Sequencing Unit Würzburg University (Germany). After DNase digestion, ribosomal RNA depletion, library preparation and sequencing (all carried out by the Core Sequencing Unit Würzburg University, the obtained reads were analysed with the help of Dr Karsten Hokamp (Smurfit Institute, Department of Genetics, TCD) and Dr Anna Ershova (Moyne Institute of Preventive Medicine, Department of Microbiology, TCD). Thirteen to 24 million reads per sample were obtained, which is sufficient for complete coverage of the bacterial transcriptome (Haas *et al.*, 2012) (Figure 3.4 and Table 3.3). After read mapping, between 73 and 93% of reads mapped to coding genes (Table 3.4). The lowest percentage of reads (73-75%) mapping to coding genes was observed in the LSP growth condition. In this condition, we expect more reads mapping to non-coding features, such as sRNAs as this has been observed in other Gram-negative bacteria such as *Salmonella enterica* (Kröger *et al.*, 2013).

3.6 Reproducibility of RNA-seq biological replicates

For each condition, we sequenced three biological replicates. After analysis of RNA-seq data, most of the biological replicates showed excellent agreement (Figure 3.5). Principal component analysis and hierarchical clustering highlights the strong agreement of biological replicates. The greatest variation was observed for the temperature-shift experiment (Figure 3.6).

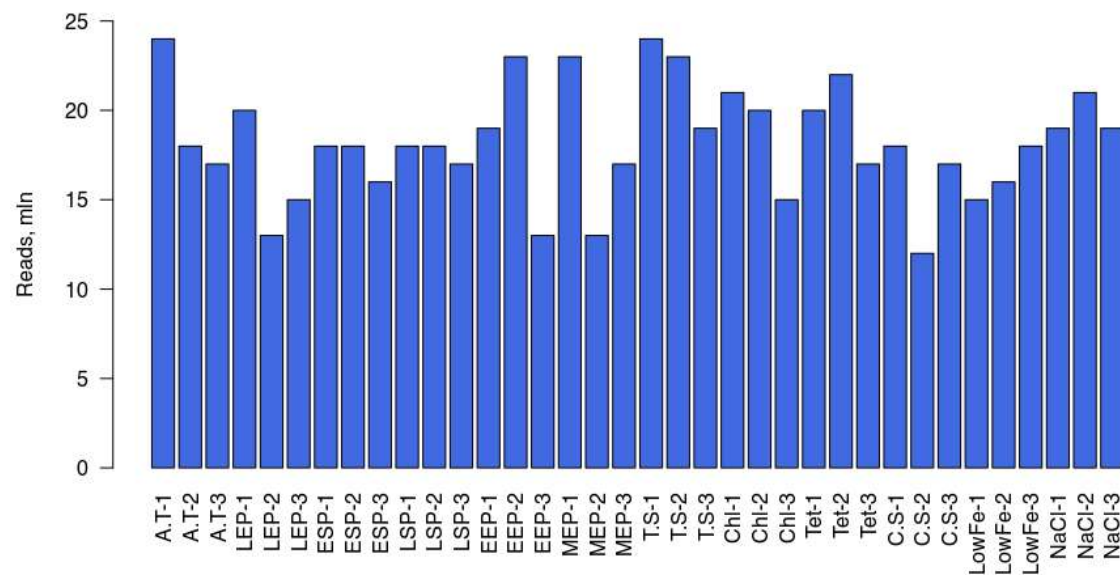


Figure 3.4: The histogram shows the number of million mapped reads per sample. The short fragments were mapped by READemption. The numbers indicate biological replicates.

Table 3.3: Sequencing statistics. Number of reads obtained from RNA-seq and aligned reads
Reference: GCF_000963815.1_ASM96381v1_genomic Mapper: READemption version: 0.4.5
Counting: READemption version: 0.4.5

Sample	No. of input reads	No. of reads - Long enough and used for alignment	Total no. of aligned reads	Total no. of unaligned reads	Total no. of uniquely aligned reads	Total no. of alignments	Percentage of aligned reads (compared to no. of input reads)	Percentage of uniquely aligned reads (in relation to all aligned reads)
EEP-1	19,096,721	19,096,721	16,199,893	2,896,828	15,573,145	18,232,681	84.83	96.13
EEP-2	22,617,453	22,617,453	19,011,993	3,605,460	18,284,025	21,332,342	84.06	96.17
EEP-3	12,748,136	12,748,136	11,168,414	1,579,722	10,885,092	11,923,636	87.61	97.46
MEP-1	22,062,156	22,062,156	18,710,708	3,351,448	18,034,684	20,923,901	84.81	96.39
MEP-2	13,007,269	13,007,269	11,339,691	1,667,578	11,092,607	11,872,456	87.18	97.82
MEP-3	16,380,716	16,380,716	14,313,018	2,067,698	13,914,543	15,414,132	87.38	97.22
LEP-1	19,883,393	19,883,393	17,109,285	2,774,108	16,513,679	19,401,529	86.05	96.52
LEP-2	13,321,079	13,321,079	10,836,936	2,484,143	10,458,329	12,256,694	81.35	96.51
LEP-3	14,661,493	14,661,493	12,489,984	2,171,509	12,086,381	14,014,436	85.19	96.77
ESP-1	16,717,174	16,717,174	14,333,406	2,383,768	13,840,948	16,066,782	85.74	96.56
ESP-2	16,922,132	16,922,132	14,228,373	2,693,759	13,740,677	15,926,122	84.08	96.57
ESP-3	15,023,991	15,023,991	12,833,387	2,190,604	12,443,543	14,134,992	85.42	96.96
LSP-1	16,443,387	16,443,387	14,184,695	2,258,692	13,887,330	15,159,447	86.26	97.9
LSP-2	15,813,812	15,813,812	14,055,436	1,758,376	13,673,764	15,369,897	88.88	97.28
LSP-3	15,702,036	15,702,036	13,821,145	1,880,891	13,512,634	14,777,888	88.02	97.77
NaCl-1	18,210,807	18,210,807	15,310,955	2,899,852	14,788,009	17,006,606	84.08	96.58
NaCl-2	20,195,333	20,195,333	17,375,362	2,819,971	16,839,984	19,013,045	86.04	96.92
NaCl-3	18,290,263	18,290,263	15,495,191	2,795,072	15,044,295	16,835,816	84.72	97.09
LowFe-1	14,692,255	14,692,255	12,076,077	2,616,178	11,720,498	13,144,388	82.19	97.06
LowFe-2	15,310,723	15,310,723	12,873,315	2,437,408	12,507,667	13,958,626	84.08	97.16
LowFe-3	17,322,911	17,322,911	14,559,408	2,763,503	14,077,186	16,114,317	84.05	96.69
Chl-1	20,921,365	20,921,365	17,708,664	3,212,701	16,929,797	20,494,137	84.64	95.6
Chl-2	20,260,927	20,260,927	17,096,912	3,164,015	16,248,552	20,184,428	84.38	95.04
Chl-3	15,665,739	15,665,739	13,073,514	2,592,225	12,343,862	15,749,793	83.45	94.42
Tet-1	20,547,215	20,547,215	17,069,266	3,477,949	16,065,470	20,889,125	83.07	94.12
Tet-2	22,399,615	22,399,615	19,142,810	3,256,805	18,341,092	22,139,727	85.46	95.81
Tet-3	17,202,083	17,202,083	14,564,623	2,637,460	13,783,639	17,458,702	84.67	94.64
AT1	22,571,351	22,571,351	19,258,033	3,313,318	18,739,521	20,858,536	85.32	97.31
AT2	17,756,235	17,756,235	15,206,541	2,549,694	14,801,092	16,409,724	85.64	97.33
AT3	16,394,928	16,394,928	14,104,310	2,290,618	13,742,334	15,198,072	86.03	97.43
Col-1	17,995,630	17,995,630	14,770,274	3,225,356	14,074,442	17,362,285	82.08	95.29
Col-2	12,505,322	12,505,322	10,464,689	2,040,633	9,912,214	12,473,091	83.68	94.72
Col-3	16,586,213	16,586,213	14,380,181	2,206,032	13,647,946	17,158,944	86.7	94.91
TS-1	23,810,861	23,810,861	20,485,156	3,325,705	19,955,179	22,235,842	86.03	97.41
TS-2	23,094,822	23,094,822	20,140,906	2,953,916	19,603,293	21,878,764	87.21	97.33
TS-3	18,966,231	18,966,231	16,489,068	2,477,163	16,125,787	17,502,821	86.94	97.8
TS-4	16,569,691	16,569,691	14,125,700	2,443,991	13,843,417	14,862,042	85.25	98

Table 3.4: Sequencing statistics. Percentage of reads mapping to genomic feature: CDS, sense_ncRNA, sense_rRNA, sense_tRNA, without classification, unmapped.

sample	CDS	ncRNA	sRNA	rRNA	tRNA	tmRNA	Assigned	Unassigned Unmapped	Unassigned No Features
EEP-1	94.22	0.14	3.25	0.80	1.46	1.45	95.58	1.16	3.24
EEP-2	94.94	0.16	1.09	0.70	1.51	1.46	96.13	0.91	2.94
EEP-3	99.23	0.12	3.69	0.59	0.64	1.05	97.78	0.24	1.97
MEP-1	96.67	0.10	1.06	0.63	1.72	1.20	97.29	0.11	2.58
MEP-2	99.25	0.13	2.63	0.29	0.47	1.11	97.41	0.28	2.29
MEP-3	98.79	0.12	5.26	0.79	0.57	1.22	97.93	0.19	1.87
LEP-1	92.77	0.34	2.66	1.99	0.46	2.84	97.55	0.43	2.00
LEP-2	92.02	0.30	4.68	1.76	0.70	2.40	96.50	0.91	2.58
LEP-3	91.95	0.28	8.49	1.63	0.70	2.16	96.59	0.64	2.75
ESP-1	89.49	0.49	7.71	1.69	0.35	5.82	97.42	0.35	2.21
ESP-2	89.62	0.50	5.46	1.60	0.41	5.92	97.56	0.25	2.18
ESP-3	91.44	0.32	14.92	1.33	0.34	4.66	97.49	0.29	2.20
LSP-1	82.96	0.67	16.69	0.55	0.43	8.58	96.08	0.39	3.51
LSP-2	78.99	0.86	16.10	1.07	0.41	12.20	96.43	0.65	2.91
LSP-3	80.63	0.86	3.36	0.54	0.43	10.47	96.43	0.40	3.16
NaCl-1	95.20	0.20	4.20	0.94	1.28	1.72	98.05	0.28	1.65
NaCl-2	95.63	0.19	2.44	0.71	1.17	1.79	97.95	0.26	1.78
NaCl-3	96.85	0.14	3.99	0.61	1.27	1.12	97.91	0.26	1.82
LowFe-1	95.43	0.19	3.63	0.57	1.20	2.02	98.11	0.21	1.67
LowFe-2	96.18	0.14	3.91	0.53	1.23	1.72	98.06	0.29	1.63
LowFe-3	95.72	0.17	3.98	0.90	1.40	1.53	98.13	0.20	1.66
Chl-1	94.54	0.05	1.03	1.17	1.84	0.29	95.15	0.46	4.38
Chl-2	93.75	0.071	1.00	1.04	2.26	0.22	94.80	0.25	4.94
Chl-3	91.34	0.10	1.34	1.43	2.36	0.26	93.18	0.92	5.89
Tet-1	93.04	0.12	0.97	1.31	2.92	0.38	94.69	0.24	5.06
Tet-2	95.39	0.08	0.75	1.35	1.68	0.53	95.49	0.43	4.06
Tet-3	92.79	0.12	1.55	1.13	2.53	0.34	93.75	0.39	5.84
AT1	96.25	0.21	2.57	0.98	0.53	2.92	98.37	0.26	1.35
AT2	97.03	0.17	3.56	0.86	0.51	2.17	98.12	0.19	1.67
AT3	96.65	0.22	5.11	0.96	0.49	2.75	98.51	0.20	1.28
Col-1	95.27	0.11	1.06	0.76	2.82	0.66	96.40	0.26	3.32
Col-2	94.09	0.08	2.11	0.69	2.77	0.52	95.14	0.37	4.48
Col-3	94.59	0.09	3.53	0.53	3.26	0.58	95.83	0.26	3.89
TS-1	94.43	0.17	2.93	1.18	0.35	1.89	97.44	0.58	1.96
TS-2	95.05	0.15	1.68	1.12	0.40	1.70	96.99	0.69	2.31
TS-3	97.24	0.09	1.14	0.55	0.44	0.95	97.18	0.53	2.27
TS-4	95.28	0.16	NA	0.40	0.62	2.41	98.09	0.26	1.63

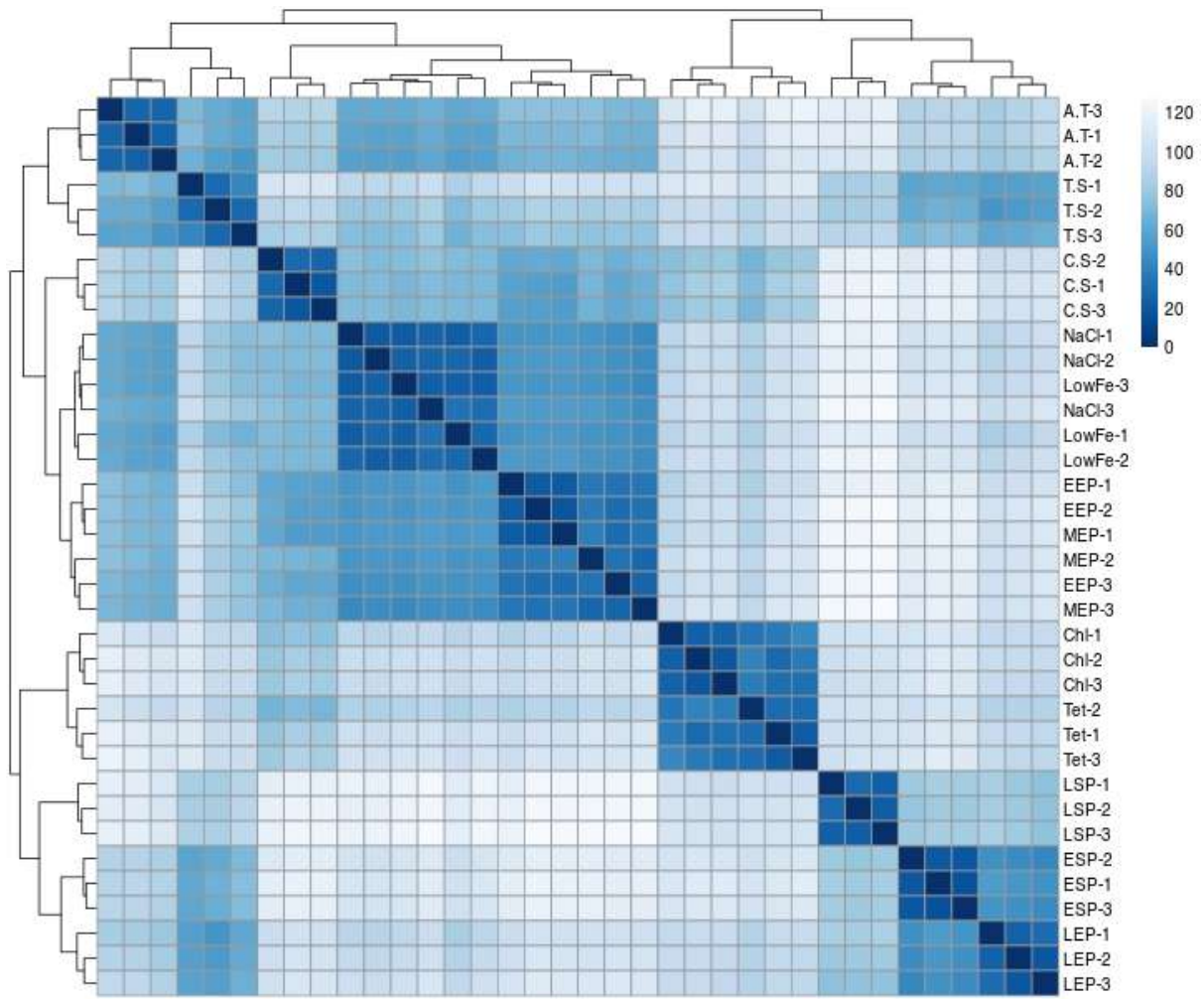


Figure 3.5: Heatmap showing sample similarity generated by DESeq2. Clustering of condition-specific RNA-seq shows excellent agreement of biological replicates. A.T (ambient temperature, 22°C), T.S (Temperature shift), C.S (Cold shock), EEP (Early Exponential Phase), MEP (Mid-Exponential Phase), LSP (Late Exponential Phase), ESP (Early Stationary Phase), LSP (Late Stationary Phase), NaCl (osmotic shock), LowFe (Low Iron shock), Tet (Tetracycline shock), Chl (Chloramphenicol shock).

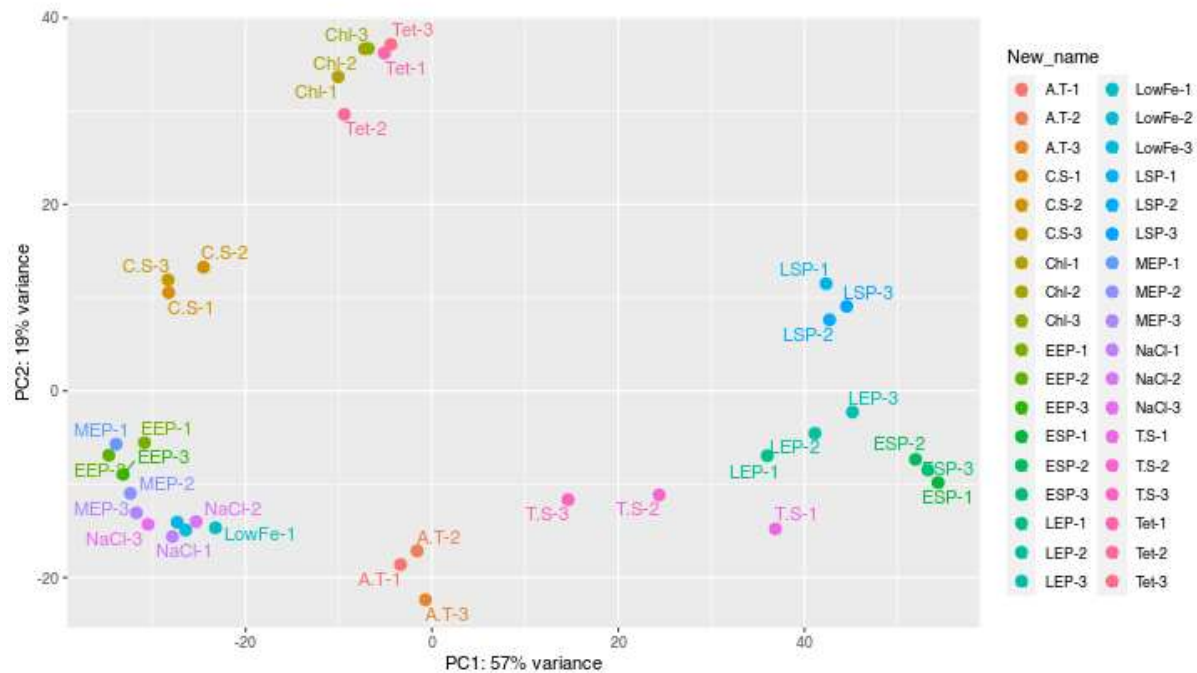


Figure 3.6: Principal component analysis of biological replicates generated by DESeq2. Biological replicates show mostly good agreement of gene expression. A.T (ambient temperature, 22°C), T.S (Temperature shift), C.S (Cold shock), EEP (Early Exponential Phase), MEP (Mid-Exponential Phase), LSP (Late Exponential Phase), ESP (Early Stationary Phase), LSP (Late Stationary Phase), NaCl (osmotic shock), LowFe (Low Iron shock), Tet (Tetracycline shock), Chl (Chloramphenicol shock).

3.7 Differential expression analysis

In order to gain insights into cellular responses, RNA-Seq can analyze global gene expression changes and therefore this method can be very instructive when contrasting various physiological states or strains (Utturkar *et al.*, 2020). To study genes involved in antimicrobial resistance, virulence or general physiology, it is necessary to discover when these genes are expressed to gain a deeper understanding of *A. baumannii* biology and to uncover the conditions when their gene regulation can be studied *in vitro*. For example, in *S. enterica*, specific environmental conditions induce the expression of different pathogenicity islands and therefore these conditions to be used to study their genetic regulation *in vitro* and allow to infer the environmental queues that induce their expression (Kröger *et al.*, 2013) *in vivo*.

3.7.1 Gene expression throughout growth phases of AB5075

Bacteria grown in batch culture in the lab in rich media undergo different phases of growth. After inoculating cells into fresh medium, they first undergo an adaptation phase, where cells start to take up nutrients and prepare for exponential growth (Rolfe *et al.*, 2012). During exponential growth, cells possess the shortest generation time (i.e., multiply fastest) but once the culture gets depleted of essential nutrients, cells will start to enter stationary phase, which is characterised by growth cessation. The transcriptome profiles of *A. baumannii* AB5075 cells in different growth stages (EEP, MEP, LSP, ESP and LSP, Table 3.1) were analysed by high-throughput sequencing as described above. We performed DESeq2 to determine which genes are expressed at different levels between conditions by taking the normalized read count data and performing statistical analysis to discover quantitative changes in expression levels between experimental groups. By taking cut-off values for gene expression fold change (FC) to see how many genes are up- or downregulated per comparison. Growth-phase comparisons were compared with MEP. Table 3.5 and Figure 3.7 show how many genes are up- or down-regulated when cells were grown in L-broth when compared to the MEP condition. All gene expression data can be found in Appendix 1. We also considered the “absolute expression” values as expressed at transcripts per million

(TPM) values (Wagner and Romby, 2015), which give an indication of the overall abundance of transcripts in the different growth conditions.

Table 3.5: Numbers of genes up- and downregulated in EEP, LEP, ESP and LSP compared to the MEP growth condition. The numbers were calculated based on DESeq2 values.

Cut-off	No. of genes > 2-fold up	No. of genes unchanged	No. of genes > 2-fold down
EEP/MEP	0 (0%)	4034 (100%)	0 (0%)
LEP/MEP	1003 (24.9%)	2148 (53.2%)	883 (21.9%)
ESP/MEP	1125 (27.9%)	1992 (49.4%)	917 (22.7%)
LSP/MEP	1227 (30.4%)	1728 (42.9%)	1079 (26.7%)

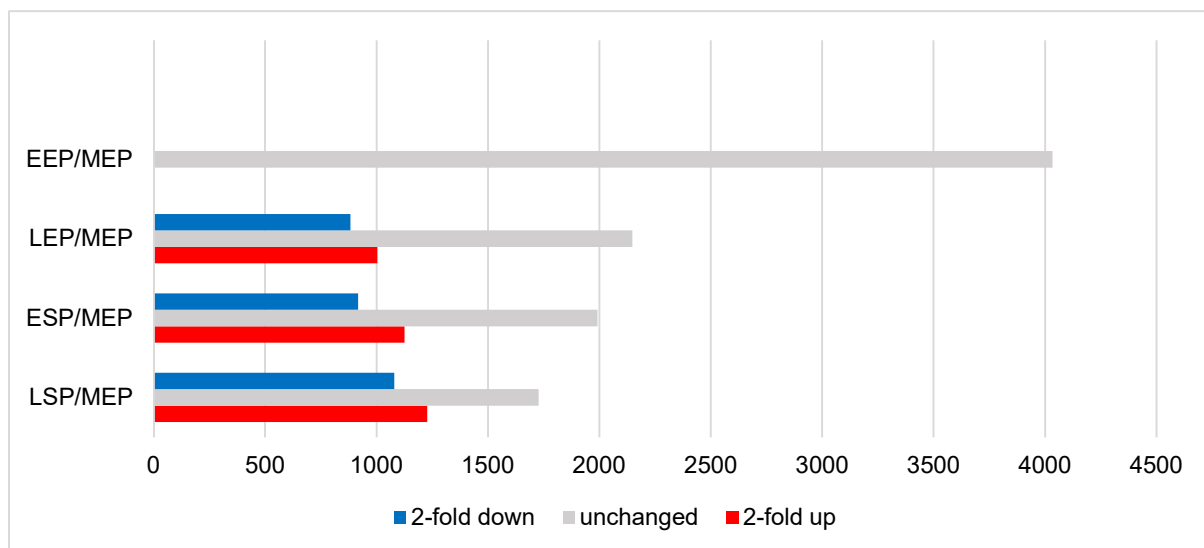


Figure 3.7: Gene expression changes in L-broth. Using a cut-off value (DESeq2) of 2-fold in difference of gene expression, the bar chart shows the numbers of genes that are up- or downregulated or unchanged in EEP, LEP, ESP and LSP compared to the MEP growth condition.

3.7.1.1 Growth-phase comparison of EEP, LEP, ESP and LSP with MEP

Overall, we see no significant difference ($P_{\text{adj}} < 0.05$) between gene expression in early and mid-exponential growth phase (EEP vs. MEP). These two conditions cluster closely in Figure 3.8 indicating that gene expression in these early exponential growth phases is very similar. Conversely, the largest difference is between mid-exponential phase and late stationary phase (MEP vs. LSP) (1537 genes up-, 1649 genes down-regulated, Figure 3.11). To get a first indication of what genes show the largest difference between conditions, and therefore might be most relevant and indicative of the respective growth condition, we listed the ten genes that showed largest up- or downregulation compared to the MEP condition and assessed their functions.

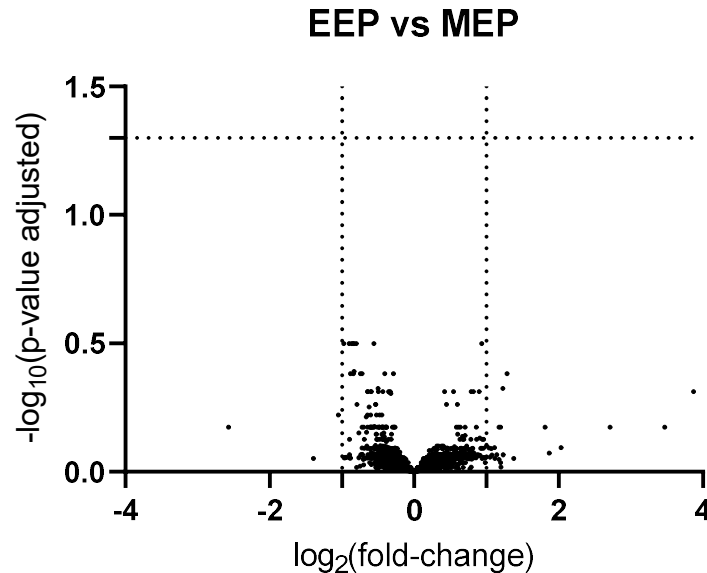


Figure 3.8: Volcano plot showing genes up- and down-regulated genes in EEP vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots would indicate genes that are up-regulated in the EEP condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots would indicate genes that are down-regulated in the EEP condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005.

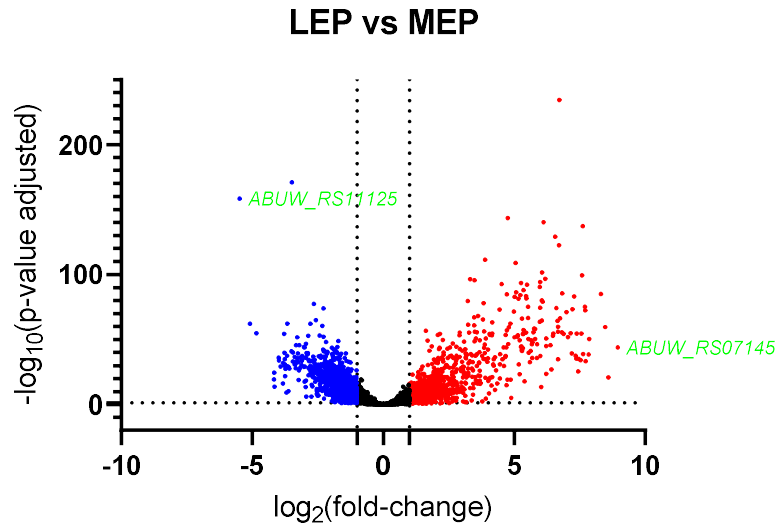


Figure 3.9: Volcano plot showing genes up- and down-regulated genes in LEP vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the LEP condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the LEP condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005. 1461 (36.2%) genes up- and 1418 (35.2%) genes down-regulated out of 4034 genes in LEP/MEP.

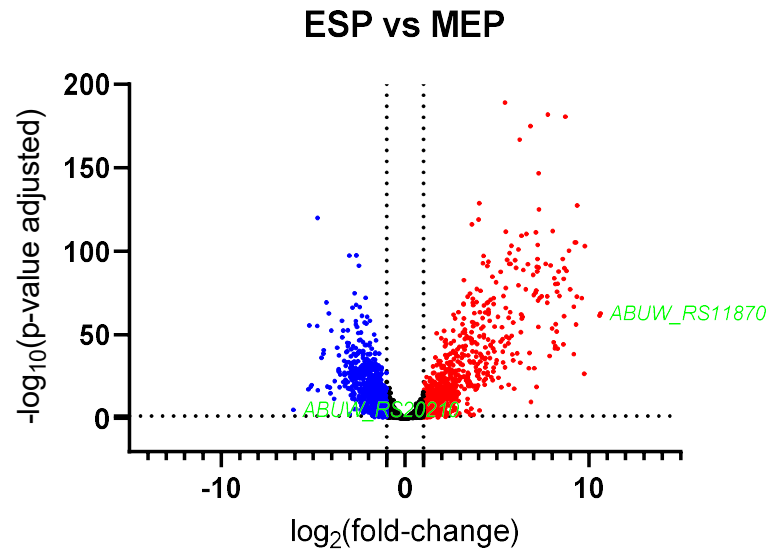


Figure 3.10: Volcano plot showing genes up- and down-regulated genes in ESP vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the ESP condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the ESP condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005. 1487 (36.9%) genes up- and 1468 (36.4%) genes down-regulated out of 4034 genes in ESP/MEP.

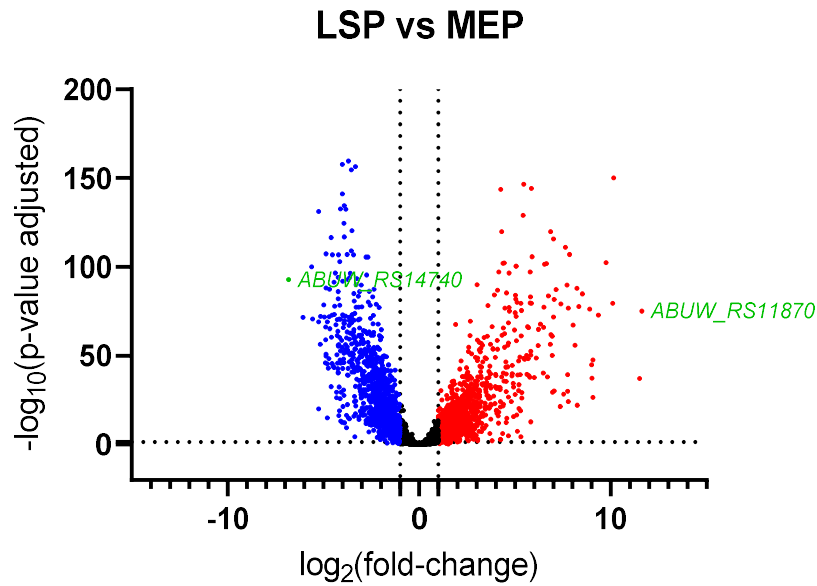


Figure 3.11: Volcano plot showing genes up- and down-regulated genes in LSP vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the LSP condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the LSP condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005. 1537 (38.1%) genes up- and 1649 (40.9%) genes down-regulated out of 4034 genes in LSP/MEP.

Expression of ribosomal protein encoding genes Rps and Rpl. When cells are at their fastest growth (i.e., when growing exponentially), they require enzymes and structural proteins to provide all building blocks for cell division. To generate enough proteins for growth, cells can increase their abundance of ribosomes by up-regulating the expression of rRNA genes and genes that encode for ribosomal proteins (Rps: proteins of small ribosomal subunit, Rpl, Rpm: proteins of large ribosomal subunit). As samples were depleted for rRNA, the levels of *rps*, *rpl*, *rpm* genes that encode for the proteins of the ribosomes were measured (Figure 3.12). As expected, genes encoding for ribosomal protein are most up-regulated when cells are growing exponentially and abundance of *rps*, *rpl*, *rpm* transcripts gradually decrease when cells transition through LEP, ESP and LSP.

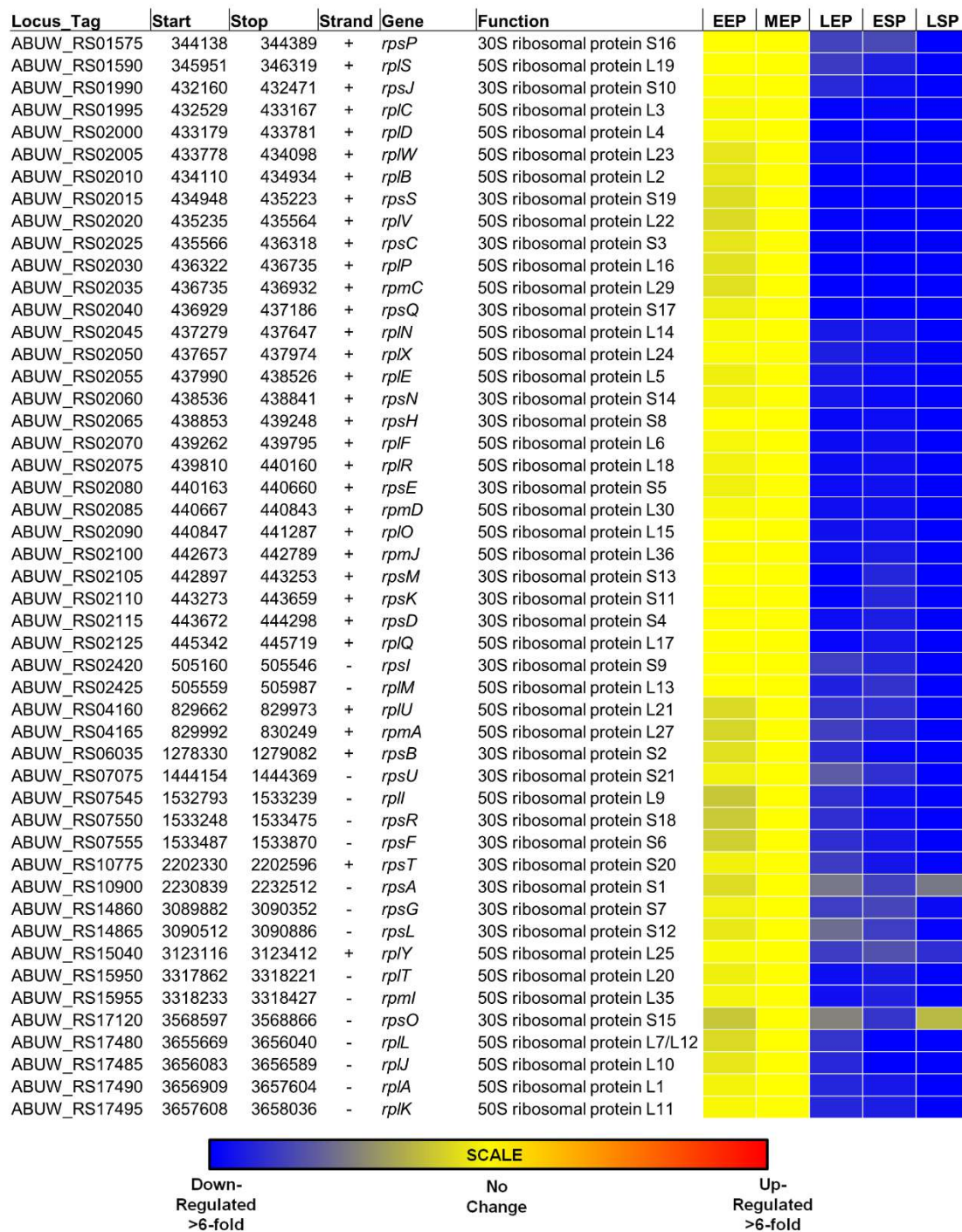


Figure 3.12: Heatmap showing relative gene expression (TPM values) of genes encoding for ribosomal proteins (*rps*, *rpl* and *rpm*) in L-broth throughout growth phases. The MEP condition is used as a comparator. The heatmap shows down-regulation of *rps*, *rpl* and *rpm* genes when entering late exponential growth phase.

By further analysing differentially expressed genes, we focussed on genes and pathways with annotated function (Figure 3.13). Up-regulated genes and pathways that stood out were genes of the phenyl acetic acid (*paa*) pathway (especially in LEP), the catalase-encoding gene *katE*, genes of malonate degradation (*mdc*, *mad*), genes of the *otsAB* operon and the genes that encode the chaperone-usher pilus system (*csu*) that were down-regulated. These pathways will be analyzed in more depth below.

The phenyl acetic acid (*paa*) pathway:

The Paa pathway is repressed by BaeRS (Hooppaw *et al.*, 2022a; Liu *et al.*, 2023) and regulated by GacS (Cerqueira *et al.*, 2014a) and it influences infection outcome through a direct effect on neutrophil chemotaxis (Bhuiyan *et al.*, 2016a). The *paa* operon in *A. baumannii* is similar to the well-studied *paa* system in *E. coli* (Cerqueira *et al.*, 2014). The aromatic compounds phenylacetate and phenylalanine are converted into acetyl- and succinyl-CoA and fed into the tricarboxylic acid cycle. Research has demonstrated that the *paa* operon, which is in charge of PAA degradation, is one of the pathways that is most differently regulated in response to a variety of stressors and is significantly increased while receiving antibiotics (Rumbo-Feal *et al.*, 2013; Ohneck *et al.*, 2018; Qin *et al.*, 2018; Quinn *et al.*, 2018; Alkasir *et al.*, 2018). Surprisingly, in *A. baumannii*, it was discovered that the *paa* pathway possesses a role in bacterial virulence. Inhibition of the *paa* pathway led to increased killing of *A. baumannii* in a zebrafish infection model (Bhuiyan *et al.*, 2016). Up-regulation of the *paa* pathway also coincides with down-regulation of the Csu pili in ATCC17978 when exposed to sub-inhibitory levels of sulfamethoxazole and trimethoprim (Moon *et al.*, 2017). Interrupting Paa mediated catabolism resulted in increased antibiotic and hydrogen peroxide sensitivity (Hooppaw *et al.*, 2022). Here, we see strong up-regulation of the *paa* genes (*paaA*, *paaB*, *paaC*, *paaJ*, *paaK* and *paaZ*) in LEP and ESP without the addition of any additional environmental stressors. It may be possible that the expression of the *paa* genes is a reflection of intracellular oxidative stress, because we see the katalase gene *katE* to be highly up-regulated afterwards, in ESP and LSP (see Figure 3.13). For future studies, we discovered that the conditions of LEP and ESP will be ideal conditions to study the regulation of the *paa* pathway.

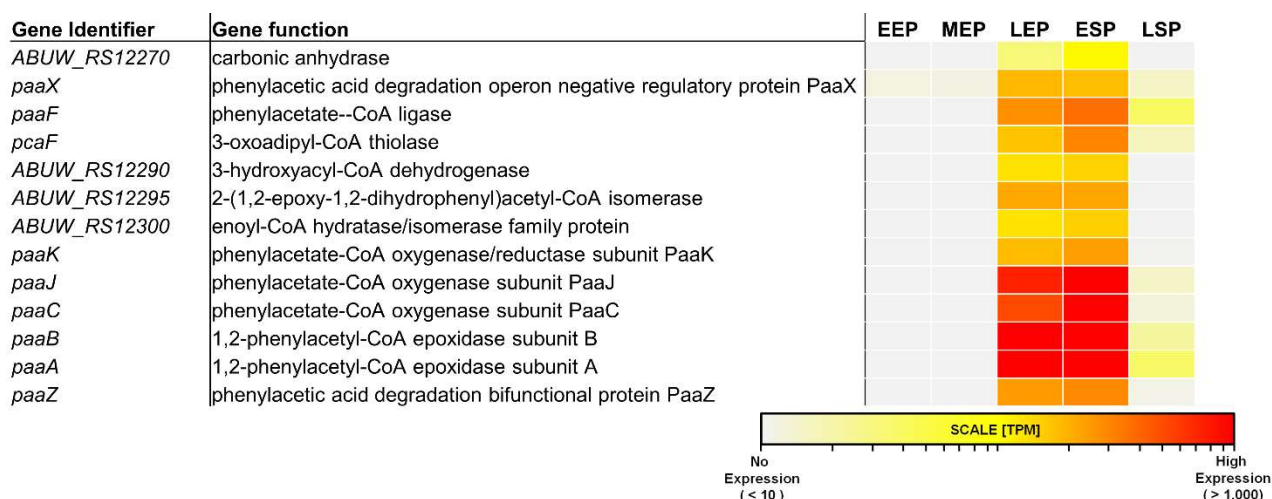


Figure 3.13: Heatmap showing gene expression of *paa* genes in L-broth across growth phases. The *paa* genes display high up-regulation in LEP and ESP and down-regulation at LSP ("Absolute gene expression" expressed by TPM values).

The malonate degradation (*mdc*) pathway and transport (*mad*):

The ability of bacteria to use malonate as a carbon source for growth is the main purpose of the Mdc pathway and Mad system. Although malonate is not a typical carbon source in many environments, organisms with this pathway can make use of molecules that contain malonate for their metabolic requirements (Koo and Kim, 1999). *Acinetobacter*'s general metabolic flexibility and ability to adapt to shifting environmental conditions are probably aided by the expression and control of the Mdc pathway and Mad system. Gaining knowledge of the regulatory mechanisms controlling these pathways may help us comprehend the ecology and physiology of *Acinetobacter* (Repizo *et al.*, 2020). A condition-specific up-regulation, in LSP, is the transport and degradation pathway of malonate. Here, *mdcA*, *mdcE* and *mdcH* (malonate degradation and *madL* and *madM* (malonate transport) showed high up-regulation in LSP (Figure 3.14). It is unclear, why malonate would be available in the medium at this later stage of growth. Potentially, dead, lysed cells could release malonate into the cell medium and would provide a source of energy when other sources have been depleted over the time of the growth curve.

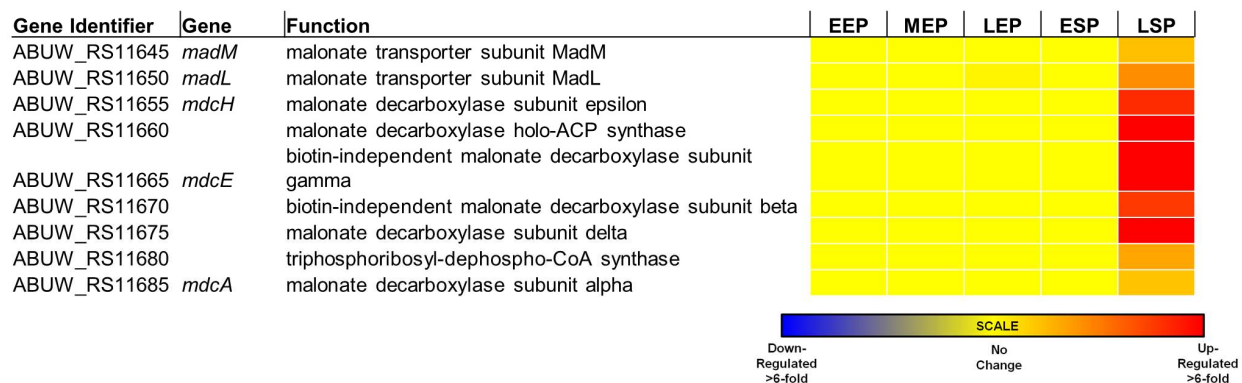


Figure 3.14: Heatmap showing gene expression of *mad* and *mdc* genes in L-broth across growth phases. The malonate metabolism genes display high up-regulation LSP ("Relative gene expression" expressed by TPM values).

Table 3.6: Top 10 upregulated genes in different growth phases

Growth Stage	1	2	3	4	5	6	7	8	9	10
EEP	ABUW_RS20160 hypothetical protein	ABUW_RS19765 hypothetical protein	ABUW_RS12615 TetR/AcrR family transcriptional regulator	ABUW_RS20135 hypothetical protein	ABUW_RS10215 hypothetical protein	ABUW_RS02355 GFA family protein	ABUW_RS01510 bacterioferritin-associated ferredoxin	ABUW_RS14465 hypothetical protein	ABUW_RS20440 hypothetical protein	ABUW_RS20180 hypothetical protein
LEP	ABUW_RS07145 DUF2171 domain-containing protein	ABUW_RS20475 hypothetical protein	ABUW_RS07170 NirDY/gwYdel family stress tolerance protein	ABUW_RS07960 spore coat protein U domain-containing protein	ABUW_RS12300 enoyl-CoA hydratase/isomerase family protein	ABUW_RS10355 thiamine pyrophosphate-dependent dehydrogenase E1 component subunit alpha	ABUW_RS1870 hypothetical protein	ABUW_RS05445 alpha-keto acid decarboxylase family protein	ABUW_RS12295 2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	ABUW_RS10350 alpha-keto acid dehydrogenase subunit beta
ESP	ABUW_RS11870 hypothetical protein	ABUW_RS07145 DUF2171 domain-containing protein	ABUW_RS11875 hypothetical protein	ABUW_RS20475 hypothetical protein	ABUW_RS11840 stress-induced protein	ABUW_RS11855 catalase HP1	ABUW_RS07170 NirDY/gwYdel family stress tolerance protein	ABUW_RS15160 trehalose-phosphatase	ABUW_RS05445 alpha-keto acid decarboxylase family protein	ABUW_RS07960 spore coat protein U domain-containing protein
LSP	ABUW_RS11870 hypothetical protein	ABUW_RS20475 hypothetical protein	ABUW_RS12975 hypothetical protein	ABUW_RS11840 stress-induced protein	ABUW_RS11875 hypothetical protein	ABUW_RS07170 NirDY/gwYdel family stress tolerance protein	ABUW_RS20230 hypothetical protein	ABUW_RS12220 hypothetical protein	ABUW_RS10025 hypothetical protein	ABUW_RS07145 DUF2171 domain-containing protein

Table 3.7: Top 10 downregulated genes in different growth phases

Growth Stage	1	2	3	4	5	6	7	8	9	10
EEP	ABUW_RS06950 GNAT family N-acetyltransferase	ABUW_RS11865 CinA family protein	ABUW_RS13220 hypothetical protein	ABUW_RS09705 hypothetical protein	ABUW_RS07145 DUF2171 domain-containing protein	ABUW_RS01825 PspC domain-containing protein	ABUW_RS09890 hypothetical protein	ABUW_RS11870 hypothetical protein	ABUW_RS13700 hypothetical protein	ABUW_RS13395 metal-dependent hydrolase
LEP	ABUW_RS11125 trifunctional regulator/proline dehydrogenase/L-glutamate-gamma-semialdehyde dehydrogenase	ABUW_RS14445 homocysteine S-methyltransferase family protein	ABUW_RS11115 sodium/proline symporter PutP	ABUW_RS05000 sulfate ABC transporter permease subunit CysI	ABUW_RS14425 betaine-aldehyde dehydrogenase	ABUW_RS16540 TonB-dependent siderophore receptor	ABUW_RS20240 30S ribosomal protein S17	ABUW_RS08010 hypothetical protein	ABUW_RS20215 30S ribosomal protein S19	ABUW_RS14430 choline dehydrogenase
ESP	ABUW_RS20210 hypothetical protein	ABUW_RS05010 sulfate ABC transporter substrate-binding protein	ABUW_RS14740 bacteriohemerythrin	ABUW_RS05005 alpha/beta hydrolase	ABUW_RS16540 TonB-dependent siderophore receptor	ABUW_RS14445 homocysteine S-methyltransferase family protein	ABUW_RS11125 trifunctional regulator/proline dehydrogenase/L-glutamate-gamma-semialdehyde dehydrogenase	ABUW_RS11590 taurine ABC transporter substrate-binding protein	ABUW_RS08010 hypothetical protein	ABUW_RS00925 porin Omp33-36
LSP	ABUW_RS14740 bacteriohemerythrin	ABUW_RS00925 porin Omp33-36	ABUW_RS01290 hypothetical protein	ABUW_RS14445 homocysteine S-methyltransferase family protein	ABUW_RS16350 enoyl-ACP reductase	ABUW_RS18185 F0F1 ATP synthase subunit B	ABUW_RS05005 alpha/beta hydrolase	ABUW_RS09600 multidrug efflux RND transporter periplasmic adaptor subunit AdeA	ABUW_RS18180 F0F1 ATP synthase subunit delta	ABUW_RS03465 alanine cation symporter family protein

Osmoprotection of *A. baumannii* via trehalose and *otsAB*:

The biological function of OtsAB in *Acinetobacter* includes several important roles such as osmoprotection. Trehalose functions as an osmoprotectant and compatible solute, assisting bacteria such as *Acinetobacter* in surviving in conditions where osmotic pressure fluctuates or is high. Trehalose builds up inside of cells in conditions of osmotic stress, such as extreme salt concentrations or dehydration, stabilizing proteins and membranes and averting harm (Zeidler *et al.*, 2017). OtsAB-mediated trehalose buildup can provide *Acinetobacter* resistance to desiccation, enabling it to thrive in conditions with little moisture or dryness. This ability is especially crucial for persistence and resilience in the environment (Zeidler and Müller, 2018). Cellular metabolism and energy balance are closely related to trehalose metabolism. Trehalose levels are modulated to satisfy the metabolic requirements of the cell via the activity of OtsAB enzymes, which can be controlled in response to metabolic cues, environmental stressors, or developmental signals (Vanaporn and Titball, 2020). *Acinetobacter* spp. can synthesise trehalose. The production of trehalose from UDP-glucose and glucose-6-phosphate is catalysed by the action of trehalose-6-phosphate synthetase OtsA and trehalose phosphatase OtsB (Zeidler *et al.*, 2017; Hubloher *et al.*, 2020). However, only OtsB is required for trehalose synthesis (Zeidler *et al.*, 2017). Deletion of *otsB* also led to reduced virulence in the *Galleria mellonella* larvae infection model and to impaired growth at 45°C and at high salinity (Hubloher *et al.*, 2020). Similar to the *paa* gene expression pattern, *otsA* and *otsB* (Figure 3.15) were up-regulated highly in LEP, ESP and LSP peaking in ESP. In *E.coli* the *otsA* and *otsB* genes are present on the same operon (McDougall *et al.*, 1993), and from our transcriptomic data, it is likely that it is an operon in *A. baumannii* as well. The up-regulation of the *otsAB* genes could mean that cells are under osmotic stress starting from LEP until LSP. Also, here the ESP condition appears ideal to study the regulation of the *otsAB* genes (in addition to the potential effect of temperature, see below).

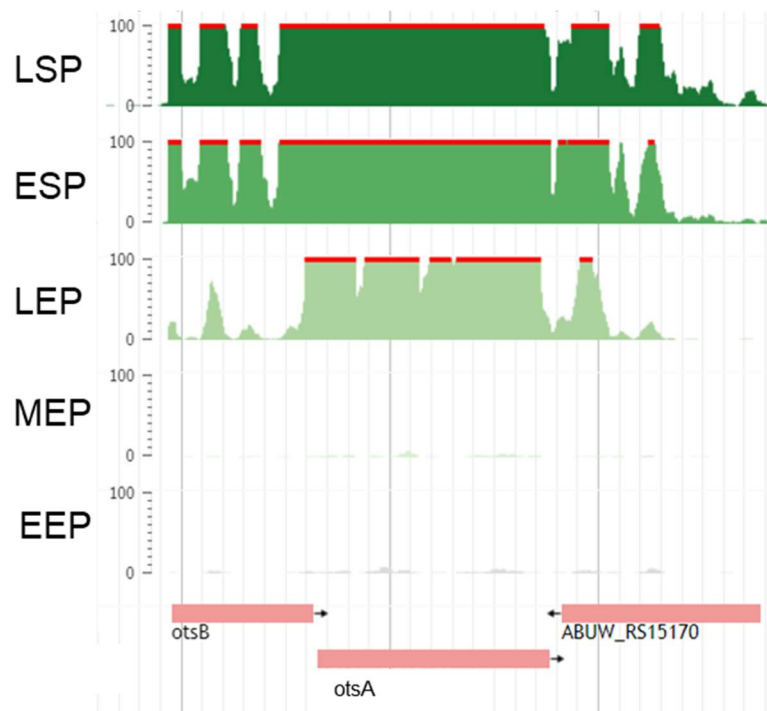


Figure 3.15: The genes *otsBA* are highly up-regulated in LEP, ESP and LSP while being not expressed in MEP and EEP. Sequence reads have been mapped, normalized, and visualized in Jbrowse. The scale is 0-100 normalized reads for all tracks.

Catalases (KatE, KatG):

Studies demonstrating the crucial role of the *katE* and *katG* gene products in *Acinetobacter* resistance to H₂O₂ showed that although deletion of both *katE* and *katG* in *Acinetobacter* compromises their capacity to reduce reactive oxygen species (ROS) production in neutrophils these catalase-deficient mutant actually exhibit great virulence in *Galleria mellonella* larvae (Sun *et al.*, 2016). KatE was highly upregulated in ESP and LSP. The induction of gene expression could mean that *A. baumannii* experiences oxidative stress during ESP and LSP.

Chaperone-usher (Csu) pathway:

The ability to form biofilm on abiotic and biotic surfaces is an important survival strategy of *A. baumannii*. To adhere to medical devices and other surfaces in the hospital environment, *A. baumannii* uses the chaperone-usher pathway, which uses Csu pili. During growth in L-broth, the *csu* genes are up-regulated in LEP, and to a lesser extent

at ESP, but otherwise switched off. Therefore, the LEP condition could be the condition that could be used to study the expression and regulation of the Csu pathway.

3.7.1.2 Functional Annotation of Differentially Expressed Genes (DEGs) in LEP/MEP

In LEP/MEP, the KEGG pathway analysis showed that the DEGs were linked to 44 pathways, were most dominant in upregulation with two-component systems indicating that different sets of genes are expressed controlled by diverse TCSs. Genes involved in oxidative phosphorylation was the most dominant set to be down-regulated, which indicates that growth slows down when cells leave the height of exponential growth phase (Figure 3.16). We also see the phenylalanine (*paa*) metabolism up-regulated as shown by individual gene analysis earlier. Quorum sensing genes are also up-regulated, likely reflecting the increase in cell density in the culture as cell numbers grow. Other biosynthetic pathways, such as amino acid biosynthesis pathways are up-regulated, which could be due to bacteria slowly running out of easily available nutrients that they may take up from the growth media and switch to anabolic reactions and endogenous amino acid production. Purine and pyrimidine metabolism is slightly down-regulated which could indicate that less nucleotides for DNA replication and rRNA/mRNA are required.

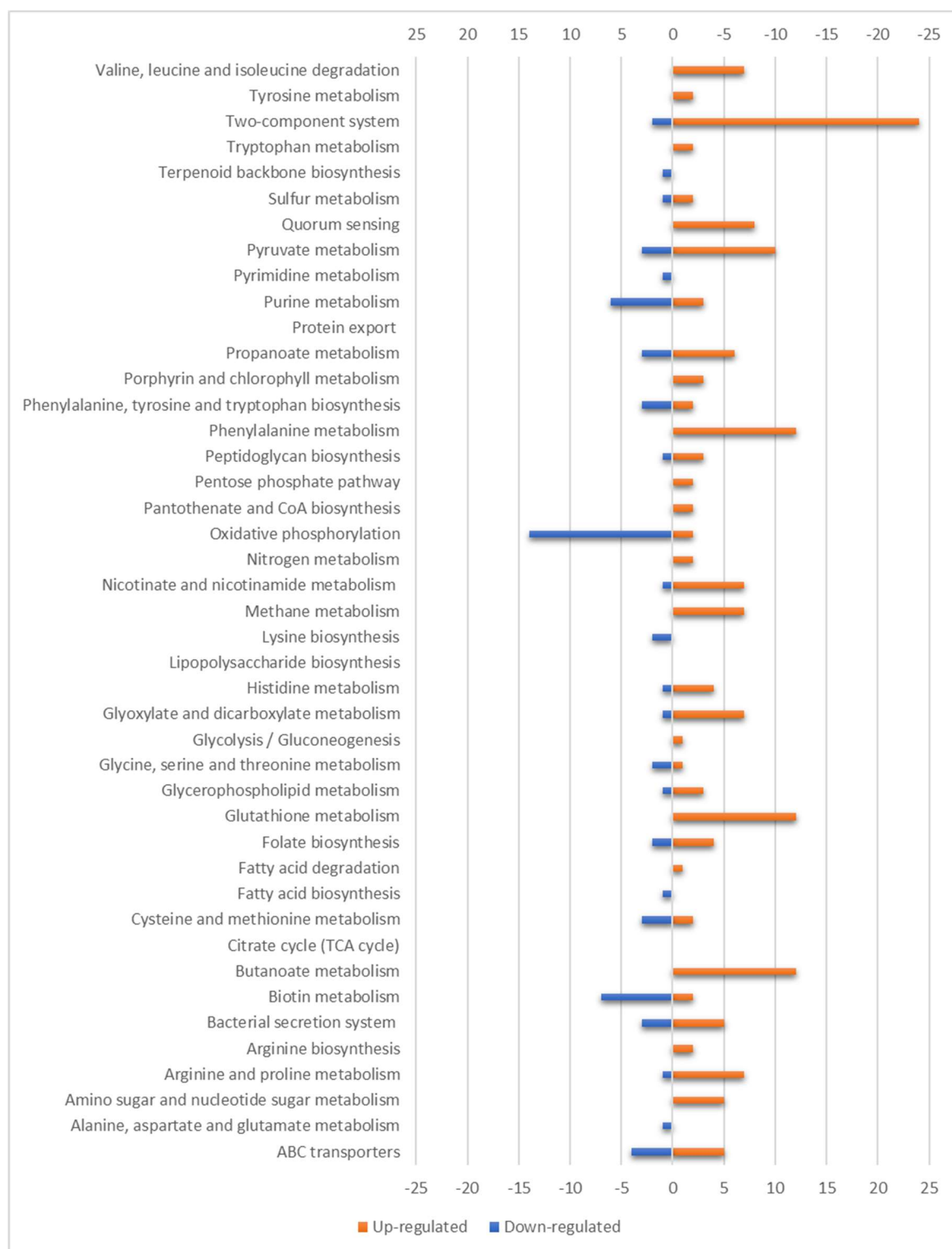


Figure 3.16: Cluster of orthologous genes (COG) classification of DEGs in LEP/MEP. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category. Using TPM values (the average of the replicates of the condition).

3.7.1.3 Functional Annotation of Differentially Expressed Genes (DEG)s in ESP/MEP

In ESP/MEP, the KEGG pathway analysis revealed that the DEGs were associated with 44 pathways, with two-component systems and ABC transporters dominating in up-regulation. The up-regulation of ABC transporters could reflect the fact that cells are running out of nutrients and that additional uptake systems are switched on in an attempt to increase nutrient uptake. As before when comparing LEP vs. MEP, oxidative phosphorylation dominating in down-regulation as cells go deeper into early stationary phase and slow in growth (Figure 3.17). Here again, biosynthetic pathways of amino acids are switched on, which could mean that cells run out of easily available nutrients they take up from the environment. In L-broth, this includes a lot of (oligo-)peptides which could be incorporated into proteins or used as carbon and nitrogen source. Once this supply runs out, cells will need to produce amino acids for protein production.

3.7.1.4 Functional Annotation of Differentially Expressed Genes (DEG)s in LSP/MEP

In LSP/MEP, the KEGG pathway analysis showed that the most up-regulated pathways were two-component systems and ABC transporters. The difference in two-component systems suggests that different TCS control specific gene sets that are needed during exponential phase and stationary phase. As cells run out of nutrient in stationary phase, the up-regulation of ABC transporters makes sense to uptake any nutrients from the environment. Although, roughly the same number of transporters are also down-regulated which could mean that some transporters are already produced and might not be needed in excess. A deeper analysis would be needed to show which transporters are expressed in which growth phase and whether the substrates are known. As before, when cells entered late exponential and early stationary phase, oxidative phosphorylation dominated in down-regulation because cell growth ceases (Figure 3.18).

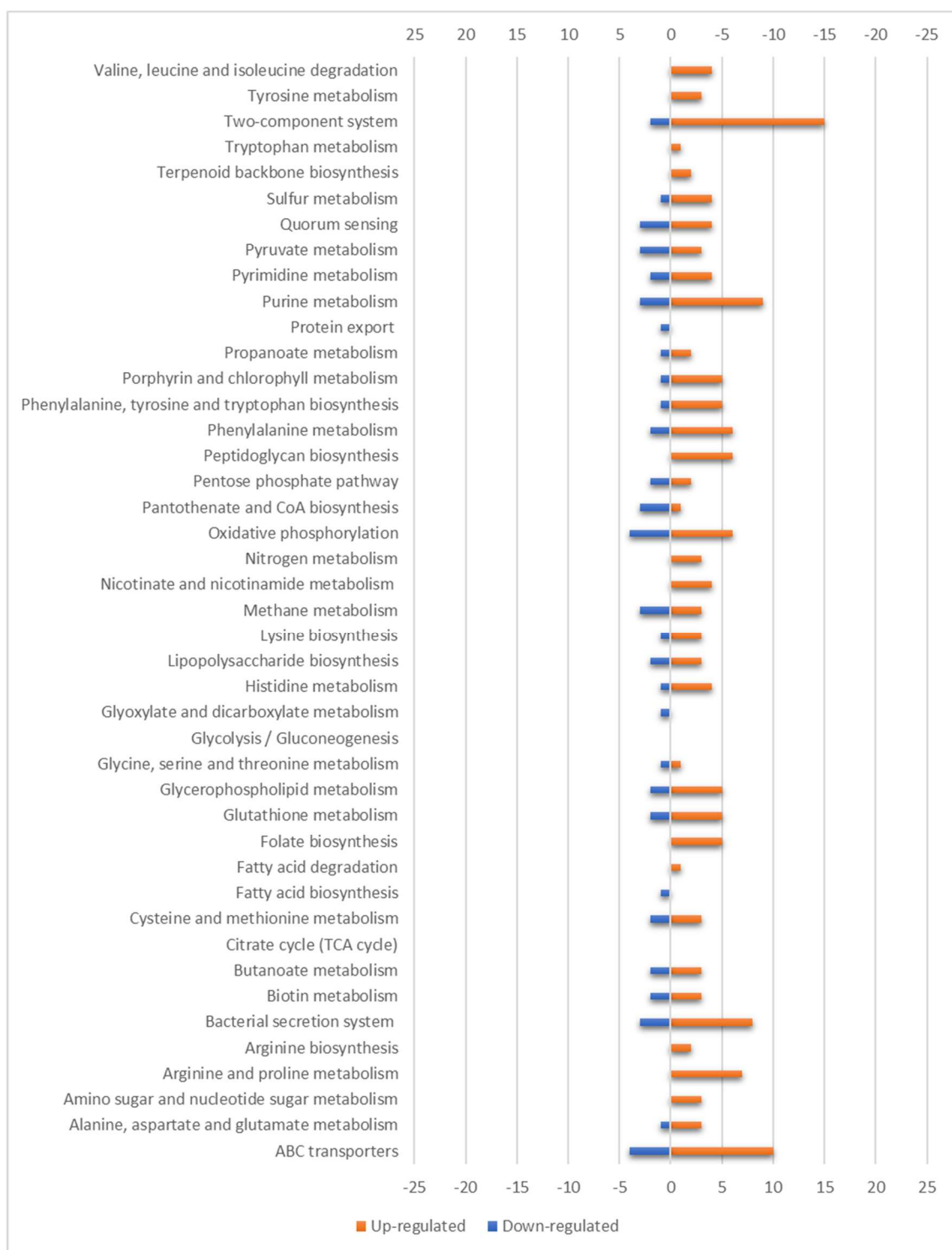


Figure 3.17: Cluster of orthologous genes (COG) classification of DEGs in ESP/MEP. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category. Using TPM values (the average of the replicates of the condition).

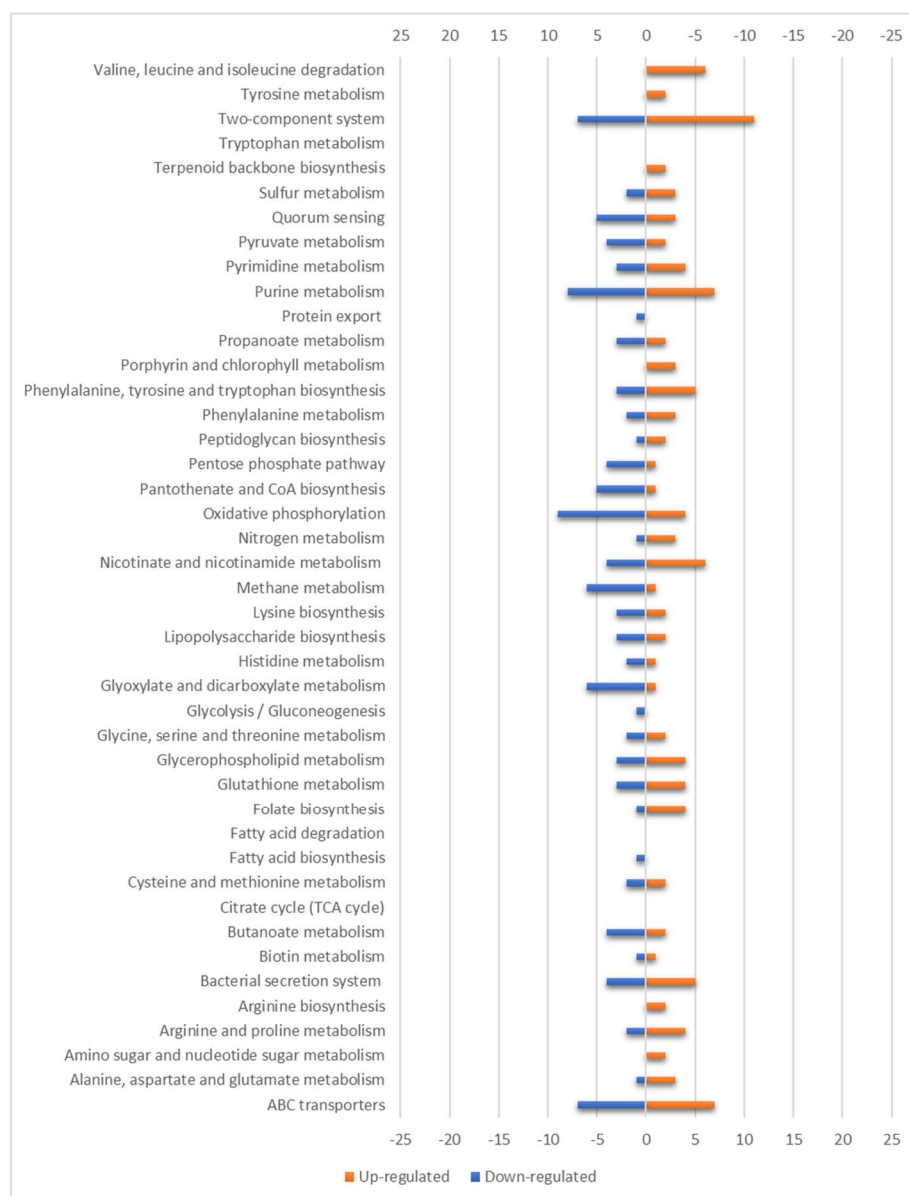


Figure 3.18: Cluster of orthologous genes (COG) classification of DEGs in LSP/MEP. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category using TPM values (the average of the replicates of the condition).

	Up-regulated				Down-regulated			
	EEp	LEp	ESp	SP	EEp	LEp	ESp	SP
ABC transporters		5	10	7		4	4	7
Alanine, aspartate and glutamate metabolism			3	3		1	1	1
Amino sugar and nucleotide sugar metabolism		5	3	2				
Arginine and proline metabolism		7	7	4		1		2
Arginine biosynthesis		2	2	2				
Bacterial secretion system		5	8	5		3	3	4
Biotin metabolism		2	3	1		7	2	1
Butanoate metabolism		12	3	2			2	4
Citrate cycle (TCA cycle)								
Cysteine and methionine metabolism		2	3	2		3	2	2
Fatty acid biosynthesis						1	1	1
Fatty acid degradation		1	1					
Folate biosynthesis		4	5	4		2		1
Glutathione metabolism		12	5	4			2	3
Glycerophospholipid metabolism		3	5	4		1	2	3
Glycine, serine and threonine metabolism		1	1	2		2	1	2
Glycolysis / Gluconeogenesis		1						1
Glyoxylate and dicarboxylate metabolism		7		1		1	1	6
Histidine metabolism		4	4	1		1	1	2
Lipopolysaccharide biosynthesis			3	2			2	3
Lysine biosynthesis			3	2		2	1	3
Methane metabolism		7	3	1			3	6
Nicotinate and nicotinamide metabolism		7	4	6		1		4
Nitrogen metabolism		2	3	3				1
Oxidative phosphorylation		2	6	4		14	4	9
Pantothenate and CoA biosynthesis		2	1	1			3	5
Pentose phosphate pathway		2	2	1			2	4
Peptidoglycan biosynthesis		3	6	2		1		1
Phenylalanine metabolism		12	6	3			2	2
Phenylalanine, tyrosine and tryptophan biosynthesis		2	5	5		3	1	3
Porphyrin and chlorophyll metabolism		3	5	3			1	
Propanoate metabolism		6	2	2		3	1	3
Protein export							1	1
Purine metabolism		3	9	7		6	3	8
Pyrimidine metabolism			4	4		1	2	3
Pyruvate metabolism		10	3	2		3	3	4
Quorum sensing		8	4	3			3	5
Sulfur metabolism		2	4	3		1	1	2
Terpenoid backbone biosynthesis			2	2		1		
Tryptophan metabolism		2	1					
Two-component system		24	15	11		2	2	7
Tyrosine metabolism		2	3	2				
Valine, leucine and isoleucine degradation		7	4	6				

Figure 3.19: Heat map shows numbers of genes associated with Cluster of orthologous genes (COG) classification that expressed in all growth phases.

3.7.2 Gene expression throughout shocks in AB5075

Bacterial transcriptomes are extremely responsive to changes in external and internal states. For example, when inoculated from spent to fresh, rich media, gene expression of hundreds of genes within 4-8 minutes (Rolfe *et al.*, 2012; Kröger *et al.*, 2013). Short (>10 min) exposures to different environmental conditions elevate the number of genes changing in expression (Kröger *et al.*, 2013), which is conserved in many bacterial pathogens (Avican *et al.*, 2021). In this study, *A. baumannii* AB5075 was exposed to four different environmental “shocks”: Osmotic shock (NaCl), iron limitation (LowFe) and antibiotic shocks (sub-inhibitory concentrations of chloramphenicol and tetracycline, Table 1.3). As above, transcriptome profiles of *A. baumannii* AB5075 cells in these different conditions were analysed by high-throughput sequencing. Cut-off values for gene expression fold change (FC) determined how many genes are up- or down-regulated per condition comparison. As the shocks were carried out at MEP, the data from the shocks were compared with MEP. Table 3.8 and Figure 3.20 show how many genes are up- or down-regulated in the different shock conditions compared to MEP.

Table 3.8: Numbers of genes up- and downregulated in NaCl, LowFe, Chl and Tet compared to the MEP growth condition. The numbers were calculated based on DESeq2 values.

Condition	No. of genes >2-fold up	No. of genes unchanged	No. of genes >2-fold down
NaCl	301 (7.5%)	3503 (86.8%)	230 (5.7%)
LowFe	307 (7.6%)	3515 (87.1%)	212 (5.3%)
Chl	1271 (31.5%)	1712 (42.4%)	1051 (26.1%)
Tet	1556 (38.6%)	1432 (35.5%)	1046 (25.9%)

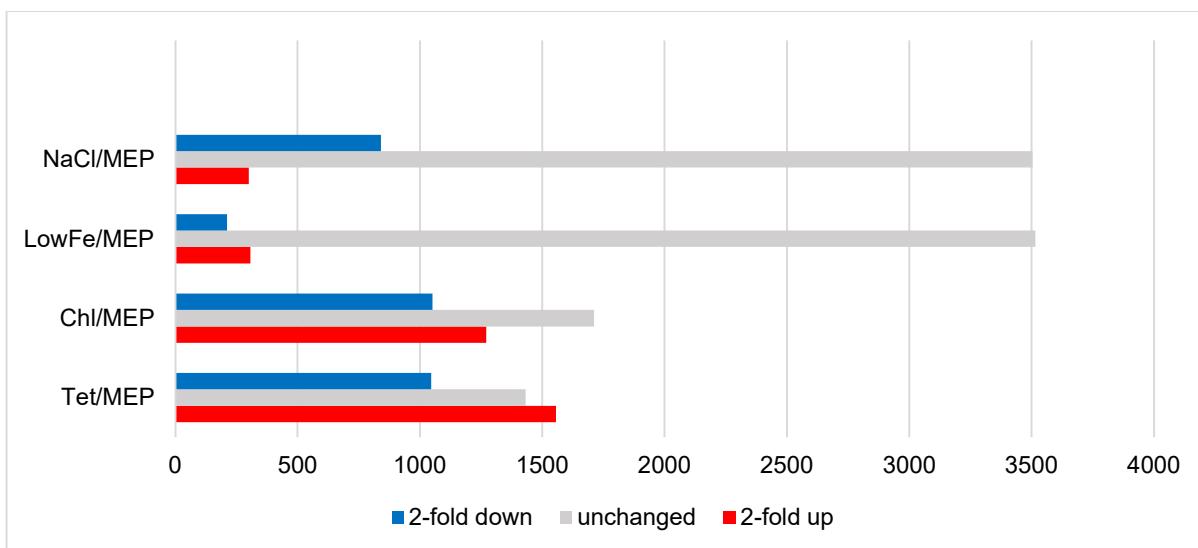


Figure 3.20: Gene expression changes in shock conditions. Using a cut-off value (DESeq2) of 2-fold in difference of gene expression, the bar chart shows the numbers of genes that are up- or downregulated or unchanged in NaCl, LowFe, Chl and Tet compared to the MEP growth condition.

Overall, we see that the transcriptional response to the changing environments is substantial, with 212-1556 genes changing in expression (using a 2-fold cut-off) across all conditions (Table 3.8 and Figure 3.20). The NaCl and LowFe conditions show similar number of genes changing (Figure 3.21, 3.22) with 301-307 up-regulated and 212-230 genes down-regulated. The two antibiotic shocks show gene expression changes to a much larger extent (Figure 3.23, 3.24) with 1271-1556 genes up-regulated and 1046-1051 genes down-regulated. This illustrates that the protein synthesis stress that the cells are exposed to in the antibiotic shocks require a much larger transcriptomic response to cope with the stress compared to the osmotic and iron limitation stress.

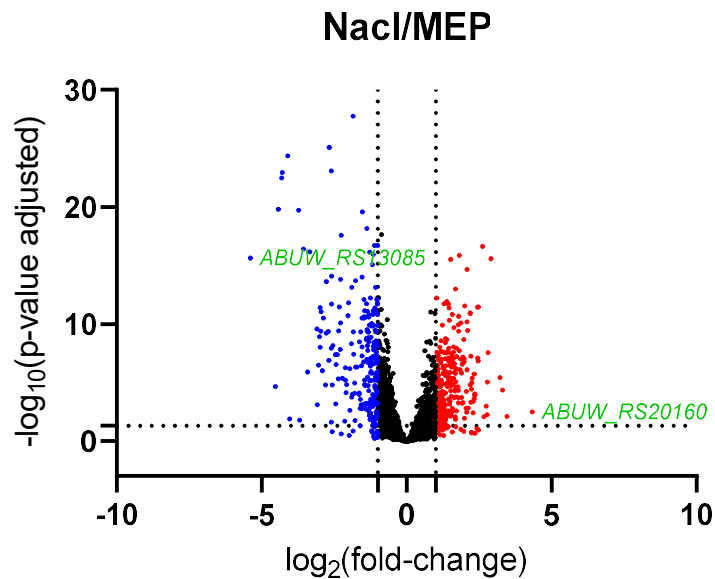


Figure 3.21: Volcano plot showing genes up- and down-regulated genes in NaCl vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the NaCl condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the NaCl condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005. 301 (7.5%) genes up- and 230 (5.7%) genes down-regulated out of 4034 genes in NaCl/MEP.

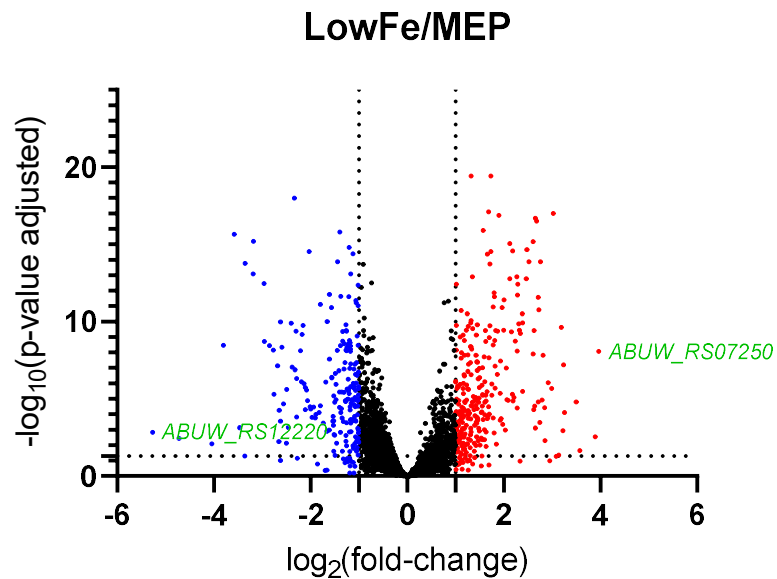


Figure 3.22: Volcano plot showing genes up- and down-regulated genes in LowFe vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the LowFe condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the LowFe condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005. 307 (7.6%) genes up- and 212 (5.3%) genes down-regulated out of 4034 genes in LowFe/MEP

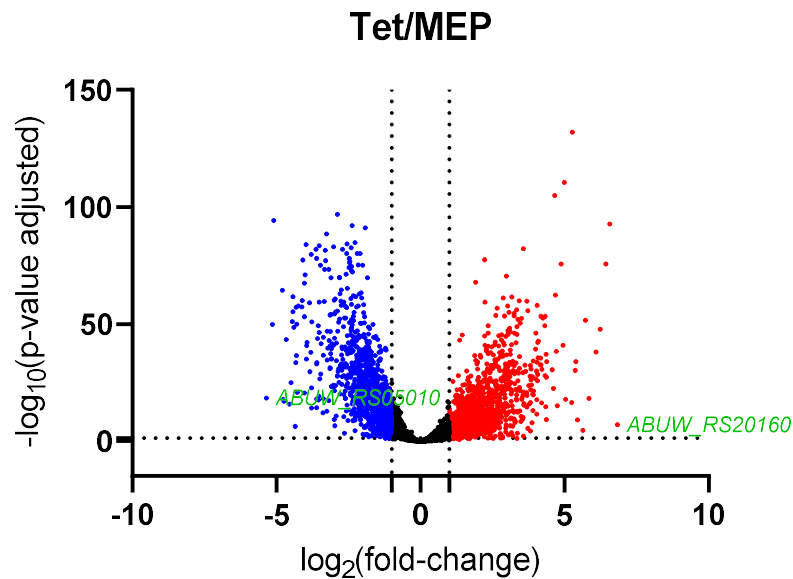


Figure 3.23: Volcano plot showing genes up- and down-regulated genes in Tet vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the Tet condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the Tet condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005. 1556 (38.6%) genes up- and 1046 (25.9%) genes down-regulated out of 4034 genes in in Tet/MEP

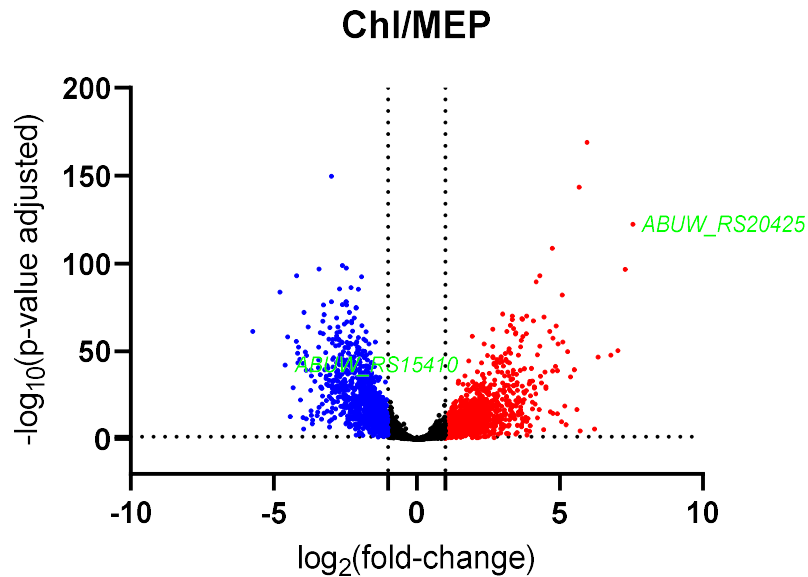


Figure 3.24: Volcano plot showing genes up- and down-regulated genes in Chl vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the Chl condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the Chl condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005. 1271 (31.5%) genes up- and 1051 (26.1%) genes down-regulated out of 4034 genes in in Chl/MEP

To obtain a first view of the genes with the largest fold-change in expression, which could indicate paramount biological importance, the top 10 genes that were up/down-regulated were calculated in each shock conditions (Table 3.9 and 3.10). The number of genes involved in the response between the different shocks conditions was overlapping between NaCl and LowFe, with seven genes up-regulated and eight down-regulated, while in antibiotic shocks (Tet and Chl) the number of genes up-regulated was seven genes and four down-regulated, indicating that these two conditions induce similar responses respectively. This is also illustrated in Figure 3.5 showing that NaCl and LowFe and Chl and Tet cluster closely, however, we also not condition-specific differences (described below). The most highly up-regulated gene in Tet and NaCl is a small pseudogene, called *ABUW_RS20160*, which has a frameshift in AB5075, which is also the 6th highest up-regulated gene in Chl and LowFe. The biological relevance of

this is doubtful, as the expression is overall at a very low level (TPM values of <30). Genes with annotated functions that stand out from this analysis are the high up-regulation of multiple genes of the fimbrial usher pathway (*csu* genes) in the osmotic shock and iron limitation conditions. In the LowFe condition, genes involved in iron uptake and metabolism (siderophore biosynthesis protein (*ABUW_RS10640*) and bacterioferritin-associated ferredoxin (*ABUW_RS01510*) are among the top10 most up-regulated genes, reflecting the response to iron depletion in the medium. These two genes were also up-regulated in the osmotic shock condition (i.e., among the top10), prompting us to compare the transcriptional response in the iron limitation and osmotic shock conditions in more depth (Figure 3.5, and see below).

Because the responses to in NaCl and LowFe and Chl and Tet were similar, respectively, we investigated more genes with annotated functions that were condition specific or with a similar transcriptional response below.

Chaperone-usher (Csu) pathway:

The Csu operon was highly upregulated in NaCl and LowFe shocks, and to a much higher extent as in LEP. However, as an exception, the Csu genes shows a different level of expression throughout the three biological replicates (Figure 3.25). The expression level in the biological replicate 2 is strongly elevated in comparison to biological replicates 1 and 3. The immediate reason for this is unclear, but it shows that the Csu pathway is transcriptionally repressed in most conditions and is only switched on under certain conditions. Whether these are NaCl and LowFe appears unlikely, because two of the three replicates do not show high up-regulation. This fact rather hints at a different level of transcriptional regulation such as mutation, epigenetic regulation, phase variation or a natural population heterogeneity. In any case, the study of the regulation appears to be an attractive target for future studies due to the clinical relevance of the Csu pathway.

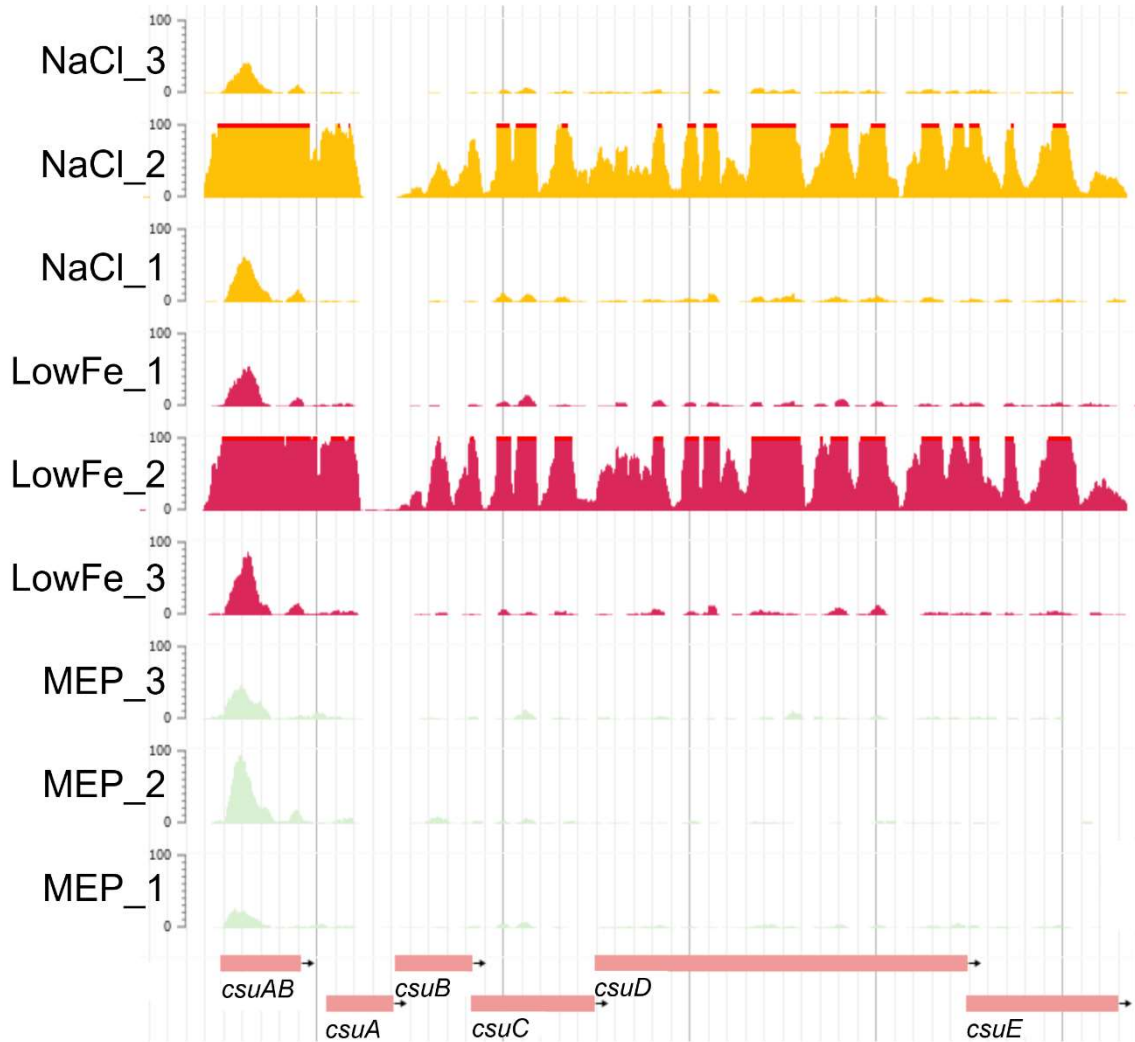


Figure 3.25: Heterogeneous up-regulation of *csu* genes in NaCl and LowFe compared to MEP only in biological replicate 2. Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number. The scale is 0-100 normalized reads for all tracks.

Acinetobactin biosynthesis and transport (Bas and Bau):

Iron uptake systems are essential to organisms ability to live in iron-deficient environments (Dorsey *et al.*, 2003; Vallenet *et al.*, 2008; Antunes *et al.*, 2014), Once *A. baumannii* is in an environment that is iron-deficient, it can generate siderophores like the acinetobactin (Dorsey *et al.*, 2003; Mihara *et al.*, 2004). There are eighteen genes (*bas* (biosynthesis) and *bau* (transport)) that make up the locus that is responsible for the synthesis, use, and secretion of acinetobactin. Within this gene group, there are

ten *bas* genes that are responsible for the synthesis of siderophores and six *bau* genes that are involved for the utilization of acinetobactin (Dorsey *et al.*, 2003; Mihara *et al.*, 2004; Vallenet *et al.*, 2008). Here several *bas* (e.g., *basF*, *basG*, *basJ*) and *bau* (*bauD*, *bauE*, *bauA*, *bauC*, (Figure 3.26) genes were upregulated in NaCl and LowFe shocks indicating that *A. baumannii* up-regulates systems to acquire iron in both NaCl and LowFe. In the case of LowFe, this appears logical, whereas the up-regulation in the NaCl conditions is more surprising. It is possible that in osmotic pressure is an additional signal for *A. baumannii* to detect that it is inside the host (the concentration of sodium in human serum is 136-146 mM).

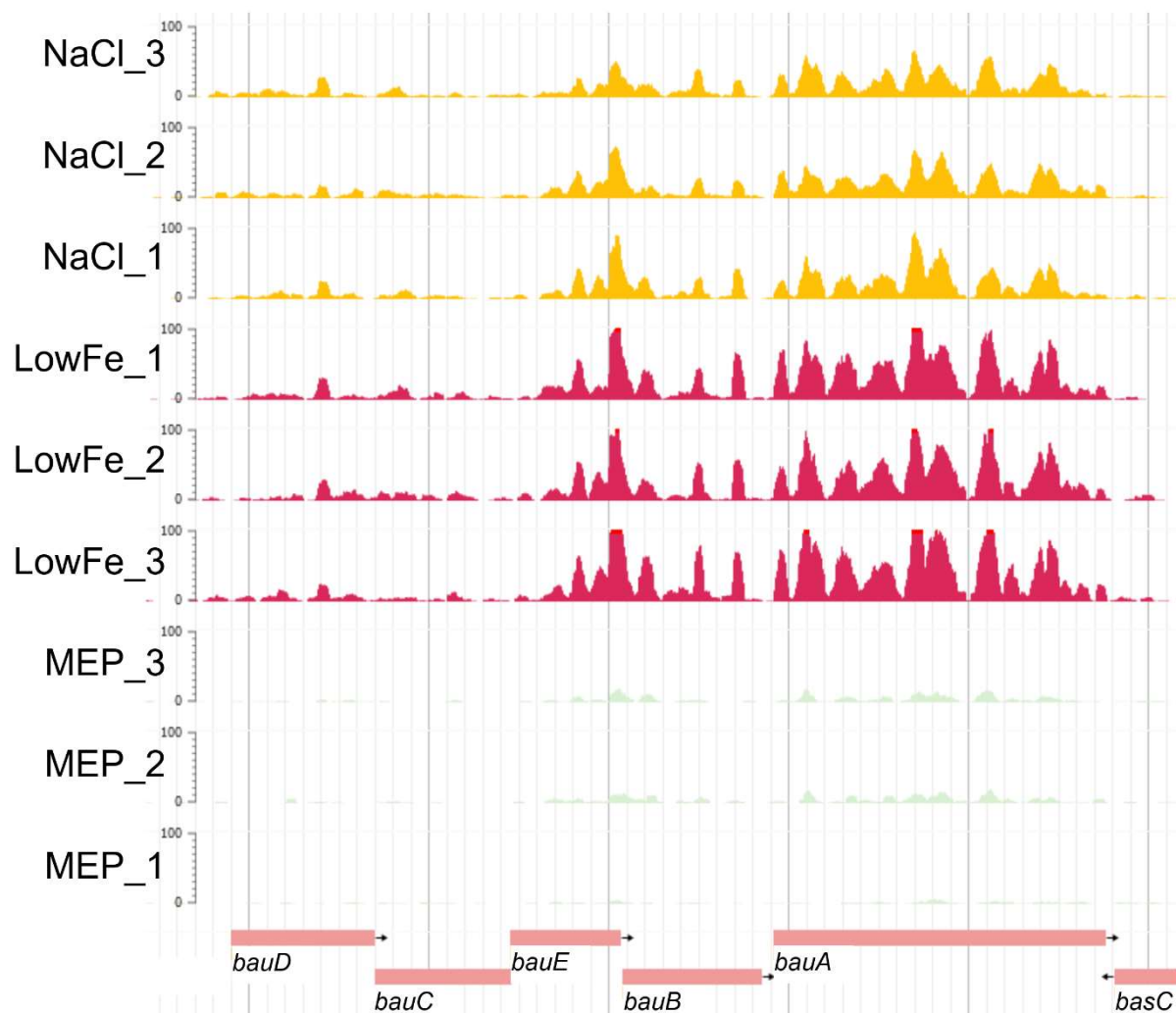


Figure 3.26: Up-regulation of *bau* genes in NaCl and LowFe compared to MEP. Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number. The scale is 0-100 normalized reads for all tracks.

Cysteine metabolism/sulfur assimilation (Cys):

The *cys* genes have been shown to be important for *A. baumannii* in multiple physiological and virulence traits (Wang *et al.*, 2014; Gebhardt *et al.*, 2015). It has been demonstrated that cysteine biosynthesis is necessary for the progression of an *A. baumannii* infection, which implicates cysteine biosynthesis as a possible target for therapeutic intervention in the fight against this increasingly dangerous disease (Gebhardt *et al.*, 2020). Here, we see the operon consisting of *ABUW_RS05010*, *ABUW_RS05005* (both annotated as sulfate ABC transporter substrate-binding protein), *cysT* (sulfate ABC transporter permease subunit), *cysW* (sulfate ABC transporter permease subunit) and *ABUW_RS04990* (sulfate ABC transporter ATP-binding protein) was downregulated in all shocks.

Table 3.9: Top 10 upregulated genes in different shocks conditions

Condition	1	2	3	4	5	6	7	8	9	10
NaC/MEP	ABUW_RS20160 hypothetical protein	ABUW_RS07250 Csu fimbrial major subunit CsuAB	ABUW_RS07270 Csu fimbrial usher CsuD	ABUW_RS07275 Csu fimbrial tip adhesin CsuE	ABUW_RS07265 Csu fimbrial biogenesis chaperone CsuC	ABUW_RS01510 bacterioferritin-associated ferredoxin	ABUW_RS10640 siderophore biosynthesis protein	ABUW_RS18405 acyl-CoA dehydrogenase family protein	ABUW_RS01275 SDR family NAD(P)-dependent oxidoreductase	ABUW_RS13520 Paal family thioesterase
LowFe/MEP	ABUW_RS07250 Csu fimbrial major subunit CsuAB	ABUW_RS07270 Csu fimbrial usher CsuD	ABUW_RS07275 Csu fimbrial tip adhesin CsuE	ABUW_RS10640 siderophore biosynthesis protein	ABUW_RS07265 Csu fimbrial biogenesis chaperone CsuC	ABUW_RS020160 hypothetical protein	ABUW_RS01510 bacterioferritin-associated ferredoxin	ABUW_RS05760 (2,3-dihydroxybenzoyl)adenylate synthase Base	ABUW_RS10635 Sida/lucD/Pda family monooxygenase	ABUW_RS10070 transcriptional repressor
Tet/MEP	ABUW_RS20160 hypothetical protein	ABUW_RS20425 hypothetical protein	ABUW_RS03205 RtcB family protein	ABUW_RS19345 molecular chaperone DnaJ	ABUW_RS09950 hypothetical protein	ABUW_RS12725 hypothetical protein	ABUW_RS12675 TetR/AcrR family transcriptional regulator	ABUW_RS09900 hypothetical protein	ABUW_RS13120 four-helix bundle copper-binding protein	ABUW_RS09895 replication initiation factor domain-containing protein
Chi/MEP	ABUW_RS20425 hypothetical protein	ABUW_RS03205 RtcB family protein	ABUW_RS09950 hypothetical protein	ABUW_RS13120 four-helix bundle copper-binding protein	ABUW_RS09900 hypothetical protein	ABUW_RS20160 hypothetical protein	ABUW_RS09895 replication initiation factor domain-containing protein	ABUW_RS09945 replication initiation factor domain-containing protein	ABUW_RS19345 molecular chaperone DnaJ	ABUW_RS11250 fimbrial protein

Table 3.10: Top 10 downregulated genes in different shocks conditions

Condition	1	2	3	4	5	6	7	8	9	10
NaC/MEP	ABUW_RS13085 transposase	ABUW_RS12225 cold-shock protein	ABUW_RS13055 cold-shock protein	ABUW_RS12115 NAD(P)H-dependent oxidoreductase	ABUW_RS01870 DEAD/DEAH box helicase	ABUW_RS11615 hypothetical protein	ABUW_RS20235 hypothetical protein	ABUW_RS14420 transcriptional regulator BetI	ABUW_RS12220 hypothetical protein	ABUW_RS14425 betaine-aldehyde dehydrogenase
LowFe/MEP	ABUW_RS12220 hypothetical protein	ABUW_RS20235 hypothetical protein	ABUW_RS06950 GNAT family N-acetyltransferase	ABUW_RS13085 transposase	ABUW_RS01870 DEAD/DEAH box helicase	ABUW_RS20210 hypothetical protein	ABUW_RS12115 NAD(P)H-dependent oxidoreductase	ABUW_RS14425 betaine-aldehyde dehydrogenase	ABUW_RS11615 hypothetical protein	ABUW_RS14420 transcriptional regulator BetI
Tet/MEP	ABUW_RS05010 sulfate ABC transporter substrate-binding protein	ABUW_RS16540 TonB-dependent siderophore receptor	ABUW_RS05005 alpha/beta hydrolase	ABUW_RS15410 NADH-quinone oxidoreductase subunit Nuof	ABUW_RS11590 taurine ABC transporter substrate-binding protein	ABUW_RS14445 homocysteine S-methyltransferase family protein	ABUW_RS15395 NADH-quinone oxidoreductase subunit Nuol	ABUW_RS15390 NADH-quinone oxidoreductase subunit J	ABUW_RS15405 NADH-quinone oxidoreductase subunit Nuog	ABUW_RS20210 hypothetical protein
Chi/MEP	ABUW_RS15410 NADH-quinone oxidoreductase subunit Nuof	ABUW_RS05010 sulfate ABC transporter substrate-binding protein	ABUW_RS13140 heavy-metal-associated domain-containing protein	ABUW_RS15390 NADH-quinone oxidoreductase subunit J	ABUW_RS05245 peptidylprolyl isomerase	ABUW_RS15395 NADH-quinone oxidoreductase subunit Nuol	ABUW_RS15405 NADH-quinone oxidoreductase subunit Nuog	ABUW_RS15385 NADH-quinone oxidoreductase subunit Nuok	ABUW_RS15400 NADH-quinone oxidoreductase subunit Nuoh	ABUW_RS12115 NAD(P)H-dependent oxidoreductase

Type 6 Secretion System (*tss* genes):

The genes that code for the 13 core proteins necessary for T6SS apparatus assembly are all clustered inside a single locus in the vast majority of bacterial species that are capable of producing a functional T6SS. In addition, the T6SS locus contains genes that code for proteins that are hypothesized to play accessory, regulatory, or effector roles within the T6SS complex. The T6SS locus is comprised of 18 genes in the majority of *A. baumannii* strains (Henry *et al.*, 2012; Weber *et al.*, 2013). Homologs of the conserved core components TssB, TssC, Hcp (also known as TssD), TssE, TssF, TssG, TssM, TssH (also known as ClpV), TssA, TssK, and TssL are encoded by these genes (Aschtgen *et al.*, 2008; Weber *et al.*, 2013). Here the genes *tssB*, *tssC*, *hcp*, *tssE*, *tssF* and *tssG* were upregulated in antibiotic shocks (Tet and Chl). Perhaps, exposure to antibiotic stress, which is potentially quickly lethal to a subset of the population provokes a response to quickly kill a nearby antibiotic producing, hostile bacteria or other microorganisms as a defense mechanism. Surprisingly, other T6SS-related genes (i.e., *tssM*, *tagF*, *tssH*, *tssA*, *tssK*) did not show an up-regulation, which suggests that they are regulated at the transcriptional level in a different way.

NADH-quinone oxidoreductase (*nuo* genes)

NADH-quinone oxidoreductase is an enzyme that is essential for oxidative phosphorylation and catalyzes the transfer of electrons from NADH to quinone in the cytoplasmic membrane. This is necessary for the formation of the proton gradient across the cytoplasmic membrane, which is required to produce energy storage molecules such as ATP via the ATP synthetase. All annotated *nuo* genes that each encode a subunit of the enzyme (Brandt, 2006) showed strong down-regulation only in antibiotic shocks (Figure 3.27). This could suggest that cells enter a growth arrest to deal with the protein biosynthesis stress caused by the antibiotics. In addition, down-regulation of NADH-quinone oxidoreductase could result in a reduced proton gradient across the cytoplasmic membrane which might inhibit transporters that rely on the proton gradient and reduce uptake of additional antibiotics.

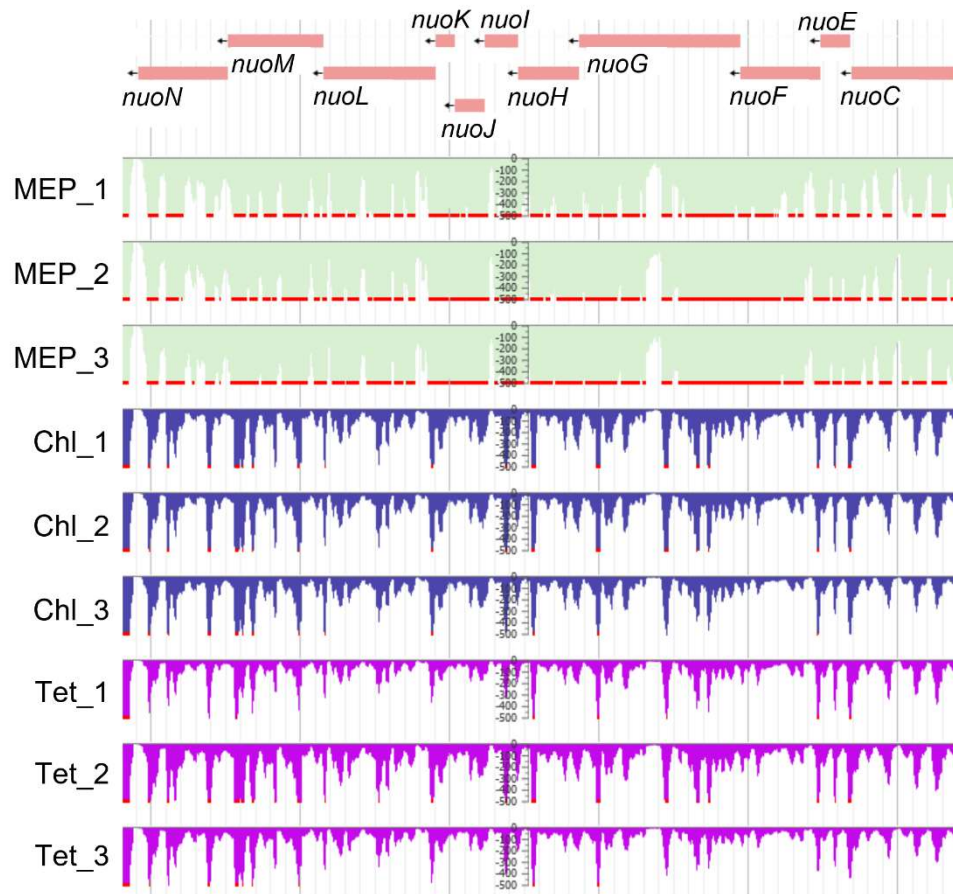


Figure 3.27: Down-regulation of *nuo* genes in Chl and Tet compared to MEP. Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number. The scale is 0-500 normalized reads for all tracks.

Bacterioferritin (*bfr*)

Bacterioferritin (Bfr) is a spherical protein that is unique to bacteria and can store up to around 3000 Fe^{3+} ions in its internal cavity, which has a diameter of approximately 80 microns (Weeratunga *et al.*, 2010; Rivera, 2017). Surprisingly, here the *bfr* was downregulated in LowFe.

3.7.2.1 NaCl/MEP vs LowFe/MEP

The results from above showing that the response to osmotic stress and iron limitation were somewhat similar prompted us to compare these two responses in more detail. The differential gene expression analysis in NaCl/MEP vs LowFe/MEP showed that 531 genes were expressed in NaCl/MEP (Figure 3.28 and 3.29) including 301 genes that were upregulated, and 230 genes that were downregulated. While in LowFe/MEP 519 genes were expressed (Figure 3.32 and 3.33), including 307 genes that were upregulated and 212 genes that were downregulated. 397 genes were overlap differentially expressed between NaCl/MEP vs LowFe/MEP.

		NaCl vs MEP	
		Differentially Expressed	Differentially Non-Expressed
LowFe vs MEP	Differentially Expressed	397	124
	Differentially Non-Expressed	134	3379

Figure 3.28: Differential gene expression analysis in NaCl/MEP vs LowFe/MEP using DESeq2 values that showing numbers of genes differentially expressed and differentially non-expressed.

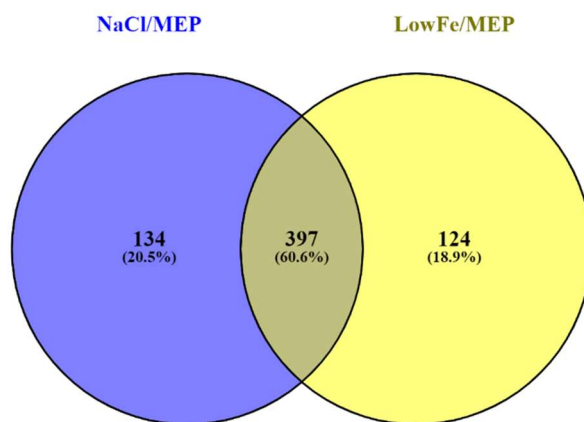


Figure 3.29: Venn diagram illustrate the overlap genes that differentially expressed between **NaCl/MEP** (blue circle) and **LowFe/MEP** (yellow circle) using DESeq2 values, 397 genes were overlapped.

3.7.2.2 Functional Annotation of Differentially Expressed Genes (DEG)s in NaCl/MEP

In NaCl/MEP, the KEGG pathway analysis showed that the DEGs were associated with 44 pathways, with arginine and proline metabolism and purine metabolism dominating in upregulation and pyruvate metabolism dominating in downregulation (Figure 3.30).

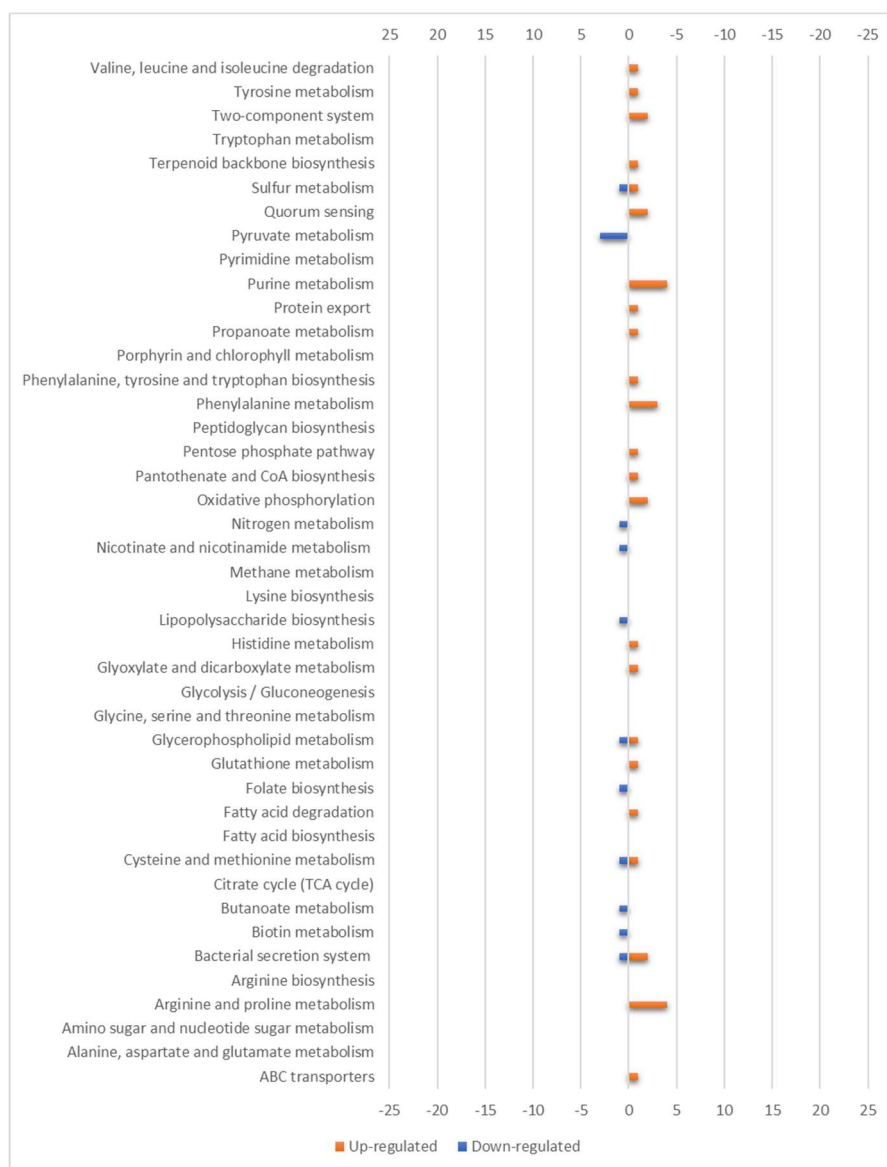


Figure 3.30: Cluster of orthologous genes (COG) classification of DEGs in NaCl/MEP. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category. Using TPM values (the average of the replicates of the condition and considering all values below 10 equals to 10).

3.7.2.3 Functional Annotation of Differentially Expressed Genes (DEG)s in LowFe/MEP

In LowFe/MEP, the KEGG pathway analysis showed that the DEGs were associated with 44 pathways, with arginine and proline metabolism and bacterial secretion systems dominating in upregulation and pyruvate metabolism dominating in downregulation (Figure 3.31).



Figure 3.31: Cluster of orthologous genes (COG) classification of DEGs in LowFe/MEP. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category. Using TPM values (the average of the replicates of the condition and considering all values below 10 equals to 10).

3.7.2.4 Tet/MEP vs Chl/MEP

Similar to the comparison between the osmotic and iron limitation responses, the response to exposure to sub-inhibitory antibiotics that both inhibit the protein biosynthesis by binding to the ribosome, were similar and they overall clustered closely (refer to Figure above, heatmap with conditions). Overall, the response was more pronounced in the antibiotic shocks compared to the NaCl and LowFe conditions as more genes were differentially expressed. Analysis of differential gene expression between Tet/MEP and Chl/MEP revealed that there was a large overlap in the responses. 2014 differentially expressed overlapped (1102 genes up-regulated and 911 genes down-regulated overlap).

The responses (for example: *ABUW_RS06230* (hypothetical protein), *ABUW_RS14595* (single-stranded DNA-binding protein) and only for example: *ABUW_RS04200* (flavodoxin family protein) were not identical though. We found seven up-regulated gene in Tet/MEP that were down-regulated in Chl/MEP and, conversely, two genes were down-regulated in Tet/MEP that were upregulated in Chl/MEP.

		Tet vs MEP	
		Differentially Expressed	Differentially Non-Expressed
Chl vs MEP	Differentially Expressed	2014	308
	Differentially Non-Expressed	288	1424

Figure 3.32: Differential gene expression analysis in Tet/MEP vs Chl/MEP using DESeq2 values that showing numbers of genes differentially expressed and differentially non-expressed.

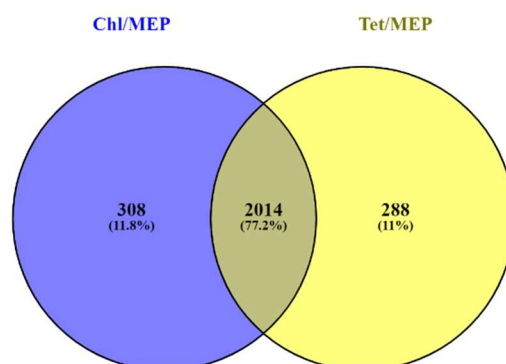


Figure 3.33: Venn diagram illustrate the overlap genes that differentially expressed between Chl/MEP (blue circle) and Tet/MEP (yellow circle) using DESeq2 values, 2014 genes were overlapped.

3.7.2.5 Functional Annotation of Differentially Expressed Genes (DEGs) in Tet/MEP

In Tet/MEP, the KEGG pathway analysis showed that the DEGs were associated with 44 pathways, with purine metabolism dominating in upregulation and oxidative phosphorylation dominating in downregulation (Figure 3.34).

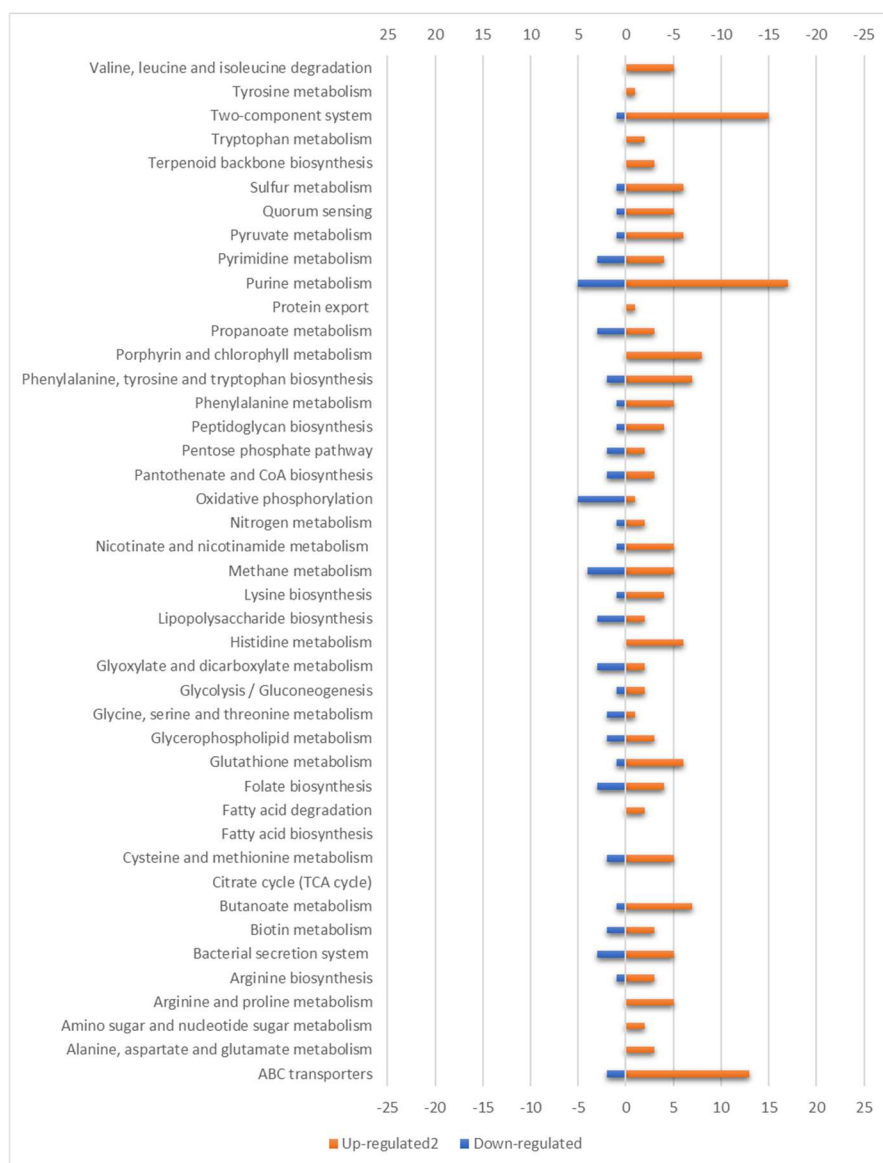


Figure 3.34: Cluster of orthologous genes (COG) classification of DEGs in Tet/MEP. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category. Using TPM values (the average of the replicates of the condition and considering all values below 10 equals to 10).

3.7.2.6 Functional Annotation of Differentially Expressed Genes (DEG)s in Chl/MEP

In Chl/MEP, the KEGG pathway analysis showed that the DEGs were associated with 44 pathways, with purine metabolism dominating in upregulation and oxidative phosphorylation dominating in downregulation (Figure 3.35).

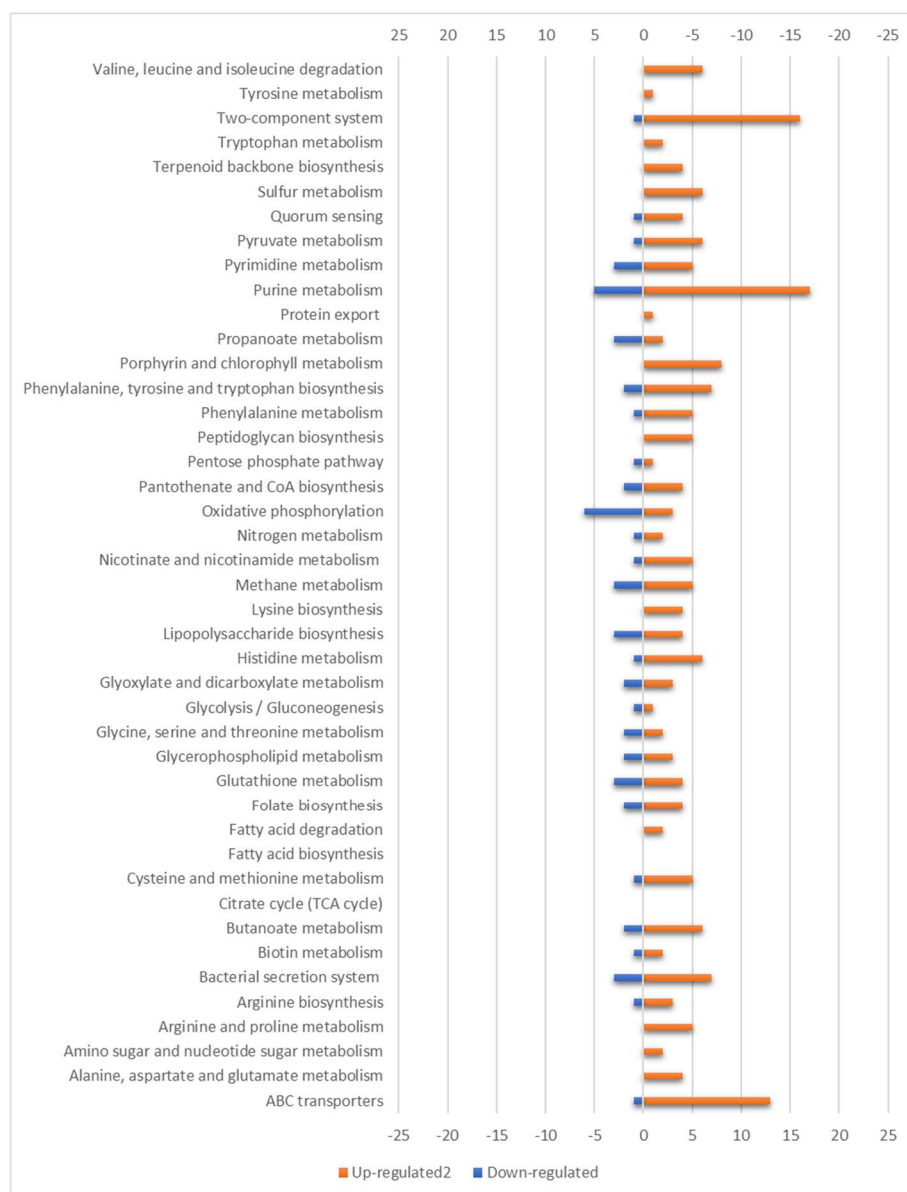


Figure 3.35: Cluster of orthologous genes (COG) classification of DEGs in Chl/MEP. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category. Using TPM values (the average of the replicates of the condition and considering all values below 10 equals to 10).

	Up-regulated				Down-regulated			
	NaCl	LowFe	Tet	Chl	NaCl	LowFe	Tet	Chl
ABC transporters	1	1	13	13			2	1
Alanine, aspartate and glutamate metabolism			3	4				
Amino sugar and nucleotide sugar metabolism			2	2				
Arginine and proline metabolism	4	3	5	5				
Arginine biosynthesis		1	3	3			1	1
Bacterial secretion system	2	3	5	7	1		3	3
Biotin metabolism			3	2	1	1	2	1
Butanoate metabolism			7	6	1		1	2
Citrate cycle (TCA cycle)								
Cysteine and methionine metabolism	1		5	5	1	1	2	1
Fatty acid biosynthesis								
Fatty acid degradation	1	1	2	2				
Folate biosynthesis		1	4	4	1	1	3	2
Glutathione metabolism	1	1	6	4			1	3
Glycerophospholipid metabolism	1	1	3	3	1	1	2	2
Glycine, serine and threonine metabolism		1	1	2			2	2
Glycolysis / Gluconeogenesis			2	1			1	1
Glyoxylate and dicarboxylate metabolism	1		2	3			3	2
Histidine metabolism	1	2	6	6				1
Lipopolysaccharide biosynthesis		1	2	4	1	1	3	3
Lysine biosynthesis		1	4	4			1	
Methane metabolism			5	5		1	4	3
Nicotinate and nicotinamide metabolism			5	5	1	1	1	1
Nitrogen metabolism			2	2	1	1	1	1
Oxidative phosphorylation	2	2	1	3			5	6
Pantothenate and CoA biosynthesis	1		3	4			2	2
Pentose phosphate pathway	1	1	2	1			2	1
Peptidoglycan biosynthesis			4	5			1	
Phenylalanine metabolism	3	2	5	5			1	1
Phenylalanine, tyrosine and tryptophan biosynthesis	1	1	7	7			2	2
Porphyrin and chlorophyll metabolism			8	8				
Propanoate metabolism	1	1	3	2			3	3
Protein export	1	1	1	1				
Purine metabolism	4	2	17	17			5	5
Pyrimidine metabolism			4	5			3	3
Pyruvate metabolism			6	6	3	3	1	1
Quorum sensing	2	2	5	4		1	1	1
Sulfur metabolism	1	1	6	6	1	1	1	
Terpenoid backbone biosynthesis	1	1	3	4				
Tryptophan metabolism			2	2				
Two-component system	2	3	15	16			1	1
Tyrosine metabolism	1	1	1	1				
Valine, leucine and isoleucine degradation	1	1	5	6				

Figure 3.36: Heat map shows numbers of genes associated with Cluster of orthologous genes (COG) classification that expressed in shocks conditions

3.7.3 Gene expression throughout different temperatures in AB5075

To mimic transitions from ambient to body temperature and back, *A. baumannii* AB5075 was grown at ambient temperature and two temperature shifts were performed: AT, Col and TS (Table 3.1). As above, the transcriptome profiles of *A. baumannii* AB5075 were analysed by RNA-sequencing. We performed DESeq2 to determine which genes are expressed at different levels between heat shocks conditions by taking the normalized read count data and performing statistical analysis to discover quantitative changes in expression levels between experimental groups. Ambient temperature growth at 22°C (AT) and cold shock (37°C → 22°C, Col) conditions were compared with MEP (37°C) and AT (22°C) compared again with TS (22°C → 37°C). Table 3.11 and Figure 3.37 show how many genes are up- or down-regulated per comparison of the different conditions and temperature transitions. Overall, we see that there are quite large changes to the transcriptome in all comparisons (12-19% of genes are changing expression >2-fold). The transcriptome signatures are distinct for each condition, however, AT and TS cluster more closely together, and likewise CS and MEP (Figure 3.5).

Table 3.11: Numbers of genes up- and downregulated in AT, Col compared to the MEP growth condition and TS compared to AT. The numbers were calculated based on DESeq2 values.

Comparisons	No. of genes > 2-fold up- regulated	No. of genes unchanged	No. of genes > 2-fold down- regulated
AT/MEP	590 (14.6%)	2920 (72.4%)	524 (13%)
Col/MEP	564 (14%)	2984 (74%)	486 (12%)
TS/MEP	757 (18.8%)	2685 (66.6%)	592 (14.6%)

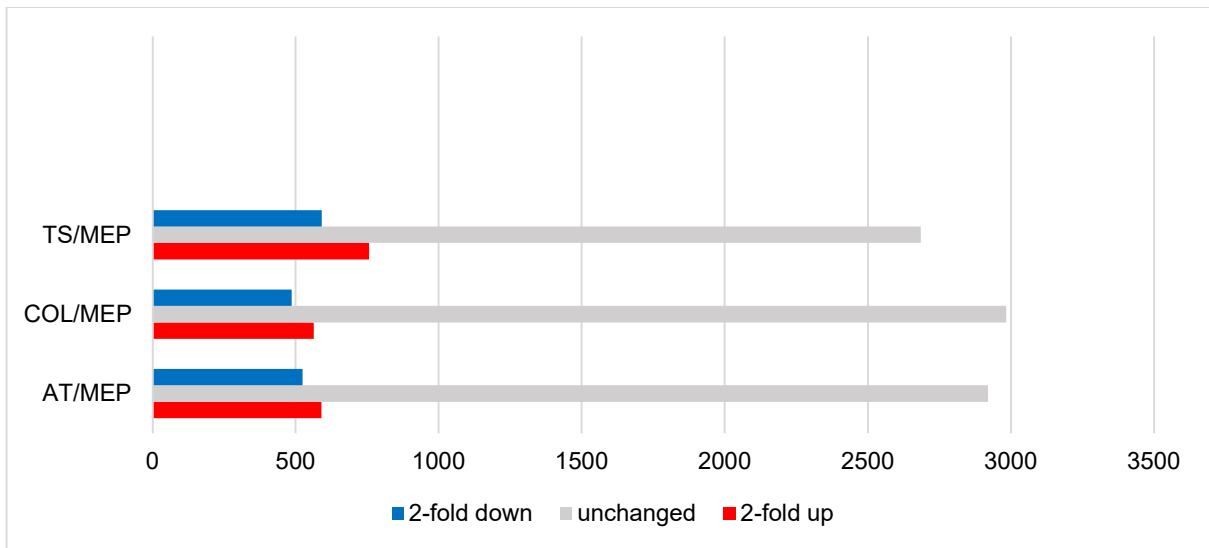


Figure 3.37: Gene expression changes in temperature shocks. Using a cut-off value (DESeq2) of 2-fold in difference of gene expression, the bar chart shows the numbers of genes that are up- or downregulated or unchanged in AT and Col, compared to the MEP growth, TS compared to AT.

Table 3.12: Top 10 upregulated genes in temperatures shocks conditions

Condition	1	2	3	4	5	6	7	8	9	10
AT/MEP	ABUW_RS12725 hypothetical protein	ABUW_RS01140 hypothetical protein	ABUW_RS10025 hypothetical protein	ABUW_RS12975 hypothetical protein	ABUW_RS07960 spore coat protein U domain-containing protein	ABUW_RS07180 hypothetical protein	ABUW_RS20475 hypothetical protein	ABUW_RS07360 acyl-CoA desaturase	ABUW_RS07145 DUF2171 domain-containing protein	ABUW_RS11885 hypothetical protein
AT/TS	ABUW_RS20475 hypothetical protein	ABUW_RS07145 DUF2171 domain-containing protein	ABUW_RS07170 NirD/YgiW/Ydel family stress tolerance protein	ABUW_RS11875 hypothetical protein	ABUW_RS11850 glucose 1-dehydrogenase	ABUW_RS11870 hypothetical protein	ABUW_RS07960 spore coat protein U domain-containing protein	ABUW_RS00260 DUF1328 domain-containing protein	ABUW_RS11840 stress-induced protein	ABUW_RS10025 hypothetical protein
Col/MEP	ABUW_RS07255 Csu fimbrial biogenesis protein CsuA	ABUW_RS07275 Csu fimbrial tip adhesin CsuE	ABUW_RS07270 Csu fimbrial usher CsuD	ABUW_RS07260 Csu fimbrial biogenesis protein CsuB	ABUW_RS07265 Csu fimbrial biogenesis chaperone CsuC	ABUW_RS07250 Csu fimbrial major subunit CsuAB	ABUW_RS00335 VOC family protein	ABUW_RS00340 maleylacetate isomerase	ABUW_RS13090 tRNA-Met	ABUW_RS12225 cold-shock protein

Table 3.13: Top 10 downregulated genes in temperatures shocks conditions

Condition	1	2	3	4	5	6	7	8	9	10
AT/MEP	ABUW_RS11280 PACE efflux transporter	ABUW_RS08010 hypothetical protein	ABUW_RS02010 hypothetical protein	ABUW_RS12115 NAD(P)H-dependent oxidoreductase	ABUW_RS08030 TetR/AcrR family transcriptional regulator	ABUW_RS05010 sulfate ABC transporter substrate-binding protein	ABUW_RS05005 alpha/beta hydrolase	ABUW_RS11590 taurine ABC transporter substrate-binding protein	ABUW_RS16080 ribosome silencing factor	ABUW_RS14420 transcriptional regulator BelI
AT/TS	ABUW_RS01495 pilin	ABUW_RS08010 hypothetical protein	ABUW_RS01430 PilN domain-containing protein	ABUW_RS01870 DEAD/DEAH box helicase	ABUW_RS01440 pilus assembly protein PilP	ABUW_RS01435 type 4a pilus biogenesis protein PilO	ABUW_RS08615 PEGA domain-containing protein	ABUW_RS01545 type IV pilus modification protein PilV	ABUW_RS17275 type II secretion system F family protein	ABUW_RS17270 type IV-A pilus assembly ATPase PilB
Col/MEP	ABUW_RS17440 outer membrane beta-barrel protein	ABUW_RS11590 taurine ABC transporter substrate-binding protein	ABUW_RS12115 NAD(P)H-dependent oxidoreductase	ABUW_RS11280 PACE efflux transporter	ABUW_RS08745 hypothetical protein	ABUW_RS06555 YfhL family 4Fe-4S cluster ferredoxin	ABUW_RS16540 TonB-dependent siderophore receptor	ABUW_RS11585 ATP-binding cassette domain-containing protein	ABUW_RS18450 D-amino acid dehydrogenase	ABUW_RS08740 cytochrome ubiquinol oxidase subunit I

Analyzing individual comparisons, we first investigated genes with an annotated function and the ten genes that showed highest differential gene expression (Table 3.12, 3.13).

Ambient temperature vs. MEP

The comparison between growth at ambient (22°C) temperature and mammalian host temperature (37°C) is not a comparison of “shock” conditions, but a comparison of genes expressed during fast growth of *A. baumannii* at the two different temperatures (measured both at OD 0.3, Figure 3.38). Genes considered up-regulated represent genes at higher gene expression at ambient temperature compared to 37°C. Of the top10 up-regulated genes, most genes are hypothetical or with predicted, but biologically non-confirmed functions. For the top10 down-regulated genes, there are a few genes that have annotated functions, including three transporter(-associated) genes (*ABUW_RS11280* (PACE efflux transporter), and *ABUW_RS05010* (sulfate ABC transporter substrate-binding protein) and *tauA* (taurine ABC transporter substrate-binding protein).

Temperature up-shift (TS)

We anticipated that a temperature shift from ambient (22°C) to body temperature (37°C) would up- and down-regulate genes that are relevant for host infection, pathogenicity and/or colonization (Figure 3.39). We first analyzed genes from the list of up- and down-regulated genes that had an annotated function.

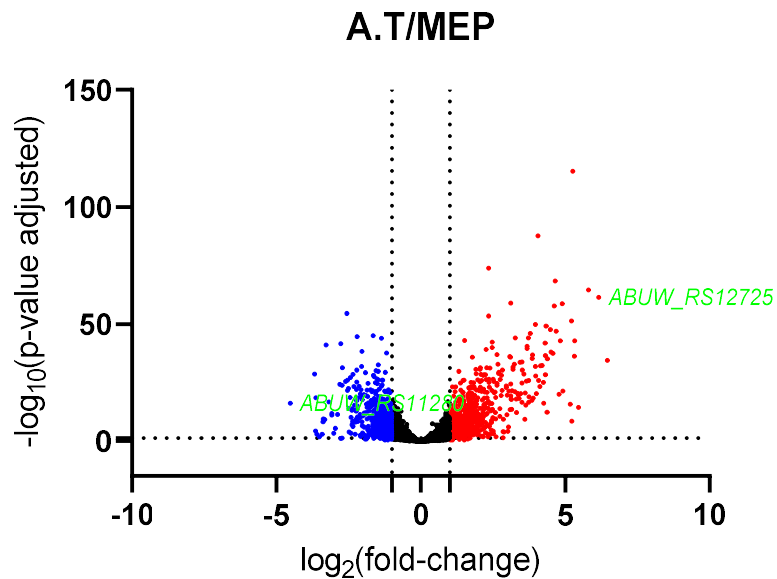


Figure 3.38: Volcano plot showing genes up- and down-regulated genes in AT vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the AT condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the AT condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005. 590 (13%) genes up- and 524 (14.6%) genes down-regulated out of 4034 genes in AT/MEP

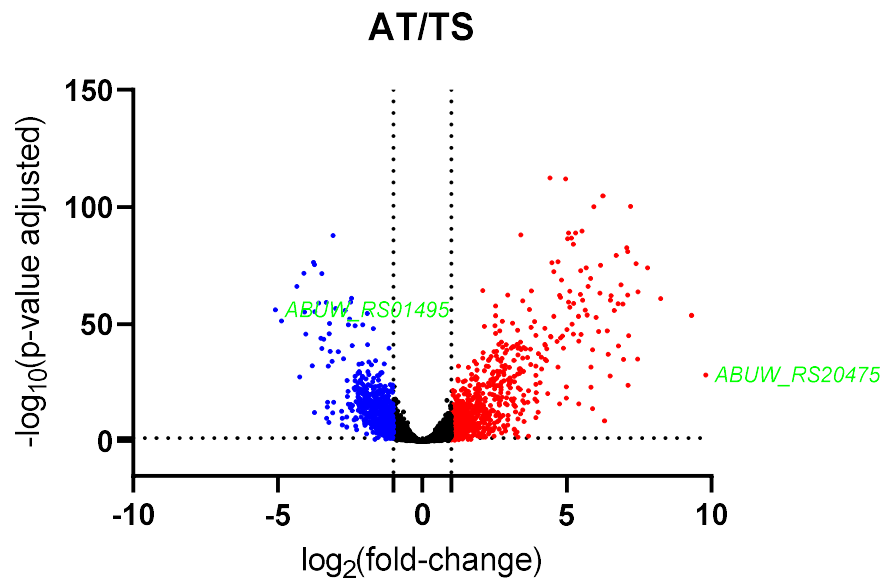


Figure 3.39: Volcano plot showing genes up- and down-regulated genes in TS vs. AT (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the TS condition >2-fold compared to the AT conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the TS condition >2-fold compared to the AT conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005. 757 (18.8%) genes up- and 592 (14.6%) genes down-regulated out of 4034 genes in TS/AT

OtsAB:

The *otsAB* operon (function described above) was strongly up-regulated upon temperature shift (*otsB*:124-fold, *otsA*: 90-fold, Figure 3.40). As these genes are involved in virulence and when deleted impair growth at 45°C, which is the highest temperature *A. baumannii* can grow at. Investigating of the regulation of these genes would be interesting to uncover the transcription factors responding to temperature upshift.

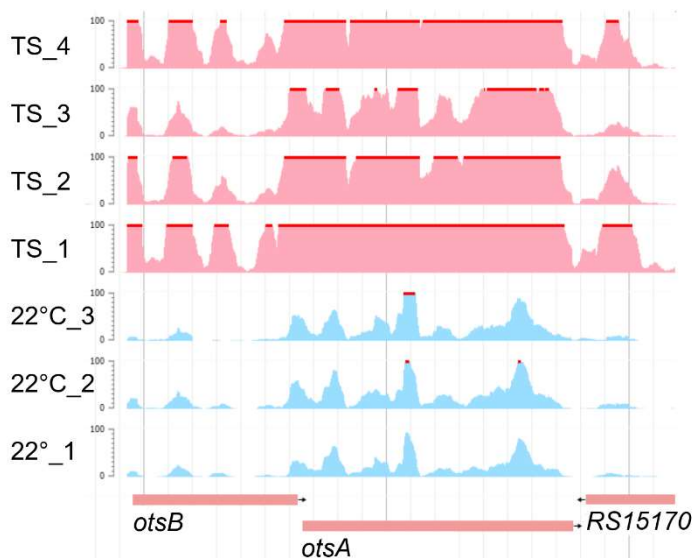


Figure 3.40: Up-regulation of *otsBA* in TS compared to 22°C. Sequence reads have been mapped, normalized, and visualized in JBrowse. The biological replicates are labelled with underscore and a number. Only the positive strand is shown for clarity.

The phenyl acetic acid (*paa*) pathway:

Many genes of the *paa* operon (function described above) were also up-regulated in temperature upshift (Two to six-fold, Figure 3.41). Most notably, the promoters of the *paaZ* gene and operon led by *paaA* were five-to-six-fold up-regulated. The induction is less strong than when cells were transitioning into LEP. Therefore, further experiments should focus at untangling the effects of growth vs. a regulatory effect caused by the temperature shift. Nevertheless, the observation that the *paa* genes are up-regulated

could hint at gene regulation by temperature and up-regulation of an important virulence trait when entering a warm-blooded host.

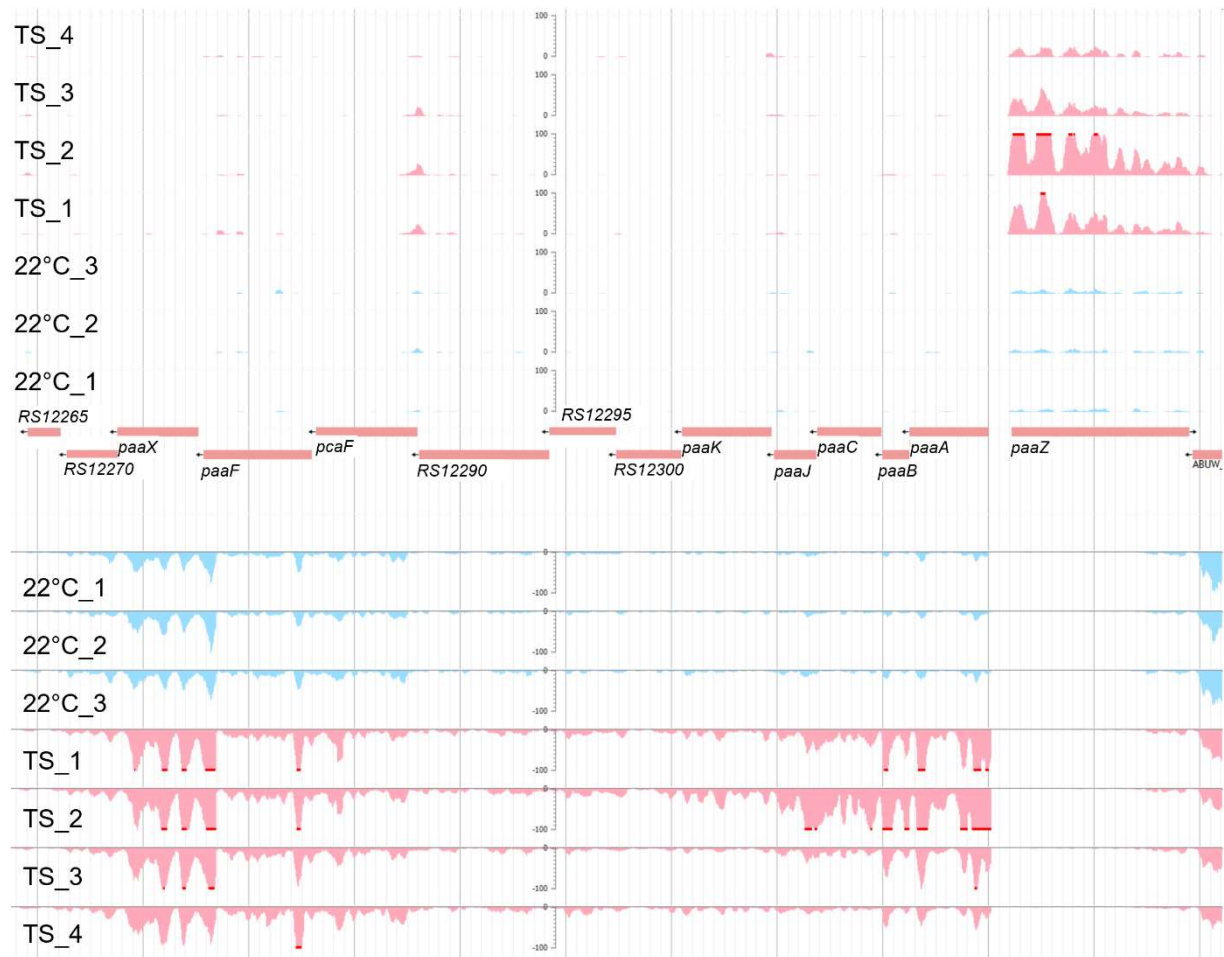


Figure 3.41: Up-regulation of the *paa* locus in TS compared to 22C°. Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number.

Type IV pilus genes.

Several genes annotated as *pil* were in the top10 down-regulated genes when cells were experiencing a temperature upshift (TS). The gene *pilA* was the most down-regulated gene (Figure 3.42), and *pilB*, *pilN*, *pilO*, *pilP* and *pilV* were also within the top10 down-regulated genes. The type IV pili are involved in DNA uptake and gene expression at ambient temperature could mean that DNA uptake is activated in the

environment, e.g., when cells are in the hospital environment. The pili are also important for cell surface motility, therefore DNA uptake and cell motility could be further investigated at different temperatures.

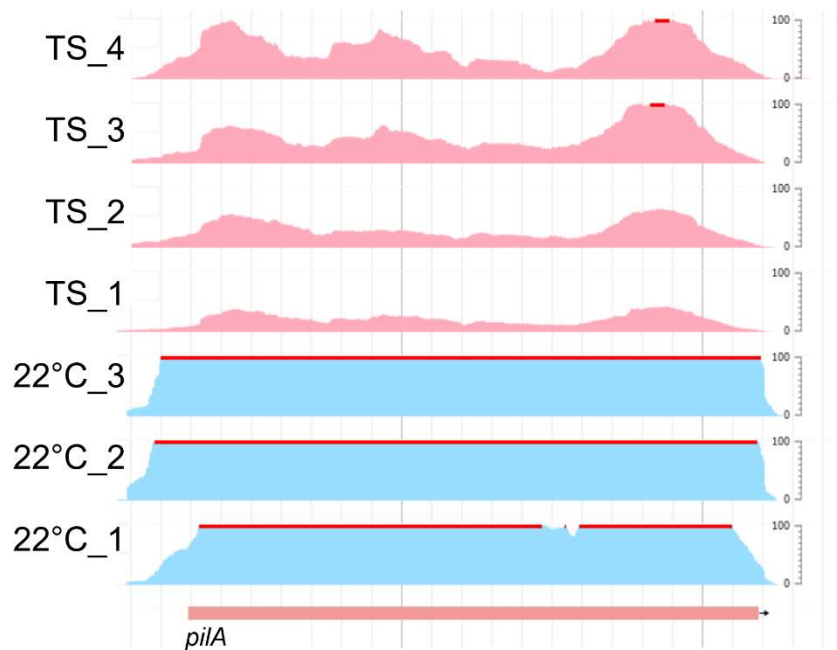


Figure 3.42: Down-regulation of *pilA* upon temperature upshift from 22°C to 37°C (TS). Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number. The scale is 0-100 normalized reads for all tracks.

Temperature down-shift (Col)

When *A. baumannii* is removed or leaves a host, it must adapt to a lower ambient temperature again to prepare for environmental survival. As previously, we first analyzed the changes in gene expression for annotated genes to obtain a first view of the adaptation of *A. baumannii* when moved from 37°C to 22°C. Gene expression changes are measured by comparing expression data for the Col condition with the MEP condition (Figure 3.43).

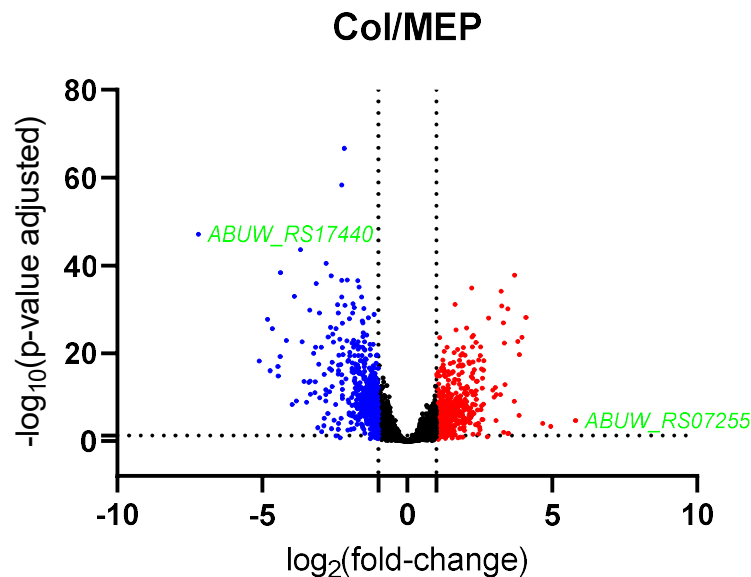


Figure 3.43: Volcano plot showing genes up- and down-regulated genes in Col vs. MEP (x-axis) and statistical analysis (y-axis). Vertical dashed line indicates two-fold up- and down-regulation cutoffs. Horizontal dashed line is drawn at an adjusted p value of 0.005. Red dots indicate genes that are up-regulated in the Col condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Blue dots indicate genes that are down-regulated in the Col condition >2-fold compared to the MEP conditions with an adjusted p value <0.005. Black dots indicate genes with an expression difference of <2-fold and/or an adjusted p value of >0.005.

Chaperone-usher (Csu) pathway:

The *csu* genes were the most highly up-regulated group of genes in temperature down-shift. As in above conditions (LowFe and NaCl), although considered a statistically significant (adjusted p value <0.005) change, it is evident that up-regulation only occurred in the replicate Col_2 (Figure 3.44). The genetic and/or biological reason for this is unclear, but it is an interesting observation and could mean that Csu expression could be stochastic.

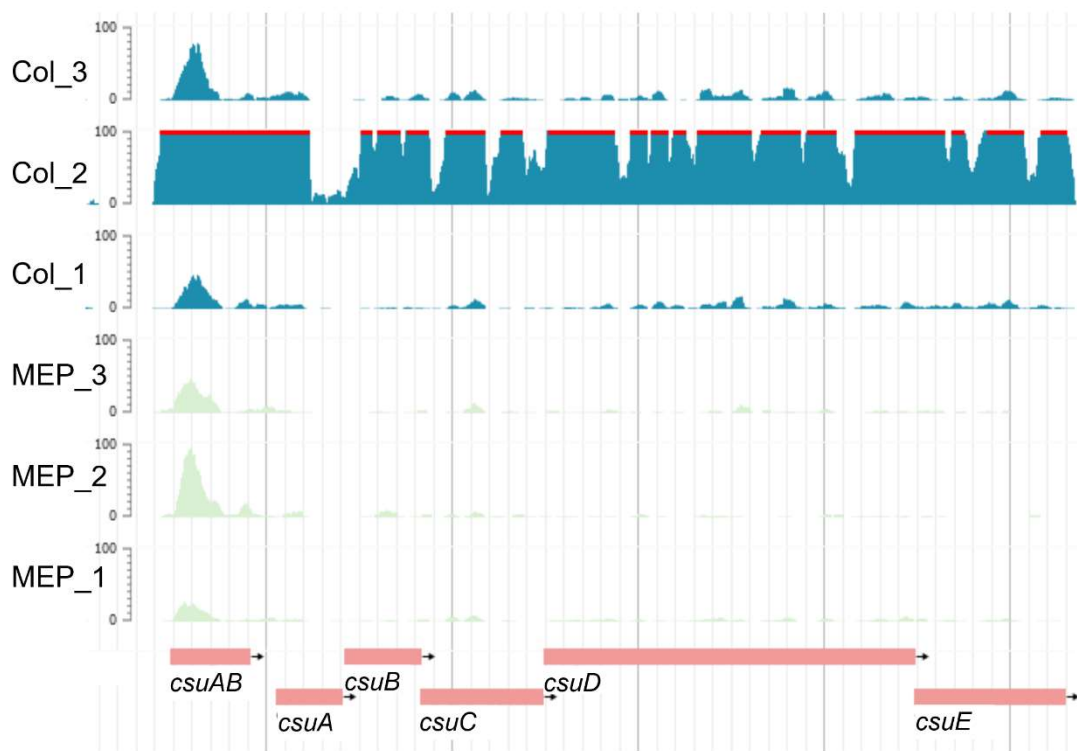


Figure 3.44: Up-regulation of *csu* genes Col compared to MEP in one of the replicates (Col_2). Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number. The scale is 0-100 normalized reads for all tracks.

Type-6-secretion system:

The type-6-secretion system is used by bacterial for interspecies microbial competition to kill potential competition for biological niches. We observe an up-regulation of *tss* and *tss*-associated genes (3 to 11-fold) upon temperature downshift from 37°C to 22°C (Figure 3.45). Changing temperature in the environment could inform *A. baumannii* that it has quickly changed environments and that in the new environment, defense systems are up-regulated to maximize chances for survival. The temperature down-shift could also prove to be an interesting condition to study the regulation of the T6SS.

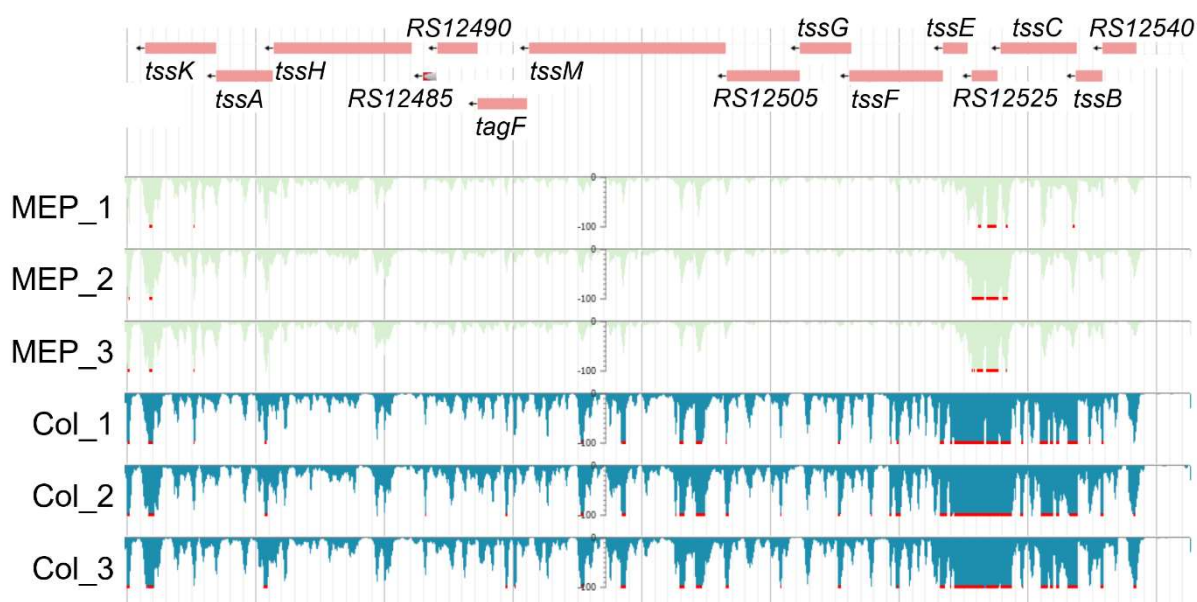


Figure 3.45: Up-regulation of *tss* genes Col compared to MEP. Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number. The scale is 0-100 normalized reads for all tracks.

Plasmid-encoded antibiotic resistance genes:

The *A. baumannii* AB5075 strain possesses many resistance genes that are located on the large, 83k bp plasmid p1AB5075. This includes several resistance genes to aminoglycosides, *aph*(6)-I (APH(6)-I family aminoglycoside O-phosphotransferase), *aph*(3'')-Ib (aminoglycoside O-phosphotransferase APH(3'')-Ib), *ABUW_RS19305* (ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2), *aadB* (ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2), *aph*(3')-VI (APH(3')-VI family aminoglycoside O-phosphotransferase) and the potential chloramphenicol resistance gene *cmIA* (chloramphenicol efflux MFS transporter) (de Dios *et al.*, 2022). When moved to lower temperature, several antibiotic resistance genes were strongly up-regulated, including *aph*(6)-I, *aph*(3'')-Ib, *ABUW_RS19305* (~6-10-fold), which might to be in an operon with *cmIA* (up-regulated ~4-fold, Figure 3.46). Other chromosomally- and plasmid-encoded aminoglycoside resistance genes showed a more mixed expression profile (*ABUW_RS18275* (aminoglycoside nucleotidyltransferase ANT(3'')-

Ila, ~3-fold up-regulated),), therefore it appears unlikely to be a specific aminoglycoside resistance gene response.

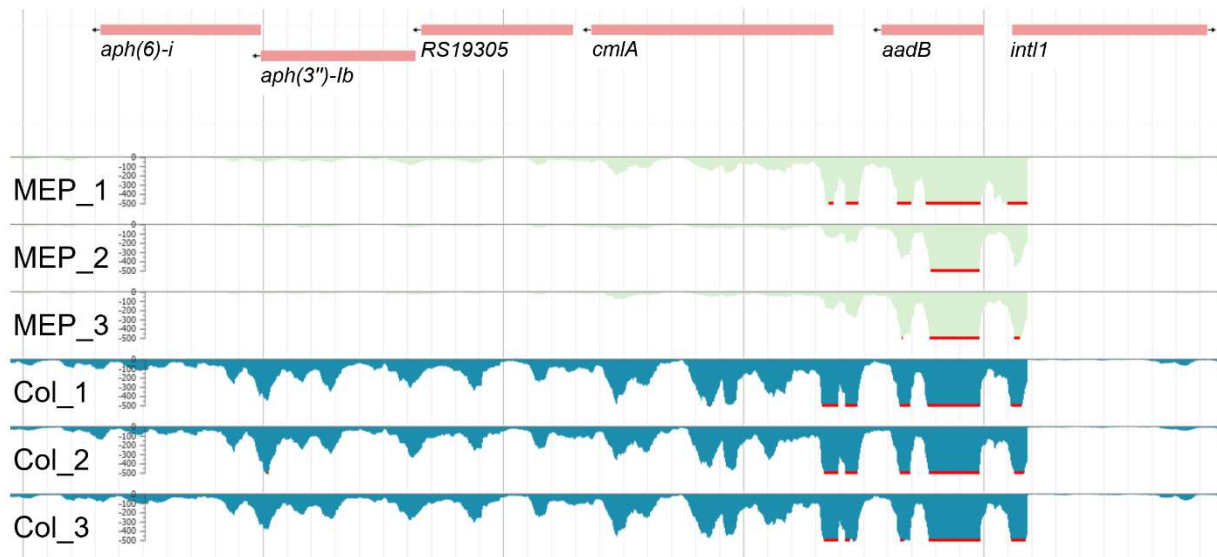


Figure 3.46: Up-regulation of antibiotic resistance genes Col compared to MEP. Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number. The scale is 0-500 normalized reads for all tracks.

Cold shock proteins

Very little is known on the function of annotated cold shock proteins in *A. baumannii*. The expectation would be that at least some predicted genes involved in the cold-shock response would be induced upon temperature down-shift. Three genes are annotated to encode for cold-shock proteins (*ABUW_RS06720*, *ABUW_RS12225* and *ABUW_RS13055*). Two of the three show strong up-regulation upon temperature down-shift (*ABUW_RS12225* is up-regulated ~15-fold, *ABUW_RS13055* is up-regulated ~8-fold, Figure 3.47). The third gene, *ABUW_RS06720*, shows only a very slight up-regulation by ~1.3-fold. Therefore, *ABUW_RS12225* and *ABUW_RS13055* could be involved in the immediate response to a drop in environmental temperature.

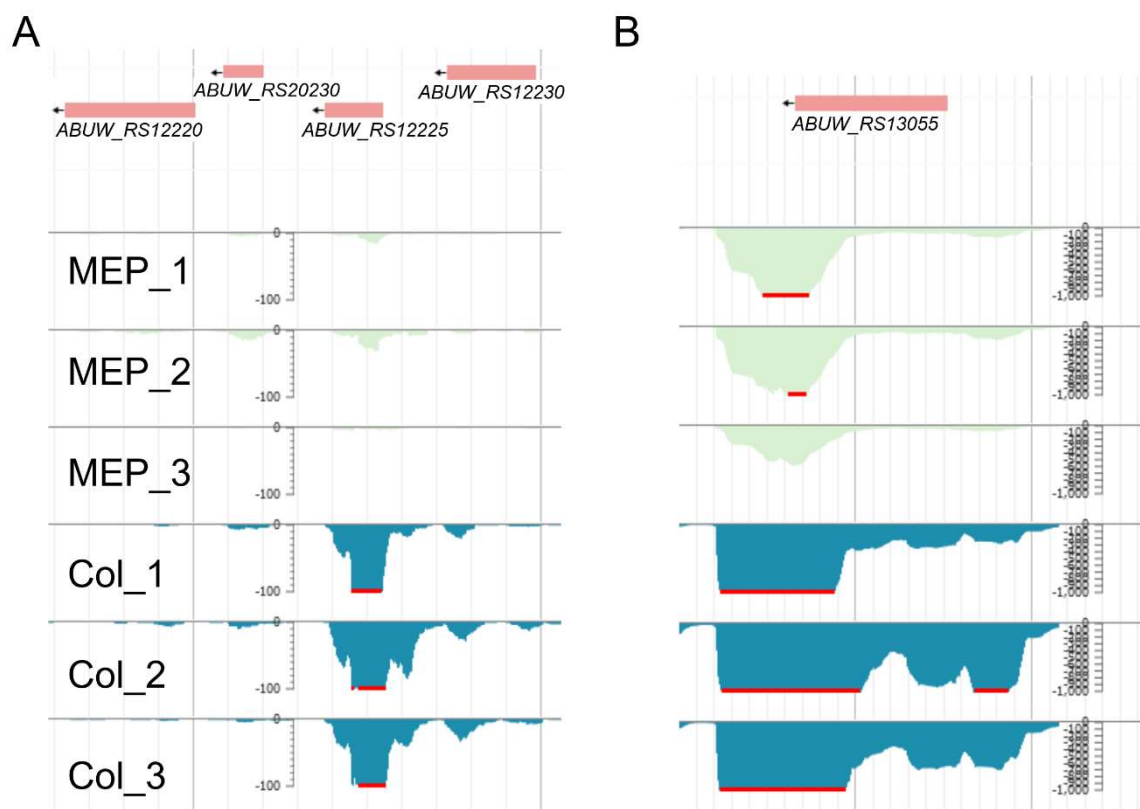


Figure 3.47: Up-regulation of cold-shock genes (*ABUW_RS12225* (A), *ABUW_RS13055* (B)) Col compared to MEP. Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number. The scale is 0-100 normalized reads for all tracks in (A) and 0-1000 normalized reads for all tracks (B).

3.7.3.1 AT/MEP vs AT/TS

According to an analysis of differential gene expression between AT/MEP and AT/TS. 2295 genes were expressed in AT/MEP (Figure 3.48 and 3.49) including 1077 genes that were upregulated and 1218 genes that were downregulated. The most upregulated genes were: *ABUW_RS12725* (hypothetical protein), *ABUW_RS01140* (hypothetical protein) and *ABUW_RS10025* (hypothetical protein). The most downregulated genes were: *ABUW_RS20210* (hypothetical protein), *ABUW_RS08010* (hypothetical protein) and *ABUW_RS11280* (PACE efflux transporter). While in AT/TS 2442 genes were expressed (Figure 3.48 and 3.49), including 1259 genes that were upregulated and 1183 genes that were downregulated. The most upregulated genes were:

ABUW_RS20475 (hypothetical protein), *ABUW_RS07145* (DUF2171 domain-containing protein) and *ABUW_RS07170* (NirD/YgiW/YdeI family stress tolerance protein). The most downregulated genes were: *ABUW_RS01430* (PilN domain-containing protein), *ABUW_RS08010* (hypothetical protein) and *ABUW_RS01495* (pilin). 1632 gene were overlap differentially expressed between AT/MEP and AT/TS. 813 genes upregulated overlapped and 703 genes were downregulated overlapped.

		AT vs MEP	
		Differentially Expressed	Differentially Non-Expressed
TS vs AT	Differentially Expressed	1632	810
	Differentially Non-Expressed	663	929

Figure 3.48: Differential gene expression analysis in AT/MEP vs TS/AT using DESeq2 values that showing numbers of genes differentially expressed and differentially non-expressed.

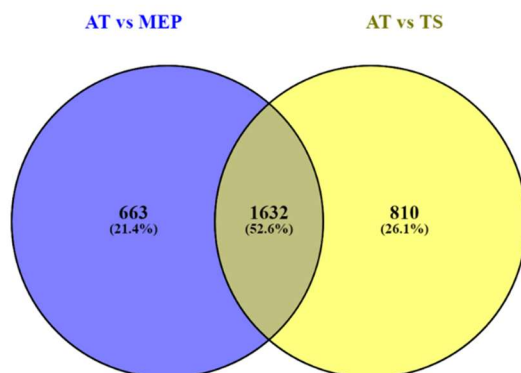


Figure 3.49: Venn diagram illustrate the overlap genes that differentially expressed between AT/MEP (blue circle) and TS/AT (yellow circle) using DESeq2 values, 1632 genes were overlapped.

3.7.3.2 Col/MEP vs AT/TS

Col/MEP expressed 2314 genes, based on an analysis of differential gene expression between Col/MEP and AT/TS. (Figure 3.50 and 3.51). 2314 genes were expressed in Col/MEP including 1228 genes that were upregulated and 1086 genes that were downregulated. The most upregulated genes were: *ABUW_RS07255* (Csu fimbrial biogenesis protein CsuA), *ABUW_RS07275* (Csu fimbrial tip adhesin CsuE) and *ABUW_RS07270* (Csu fimbrial usher CsuD). The most downregulated genes were: *ABUW_RS12115* (NAD(P)H-dependent oxidoreductase), *ABUW_RS11590* (taurine ABC transporter substrate-binding protein) and *ABUW_RS17440* (outer membrane beta-barrel protein) while in AT/TS described previously. 1436 gene were overlap differentially expressed between Col/MEP and AT/TS. 492 genes upregulated overlapped and 419 genes downregulated overlapped.

		Col vs MEP	
		Differentially Expressed	Differentially Non-Expressed
TS vs AT	Differentially Expressed	1436	1006
	Differentially Non-Expressed	878	714

Figure 3.50: Differential gene expression analysis in Col/MEP vs TS/AT using DESeq2 values that showing numbers of genes differentially expressed and differentially non- expressed.

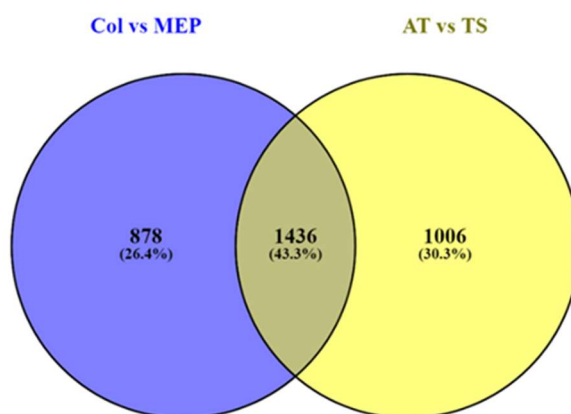


Figure 3.51: Venn diagram illustrate the overlap genes that differentially expressed between Col/MEP (blue circle) and TS/AT (yellow circle) using DESeq2 values, 1436 genes were overlapped.

3.7.3.3 Functional Annotation of Differentially Expressed Genes (DEG)s in AT/MEP

In AT/MEP, the KEGG pathway analysis showed that the DEGs were associated with 44 pathways, with ABC transporters and oxidative phosphorylation dominating in upregulation and two-component system dominating in downregulation (Figure 3.52).

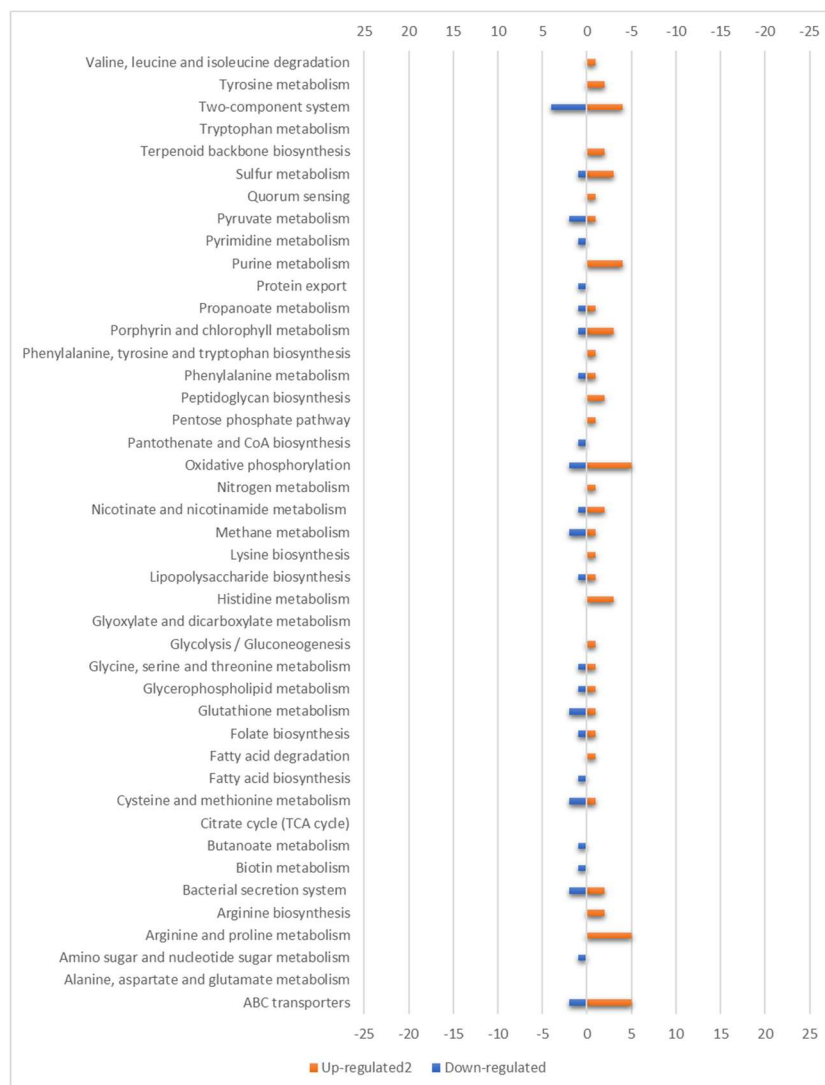


Figure 3.52: Cluster of orthologous genes (COG) classification of DEGs in AT/MEP. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category. Using TPM values (the average of the replicates of the condition and considering all values below 10 equals to 10).

3.7.3.4 Functional Annotation of Differentially Expressed Genes (DEG)s in TS/AT

In AT/TS, the KEGG pathway analysis showed that the DEGs were associated with 44 pathways, with two-component system dominating in upregulation and pyrimidine metabolism dominating in downregulation (Figure 3.53).

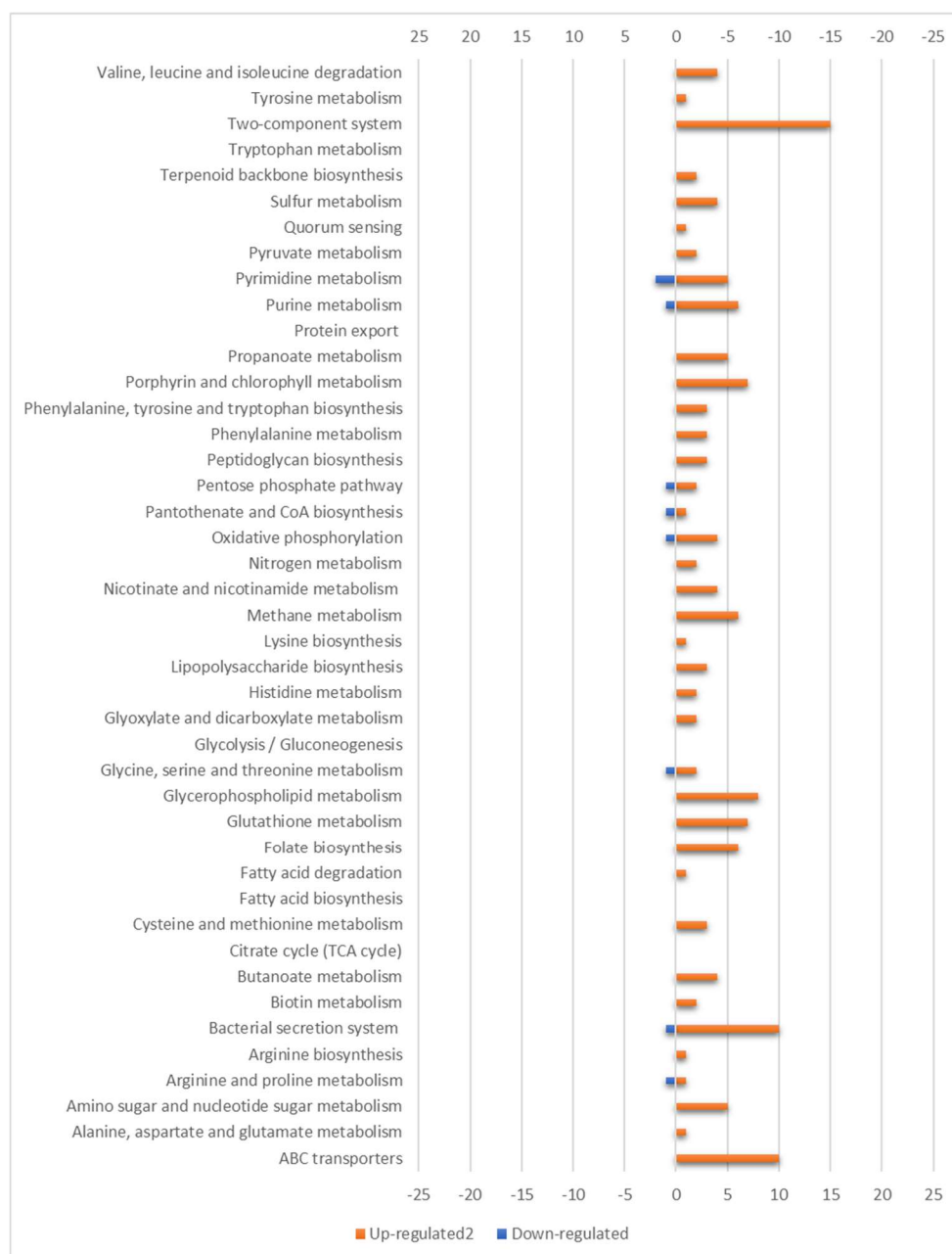


Figure 3.53: Cluster of orthologous genes (COG) classification of DEGs in TS/AT. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category. Using TPM values (the average of the replicates of the condition and considering all values below 10 equals to 10).

3.7.3.5 Functional Annotation of Differentially Expressed Genes (DEG)s in Col/MEP

In Col/MEP, the KEGG pathway analysis showed that the DEGs were associated with 44 pathways, with pantothenate and CoA biosynthesis in upregulation and purine metabolism dominating in downregulation (Figure 3.54).

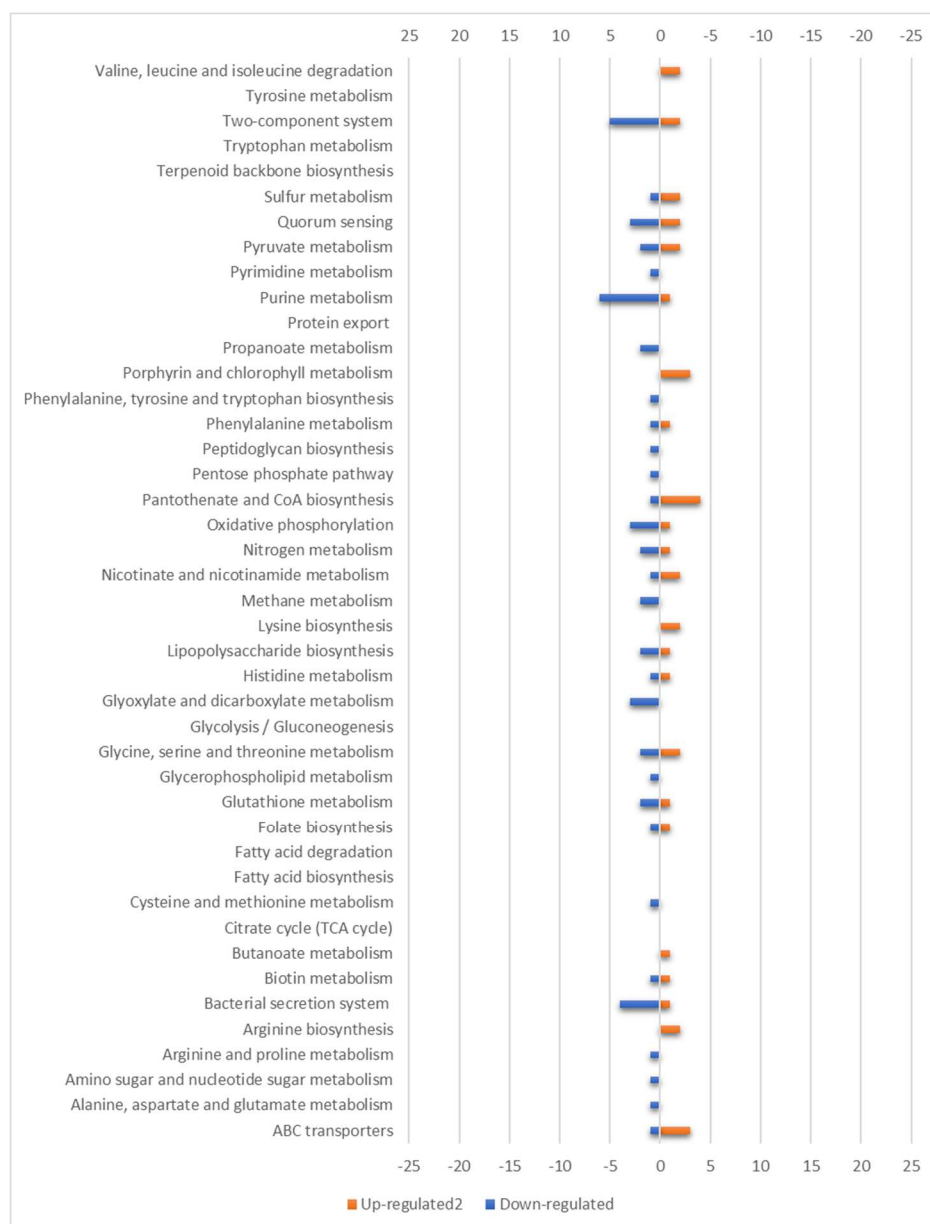


Figure 3.54: Cluster of orthologous genes (COG) classification of DEGs in Col/MEP. Red bars represent upregulated genes, and blue bars, downregulated genes in each COG category. Using TPM values (the average of the replicates of the condition and considering all values below 10 equals to 10).

	Up-regulated			Down-regulated		
	AT	TS	Col	AT	TS	Col
ABC transporters	5	10	3	2		1
Alanine, aspartate and glutamate metabolism		1				1
Amino sugar and nucleotide sugar metabolism		5		1		1
Arginine and proline metabolism	5	1			1	1
Arginine biosynthesis	2	1	2			
Bacterial secretion system	2	10	1	2	1	4
Biotin metabolism		2	1	1		1
Butanoate metabolism		4	1	1		
Citrate cycle (TCA cycle)						
Cysteine and methionine metabolism	1	3		2		1
Fatty acid biosynthesis				1		
Fatty acid degradation	1	1				
Folate biosynthesis	1	6	1	1		1
Glutathione metabolism	1	7	1	2		2
Glycerophospholipid metabolism	1	8		1		1
Glycine, serine and threonine metabolism	1	2	2	1	1	2
Glycolysis / Gluconeogenesis	1					
Glyoxylate and dicarboxylate metabolism		2				3
Histidine metabolism	3	2	1			1
Lipopolysaccharide biosynthesis	1	3	1	1		2
Lysine biosynthesis	1	1	2			
Methane metabolism	1	6		2		2
Nicotinate and nicotinamide metabolism	2	4	2	1		1
Nitrogen metabolism	1	2	1			2
Oxidative phosphorylation	5	4	1	2	1	3
Pantothenate and CoA biosynthesis		1	4	1	1	1
Pentose phosphate pathway	1	2			1	1
Peptidoglycan biosynthesis	2	3				1
Phenylalanine metabolism	1	3	1	1		1
Phenylalanine, tyrosine and tryptophan biosynthesis	1	3				1
Porphyrin and chlorophyll metabolism	3	7	3	1		
Propanoate metabolism	1	5		1		2
Protein export				1		
Purine metabolism	4	6	1		1	6
Pyrimidine metabolism		5		1	2	1
Pyruvate metabolism	1	2	2	2		2
Quorum sensing	1	1	2			3
Sulfur metabolism	3	4	2	1		1
Terpenoid backbone biosynthesis	2	2				
Tryptophan metabolism						
Two-component system	4	15	2	4		5
Tyrosine metabolism	2	1				
Valine, leucine and isoleucine degradation	1	4	2			

Figure 3.55: Heat map shows numbers of genes associated with Cluster of orthologous genes (COG) classification that expressed in heat shocks

3.8 AcinetoCom2

Acinetobacter Gene Expression Compendium (AcinetoCom) is a comprehensive database that provides valuable insights into the gene expression patterns and regulatory mechanisms. Gene expression data are very large sets data and to interrogate them, it is useful to have an accessible database. In the past, transcriptomic databases have been created by Kröger Lab (AcinetoCom 1.0) which is an online resource developed to assist the research community in making comparable discoveries *A. baumannii* ATCC17978 (Kröger *et al.*, 2018). Now, we provide the data for AcinetoCom2 which was created by Dr. Karsten Hokamp (Smurfit Institute, Department of Genetics, TCD) (Figure 66-3) that includes all of our transcriptomic data expressed as TPM values showing absolute and differential gene expression comparing different conditions. AcinetoCom2 can be used by researchers to evaluate transcriptional characteristics. The website can be reached at: [AcinetoCom2](https://www.acineto.com/).

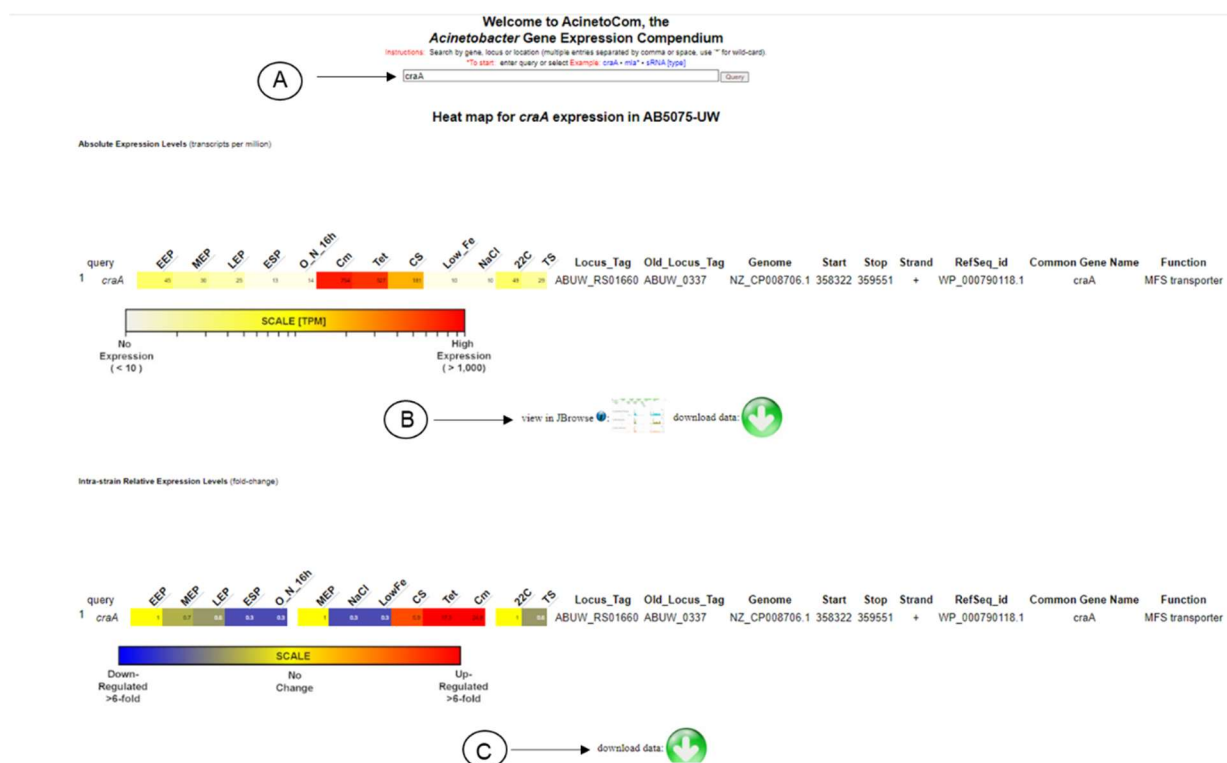


Figure 3.56: AcinetoCom2 web page interface. A: Query box that enables to search for any gene. B: Link to view data JBrowse. C: Link to download data.

Chapter 4

Global characterisation of sRNA gene expression

4.1 The expression landscape of sRNAs

The global characterisation of sRNA gene expression yields important insights into the regulation and function of these small non-coding RNA molecules in diverse biological processes across organisms and tissues (Papenfort and Melamed, 2023). Small RNAs regulate gene expression in response to both internal and external stimuli (Posner *et al.*, 2019). Multiple aspects of gene expression regulation, including regulation of transcription, mRNA turnover, and translation, have been linked to the action of sRNAs (Chen *et al.*, 2019). To characterise potentially regulatory sRNAs, it is helpful to understand when the sRNA is most highly expressed. This may indicate that this is the condition and time when the sRNA is most likely to carry out its biological role (Fender *et al.*, 2010). Even though a number of sRNAs has been discovered in the MDR *A. baumannii* strain AB5075, the physiological function(s) of these sRNAs are yet unknown. Using a method that is based on RNA sequencing, Weiss and his colleagues were able to identify 78 strain-specific small RNAs that are both short and conserved. In ATCC19787, our lab found 110 sRNA as identified by differential RNA-seq (Kröger *et al.*, 2018). sRNAs are found in substantial copy numbers inside the *A. baumannii* genome (Kröger *et al.*, 2018). Of the 110 sRNAs identified in ATCC17978, 88 sRNAs were conserved in AB5075 (Hamrock *et al.*, 2023).

4.1.1 Expression of sRNAs during growth in rich medium (L-broth)

In many bacterial species, sRNAs are involved in regulatory circuits and the responses to stress. To characterise potentially regulatory sRNAs, it is helpful to understand when the sRNA is most highly expressed. This usually indicates that this is the condition and time when the sRNA is most likely to carry out its biological role. Here, we highlight the response behaviour of small RNAs during the growth stages (EEP, MEP, LEP, ESP

and LSP) of *A. baumannii* AB5075 and compare each condition with MEP using TPM values and taking cut-off 2-fold changes. We found that many sRNAs show differences in abundance throughout growth except for the EEP condition which is very similar to MEP (Table 4.1). A set of 26 sRNAs were >2-fold up-regulated in LEP, ESP and LSP compared to MEP indicating that these sRNAs could play a role when cells enter into late exponential and stationary phase (Figures 4.1, 4.2). Few sRNAs were condition-specifically up-regulated (4 in LEP, 2 in ESP and 7 in LSP). Only very few sRNAs were down-regulated compared to MEP (Figure 4.2).

Table 4.1: sRNAs that 2-fold up- and 2-fold down-regulated sRNAs in EEP, LEP, ESP and LSP during growth in L-broth compared to MEP.

Condition	sRNA up-regulated (sRNA > 2-fold up)	sRNA down-regulated (sRNA < 2-fold down)
EEP	sRNA9, sRNA93, sRNA15	sRNA37, sRNA6
LEP	sRNA65, sRNA75, sRNA27, sRNA103, sRNA64, sRNA18, sRNA86, sRNA50, sRNA97, sRNA77, sRNA76, sRNA93, sRNA85, sRNA15, sRNA8, sRNA90, sRNA74, sRNA100, sRNA9, sRNA26, sRNA101, sRNA49, sRNA46, sRNA109, sRNA110, sRNA38, sRNA99, sRNA29, sRNA92, sRNA62, sRNA24, sRNA1, sRNA69, sRNA53, sRNA54, sRNA61, sRNA55, sRNA104, sRNA13, sRNA6, sRNA17, sRNA37, sRNA89, sRNA31, sRNA84, sRNA63, sRNA21, sRNA87, sRNA72	sRNA3, sRNA20
ESP	sRNA65, sRNA27, sRNA97, sRNA86, sRNA103, sRNA75, sRNA8, sRNA1, sRNA76, sRNA74, sRNA100, sRNA15, sRNA50, sRNA89, sRNA90, sRNA85, sRNA77, sRNA109, sRNA110, sRNA99, sRNA84, sRNA9, sRNA101, sRNA93, sRNA26, sRNA92, sRNA48, sRNA38, sRNA29, sRNA63, sRNA64, sRNA46, sRNA104, sRNA62, sRNA18, sRNA55, sRNA24, sRNA61	sRNA96, sRNA3, sRNA6, sRNA7, sRNA19, sRNA20
LSP	sRNA65, sRNA8, sRNA104, sRNA97, sRNA86, sRNA109, sRNA110, sRNA102, sRNA75, sRNA90, sRNA77, sRNA100, sRNA84, sRNA1, sRNA49, sRNA38, sRNA91,	sRNA96, sRNA20, sRNA58, sRNA95, sRNA6, sRNA3

	sRNA99, sRNA103, sRNA63, sRNA21, sRNA85, sRNA76, sRNA89, sRNA55, sRNA13, sRNA70, sRNA64, sRNA62, sRNA72, sRNA61, sRNA74, sRNA7, sRNA37, sRNA94, sRNA27, sRNA88, sRNA46, sRNA31, sRNA15, sRNA54, sRNA53, sRNA26, sRNA18	

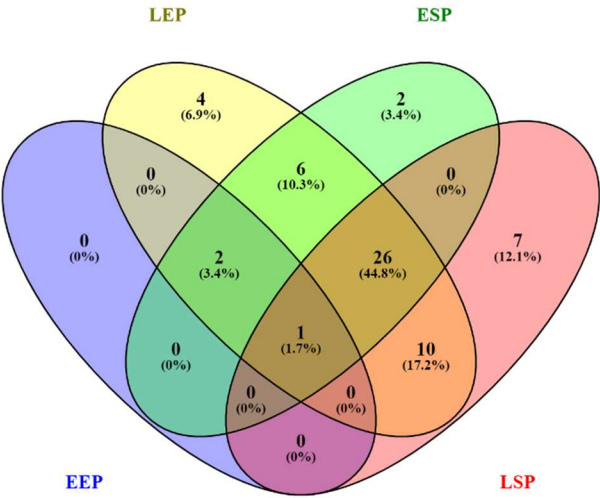


Figure 4.1: Venn diagram showing the overlap of sRNAs that are >2-fold up-regulated between EEP/MEP, LEP/MEP, ESP/MEP and LSP/MEP.

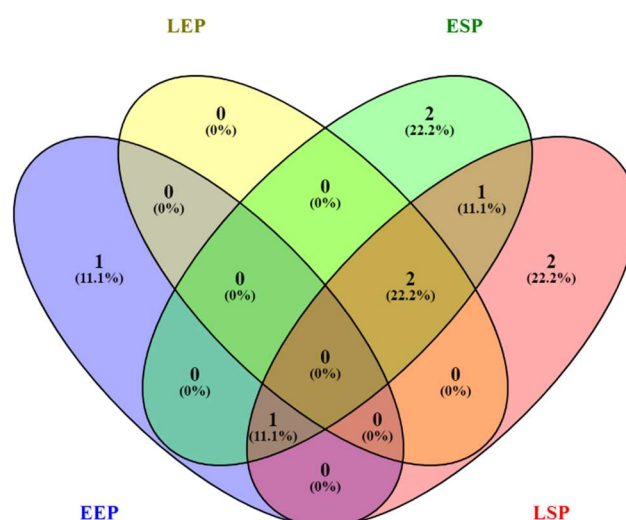


Figure 4.2: Venn diagram showing the overlap of sRNAs that are >2-fold down-regulated between EEP/MEP, LEP/MEP, ESP/MEP and LSP/MEP.

The number and percentage of up- and down-regulated sRNAs for each growth stage compared to the MEP out of a total of 88 small RNAs is shown in (Table 4.2) and (Figure 4.3). Overall, we can see that gene expression of sRNAs is much more often up- than down-regulated. This could be indicative of the potential mechanism of action of the sRNAs, as they are most often involved in down-regulation of genes or inhibition of translation through direct base-pairing.

Table 4.2: Numbers of genes go up/down per comparison different growth stages.

Cut-off	No. of sRNAs > 2-fold up	No. of sRNAs unchanged	No. of sRNAs > 2-fold down
EEP/MEP	3 (3.4%)	83 (94.4%)	2 (2.2%)
LEP/MEP	50 (56.8%)	36 (41%)	2 (2.2%)
ESP/MEP	39 (44.3%)	43 (48.9%)	6 (6.8%)
LSP/MEP	45 (51.1%)	37 (42.1%)	6 (6.8%)

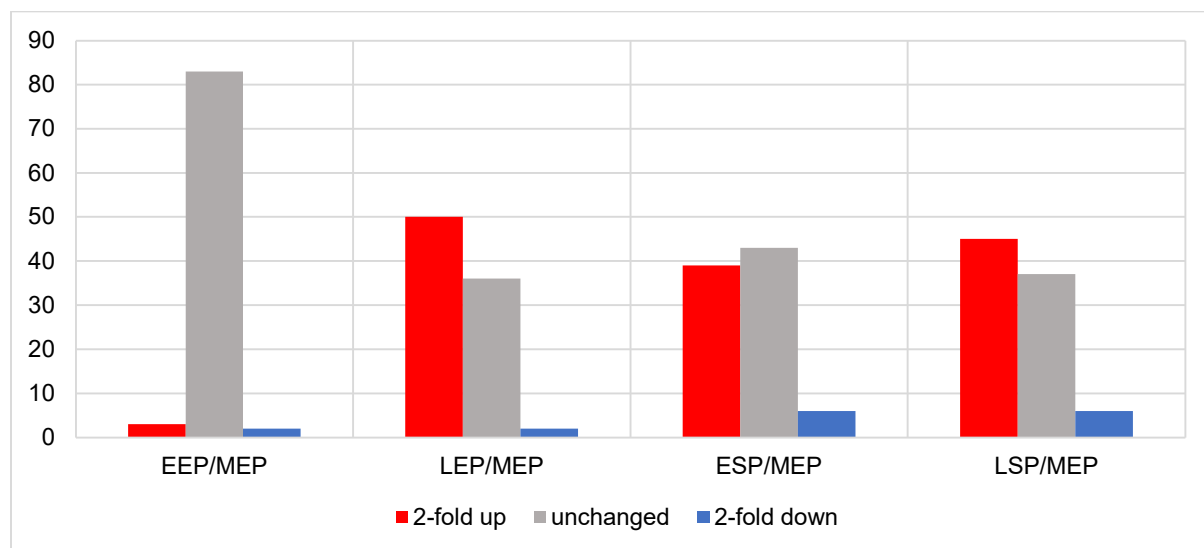


Figure 4.3: Using a cut-off value of >2-fold in difference of sRNAs expression (TPM values), the bar chart shows the number of genes that is up- or downregulated or unchanged per comparison of different growth stages.

Analysing individual transcript abundance (“absolute gene expression”) and changes in gene expression (“relative gene expression”), we observe that most sRNAs show a different abundance depending on the growth stage (Figure 4.4) indicating a dynamic change in sRNA content in the bacterial cell throughout growth offering potential for regulatory interactions. Few sRNAs are below the expression threshold (TPM >10) and are “not expressed” in L-broth. By calculating the most abundant sRNAs (top 30), Table 4.3 shows the top 30 sRNAs, we note that sRNA2 and sRNA89 were the most abundant from EEP to ESP compared to the rest of the other sRNAs (Table 4.3). Another highly changing sRNA is sRNA97, which increases hugely in LSP (1.1k-8k TPM in EEP to ESP, then 51k TPM in LSP). Other sRNAs that accumulate in LSP and that have been investigated further below are sRNA65 (<65 TPM in EEP and MEP, but 6k TPM in LSP) and sRNA100 (0.1-0.2k TPM in EEP and MEP, but 4.5k TPM in LSP).

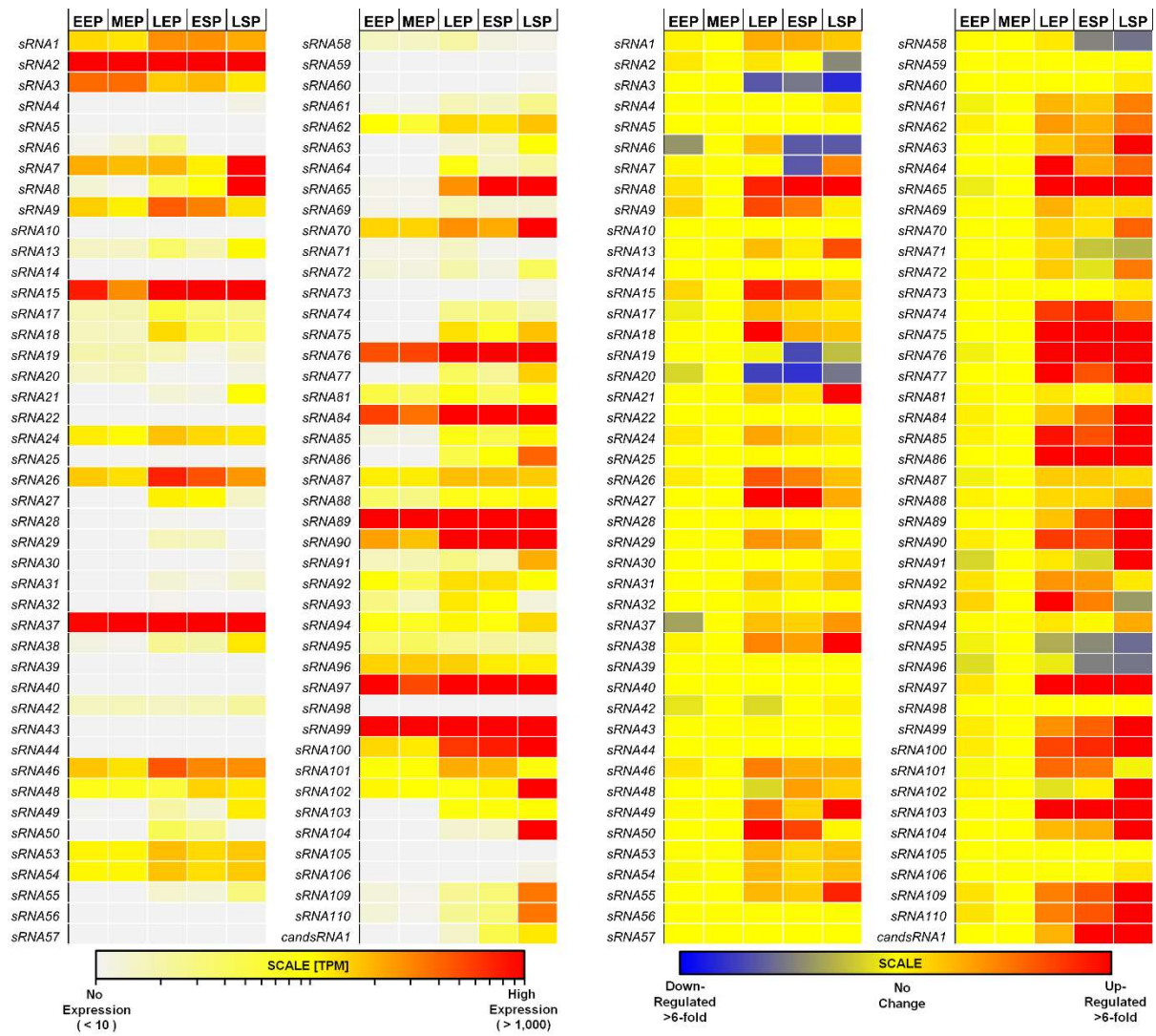


Figure 4.4: Heat map showing the abundance of sRNAs in growth phases (EEP, MEP, LEP, ESP and LSP) depending in TPM values. Left panel: “absolute” gene expression, right panel: “relative” gene expression (compared to MEP).

Table 4.3: Ranked abundance of the Top 30 sRNAs in growth phases based on TPM values.

Highlighted sRNAs that were further investigated are highlighted by colour.

	EEP	TPM	MEP	TPM	LEP	TPM	ESP	TPM	LSP	TPM
1	sRNA2	30637	sRNA2	21293	sRNA89	34466	sRNA89	72930	sRNA89	101930
2	sRNA89	17314	sRNA89	15831	sRNA2	31882	sRNA2	22057	sRNA97	51213
3	sRNA99	2479	sRNA99	1784	sRNA99	5612	sRNA97	8088	sRNA99	19726
4	sRNA97	1127	sRNA37	1407	sRNA76	4949	sRNA99	7346	sRNA2	13151
5	sRNA37	985	sRNA76	755	sRNA97	4914	sRNA76	5211	sRNA84	11728
6	sRNA15	908	sRNA97	746	sRNA37	3120	sRNA37	2671	sRNA90	8924
7	sRNA84	777	sRNA3	619	sRNA15	2759	sRNA15	2384	sRNA65	6265
8	sRNA76	723	sRNA84	607	sRNA90	1553	sRNA84	2308	sRNA76	5989
9	sRNA3	628	sRNA15	504	sRNA84	1288	sRNA90	1456	sRNA102	4655
10	sRNA90	431	sRNA7	334	sRNA26	889	sRNA65	1335	sRNA100	4587
11	sRNA7	390	sRNA90	318	sRNA100	811	sRNA100	902	sRNA37	4301
12	sRNA46	302	sRNA96	284	sRNA46	704	sRNA26	714	sRNA8	2110
13	sRNA26	284	sRNA70	253	sRNA9	672	sRNA9	538	sRNA15	1150
14	sRNA9	272	sRNA26	205	sRNA1	500	sRNA46	523	sRNA7	1122
15	sRNA96	254	sRNA46	199	sRNA70	488	sRNA1	487	sRNA104	1119
16	sRNA70	252	sRNA1	192	sRNA65	486	sRNA70	397	sRNA70	1034
17	sRNA100	238	sRNA100	172	sRNA101	396	sRNA101	356	sRNA86	650
18	sRNA1	234	sRNA87	165	sRNA7	358	sRNA3	346	sRNA109	584
19	sRNA24	169	sRNA9	146	sRNA87	332	sRNA87	331	sRNA110	584
20	sRNA87	158	sRNA53	131	sRNA53	330	sRNA48	259	sRNA46	499
21	sRNA53	137	sRNA54	127	sRNA24	318	sRNA53	236	sRNA26	462
22	sRNA54	126	sRNA24	115	sRNA54	311	sRNA24	235	sRNA1	399
23	sRNA102	125	sRNA102	104	sRNA3	282	sRNA54	219	sRNA91	391
24	sRNA92	106	sRNA101	99	sRNA96	267	sRNA92	207	sRNA75	319
25	sRNA62	102	sRNA48	89	sRNA62	239	sRNA62	204	sRNA62	302
26	sRNA101	97	sRNA94	86	sRNA18	223	sRNA96	166	sRNA53	294
27	sRNA94	95	sRNA62	80	sRNA92	214	sRNA7	153	sRNA54	289
28	sRNA48	90	sRNA92	69	sRNA75	208	sRNA102	141	sRNA87	281
29	sRNA81	73	sRNA81	65	sRNA93	181	sRNA27	118	sRNA77	268
30	sRNA88	63	sRNA95	65	sRNA27	151	sRNA8	109	sRNA94	231

The “absolute gene expression” is an informative value, however, the relative levels (proportion of the total pool of sRNA) are valuable as well (Figure 4.5). This shows that sRNA89, although its TPM value varies between 15k (MEP) and 101k (LSP), the relative levels only move between ~30-50% of the pool of sRNAs (Figure 4.6). Previous prediction suggests that sRNA89 is encoding tmRNA in *A. baumannii*, which explains the high abundance across conditions (Kröger *et al.*, 2018). In contrast, the proportion

of sRNA2 in the sRNA pool hugely decreases over time (while TPM levels only decrease ~2-fold), where it is >50% in EEP and gradually decreasing to ~6% within the pool.

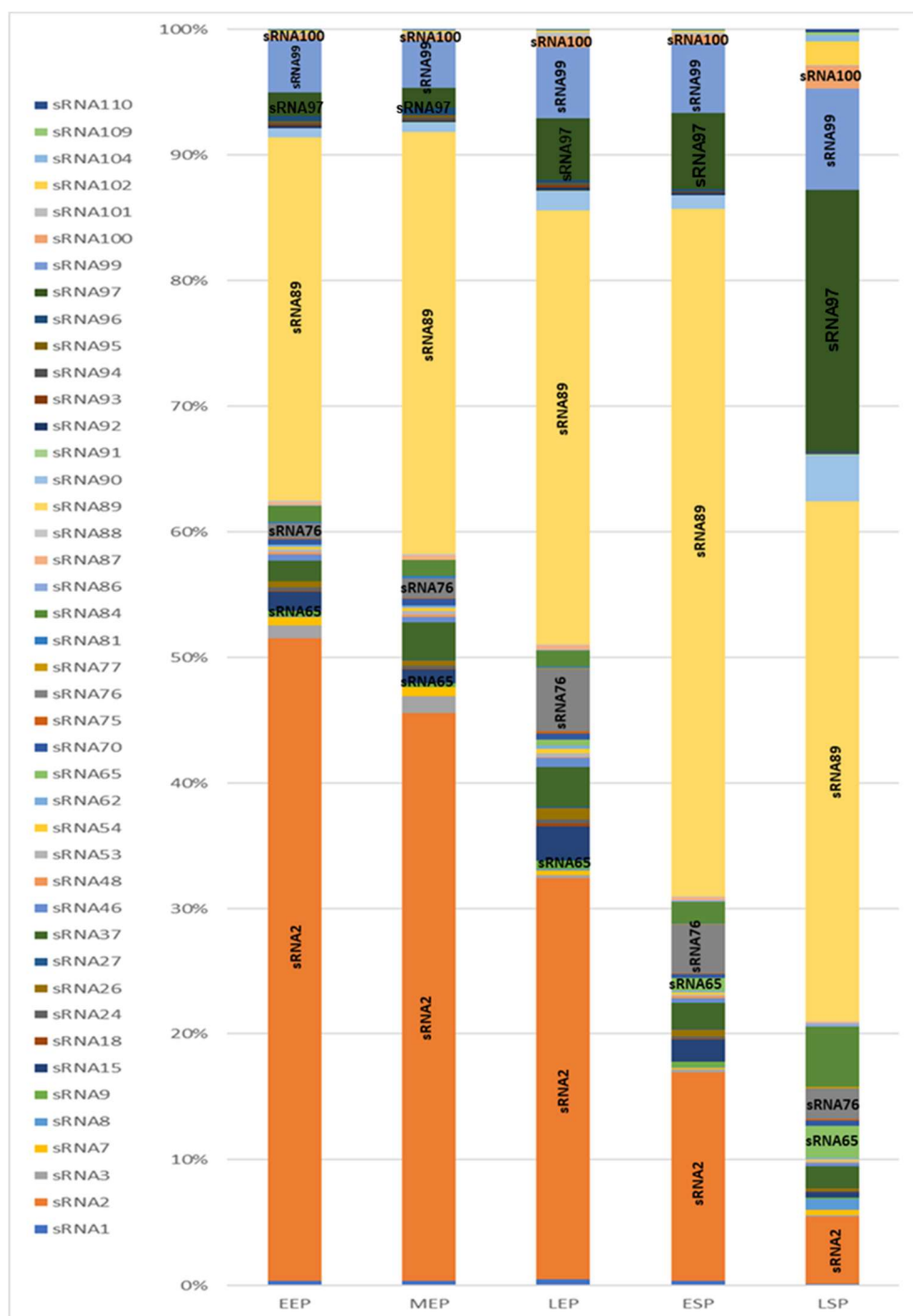


Figure 4.5: Stacked column chart showing the relative proportions of sRNAs in growth phases (EEP, MEP, LEP, ESP and LSP) based on TPM values.

4.1.2 Expression of sRNAs expression in different environmental stress conditions.

Environmental stress conditions are as important as growth stages to understand the response of bacteria to these changes and the role of sRNAs in these shock conditions. Because regulatory sRNAs are often involved in stress responses, a change in gene expression upon the short shocks applied could hint towards an involvement in adaptation to the stress applied. First, the four environmental conditions NaCl, LowFe, Tet and Chl (table 1.3) were analysed. For calculating differential gene expression, these stresses conditions were compared with MEP as above. The most up- and down-regulated sRNAs in shocks conditions are shown in (Table 4.4). As with growth in L-broth, we note that more sRNAs were up- (n=13-35) than down-regulated (n=2-8) in all shocks conditions (Table 4.5, Figure 4.6). The response of sRNAs to stressors was very similar between NaCl and LowFe where 11 up-regulated sRNAs overlapped and between Tet and Chl where 26 up-regulated sRNAs overlapped (Figure 4.7 and Figure 4.8). Six sRNAs were up-regulated in all four shock conditions, and they could represent a set of sRNAs that respond to stress more generally. There were also sRNAs that showed condition-specific up-regulation (NaCl n=1, LowFe n=2, Chl n=7 and Tet n=1). Of the down-regulated sRNAs, we noted the very strong down-regulation of sRNA99 and sRNA100 in Chl and Tet conditions (Figure 4.9), which were investigated in more detail below.

Table 4.4: Numbers of genes go up/down per comparison different stress conditions.

Cut-off	No. of sRNAs > 2-fold up	No. of sRNAs unchanged	No. of sRNAs < 2-fold down
NaCl/MEP	13 (14.8%)	72 (81.8%)	3 (3.4%)
LowFe/MEP	16 (18.3%)	70 (79.5%)	2 (2.2%)
Chl/MEP	35 (39.8%)	46 (52.3%)	7 (7.9%)
Tet/MEP	28 (31.8%)	52 (59.1%)	8 (9.1%)

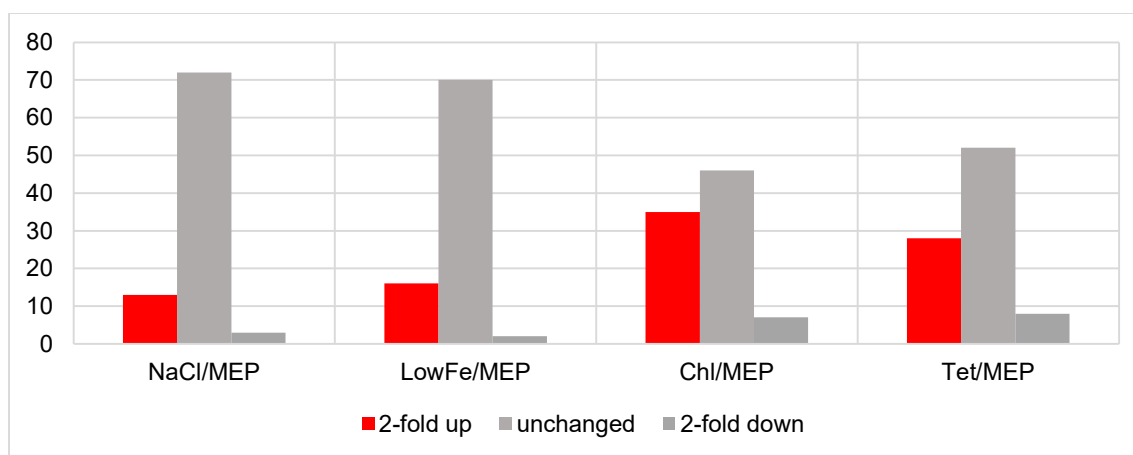


Figure 4.6: Using a cut-off value of 2-fold in difference of sRNAs expression, the bar chart shows the number of genes that are up- or downregulated or unchanged per comparison of different conditions.

Table 4.5: sRNAs that are >2-fold up- and >2-fold down-regulated in NaCl, LowFe. Tet and Chl compared to MEP.

Condition	sRNA up-regulated (> 2-fold)	sRNA down-regulated (< 2-fold)
NaCl Shock	sRNA76, sRNA93, sRNA46, sRNA86, sRNA6, sRNA50, sRNA1, sRNA8, sRNA2, sRNA37, sRNA96, sRNA64, sRNA65	sRNA72, sRNA20, sRNA7
LowFe Shock	sRNA76, sRNA6, sRNA93, sRNA50, sRNA49, sRNA46, sRNA86, sRNA8, sRNA1, sRNA99, sRNA2, sRNA58, sRNA65, sRNA37, sRNA85, sRNA26	sRNA72, sRNA20
Chloramphenicol (Chl) Shock	sRNA75, sRNA76, sRNA8, sRNA73, sRNA32, sRNA65, sRNA101, sRNA71, sRNA90, sRNA77, sRNA58, sRNA14, sRNA85, sRNA69, sRNA104, sRNA46, sRNA74, sRNA56, sRNA38, sRNA86, sRNA96, sRNA4, sRNA27, sRNA49, sRNA93, sRNA13, sRNA42, sRNA17, sRNA61, sRNA94, sRNA63, sRNA19, sRNA6, sRNA70, sRNA21	sRNA3, sRNA48, sRNA89, sRNA97, sRNA100, sRNA2, sRNA99
Tetracycline (Tet) Shock	sRNA73, sRNA65, sRNA32, sRNA8, sRNA76, sRNA101, sRNA75, sRNA71, sRNA74, sRNA69, sRNA85, sRNA77, sRNA14, sRNA38, sRNA104, sRNA58, sRNA46, sRNA50, sRNA27, sRNA61, sRNA93, sRNA49, sRNA42, sRNA86, sRNA94, sRNA21, sRNA88, sRNA13	sRNA3, sRNA91, sRNA89, sRNA97, sRNA48, sRNA100, sRNA2, sRNA99

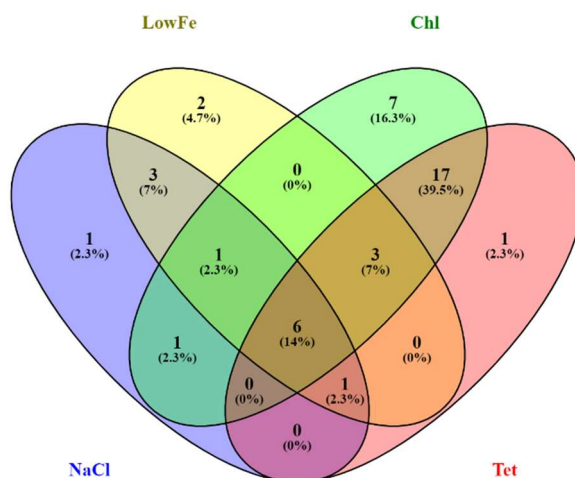


Figure 4.7: Venn diagram illustrating the overlap of >2-fold up-regulated sRNAs between NaCl/MEP, LowFe/MEP, Tet/MEP and Chl/MEP.

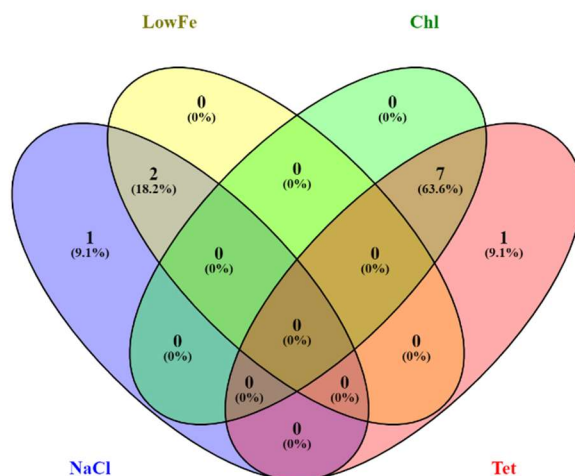


Figure 4.8: Venn diagram illustrating the overlap of >2-fold down-regulated sRNAs between NaCl/MEP, LowFe/MEP, Tet/MEP and Chl/MEP.

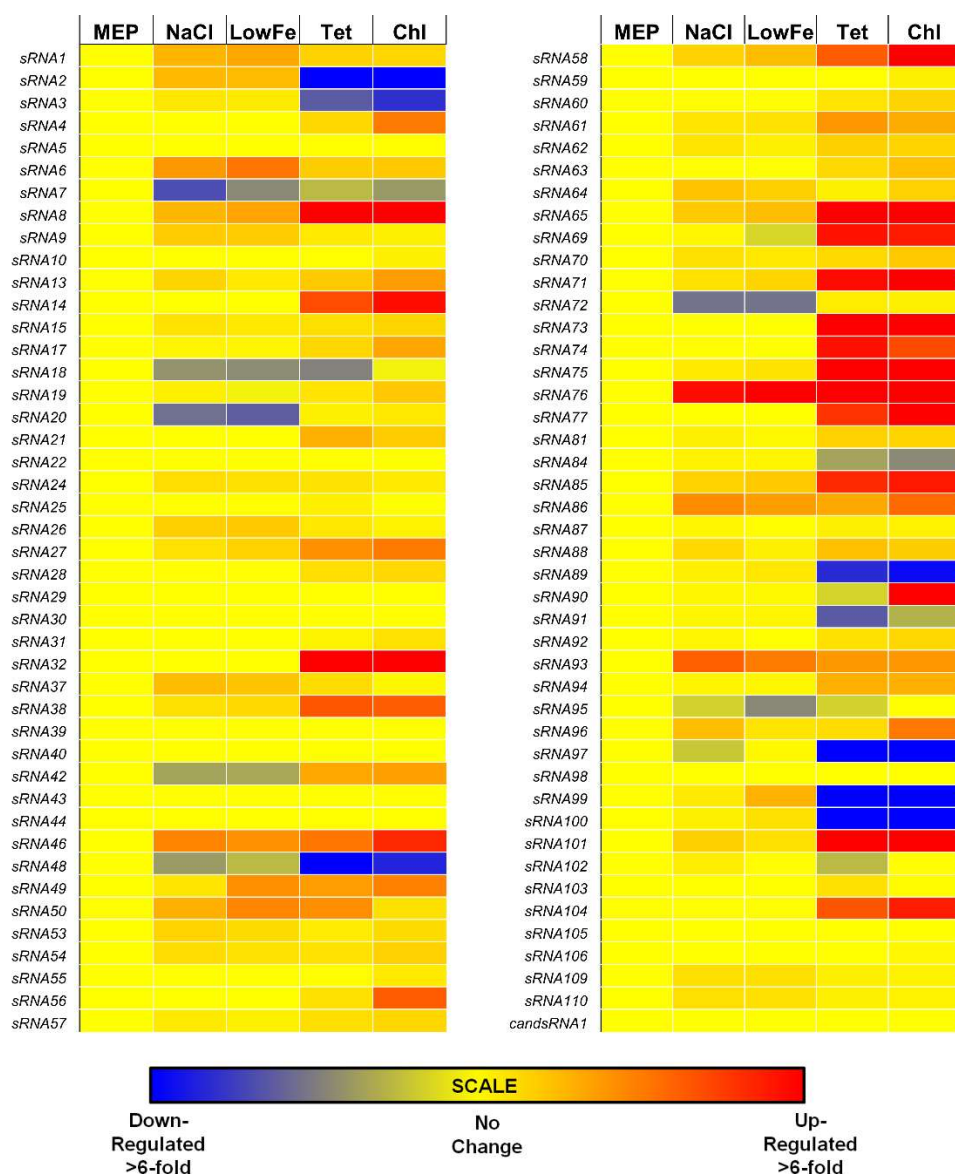


Figure 4.9: Heat map showing the relative gene expression of sRNAs in stress conditions (NaCl, LowFe, Tet, and Chl compared to MEP) based on TPM values.

Counting the most abundant sRNAs (the top 30), Table 4.6 shows the top 30 sRNAs, from the results, we note also here that sRNA2 and sRNA89 were the most abundant at high levels compared to the rest of the other sRNAs in all stress conditions (Figure 4.10).

Table 4.6: Ranked abundance of the Top 30 sRNAs in four shock conditions based on TPM values.

Highlighted sRNAs that were further investigated are highlighted by colour.

	MEP	TPM	NaCl	TPM	LowFe	TPM	Chl	TPM	Tet	TPM
1	sRNA2	21293	sRNA2	50446	sRNA2	49714	sRNA76	13930	sRNA76	5983
2	sRNA89	15831	sRNA89	20339	sRNA89	23417	sRNA89	3172	sRNA89	4888
3	sRNA99	1784	sRNA76	4377	sRNA76	4599	sRNA90	2604	sRNA37	2357
4	sRNA37	1407	sRNA37	3257	sRNA99	4484	sRNA37	1635	sRNA2	1211
5	sRNA76	755	sRNA99	2517	sRNA37	3010	sRNA2	1593	sRNA15	828
6	sRNA97	746	sRNA3	921	sRNA3	864	sRNA101	1171	sRNA46	734
7	sRNA3	619	sRNA15	778	sRNA97	832	sRNA46	1042	sRNA101	641
8	sRNA84	607	sRNA84	751	sRNA15	730	sRNA96	1041	sRNA96	477
9	sRNA15	504	sRNA46	681	sRNA84	718	sRNA15	924	sRNA70	440
10	sRNA7	334	sRNA96	643	sRNA46	630	sRNA70	523	sRNA84	428
11	sRNA90	318	sRNA97	615	sRNA1	518	sRNA84	376	sRNA1	365
12	sRNA96	284	sRNA1	471	sRNA96	430	sRNA1	349	sRNA26	306
13	sRNA70	253	sRNA26	402	sRNA26	421	sRNA26	254	sRNA3	290
14	sRNA26	205	sRNA70	402	sRNA70	363	sRNA54	243	sRNA90	273
15	sRNA46	199	sRNA90	370	sRNA90	357	sRNA7	225	sRNA7	260
16	sRNA1	192	sRNA9	293	sRNA9	293	sRNA94	222	sRNA94	222
17	sRNA100	172	sRNA53	243	sRNA100	275	sRNA53	222	sRNA87	219
18	sRNA87	165	sRNA100	223	sRNA53	22	sRNA87	205	sRNA9	208
19	sRNA9	146	sRNA54	213	sRNA7	208	sRNA3	204	sRNA54	201
20	sRNA53	131	sRNA87	192	sRNA54	198	sRNA75	194	sRNA53	180
21	sRNA54	127	sRNA101	191	sRNA24	185	sRNA9	189	sRNA24	180
22	sRNA24	115	sRNA24	191	sRNA87	173	sRNA8	182	sRNA62	154
23	sRNA102	104	sRNA102	140	sRNA101	160	sRNA65	177	sRNA73	151
24	sRNA101	99	sRNA7	140	sRNA102	110	sRNA58	169	sRNA65	151
25	sRNA48	89	sRNA62	119	sRNA62	103	sRNA24	162	sRNA81	125
26	sRNA94	86	sRNA93	118	sRNA93	102	sRNA62	147	sRNA8	116
27	sRNA62	80	sRNA94	103	sRNA94	100	sRNA73	134	sRNA58	114
28	sRNA92	69	sRNA88	90	sRNA6	79	sRNA32	128	sRNA88	113
29	sRNA81	65	sRNA81	87	sRNA81	73	sRNA92	124	sRNA92	111
30	sRNA95	65	sRNA92	81	sRNA48	69	sRNA71	121	sRNA97	102

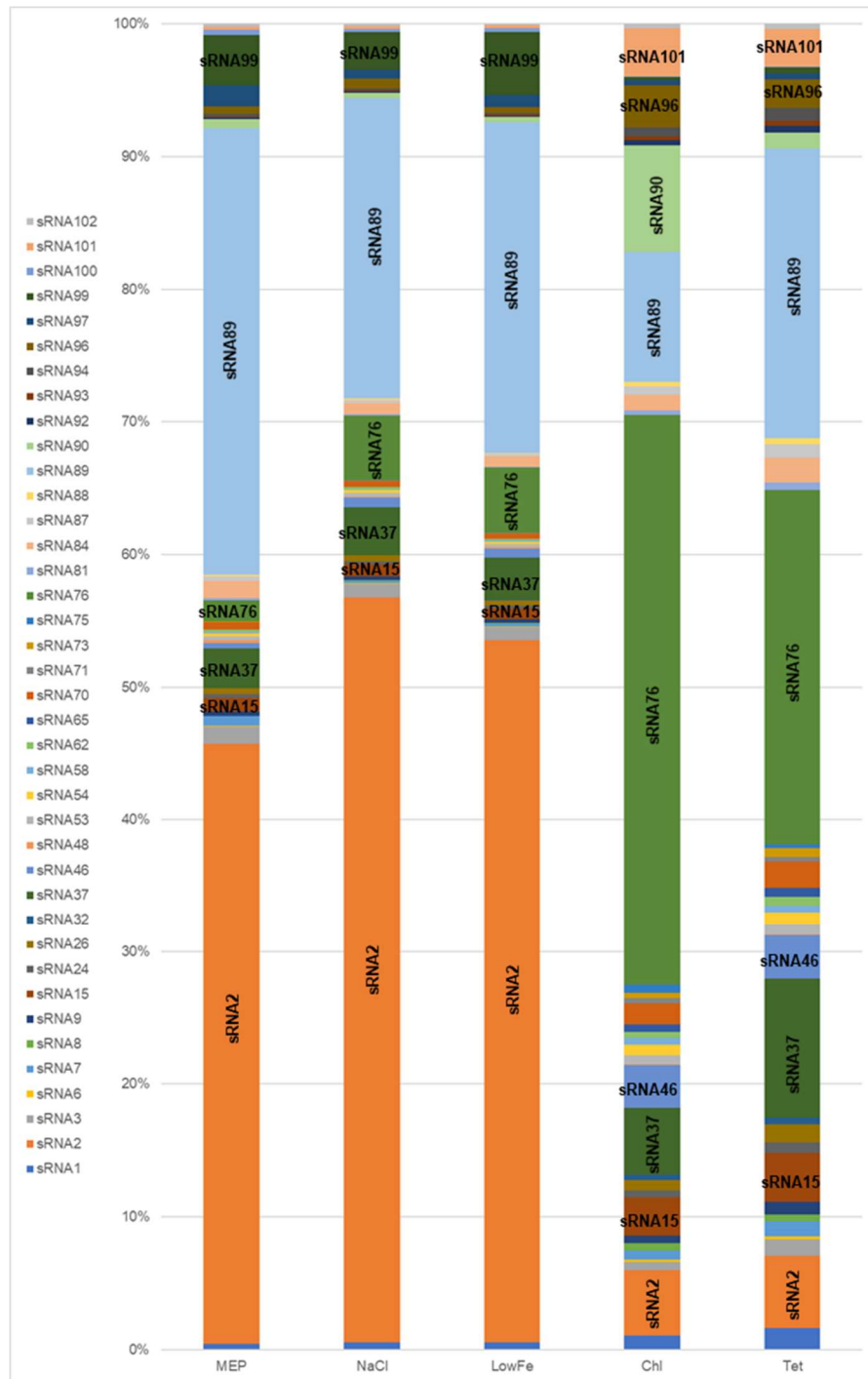


Figure 4.10: Stacked column chart showing the relative proportions of sRNAs in four shock conditions (NaCl, LowFe, Chl, and Tet) based on TPM values.

4.1.3 Expression sRNAs expression in response to temperature shifts (heat shocks)

Extreme heat or cold can be beneficial or harmful to some bacteria. The same applies to the temperature of the human body or the temperature of the surrounding environment, from this standpoint, studying the response of bacteria to temperatures, especially thermal shock when moving from one temperature to another, is of great importance. Here, when tracking the behavior of the sRNAs to respond when the bacteria move from the ambient temperature (AT) to the body temperature (TS) or vice versa, that is, when moving from the body temperature to the ambient temperature (CS), we found that the greatest response was downregulated. The most up and down regulated sRNAs in heat shocks conditions shown in (Table 4.7) and (Figures 4.11, 4.12).

Table 4.7: The most up and down regulated sRNAs in heat shocks conditions.

Condition	sRNA up-regulated (>2-fold)	sRNA down-regulated (>2-fold)
AT/TS	sRNA73	sRNA64, sRNA25, sRNA20, sRNA31, sRNA55, sRNA10, sRNA59, sRNA106, sRNA5, newcandsRNA1, sRNA105, sRNA22, sRNA29, sRNA30, sRNA39, sRNA40, sRNA43, sRNA44, sRNA98, sRNA90, sRNA95, sRNA7, sRNA102, sRNA84, sRNA18, sRNA3, sRNA91, sRNA89, sRNA97, sRNA48, sRNA100, sRNA2, sRNA99
CS/TS	sRNA73, sRNA65	sRNA72, sRNA87, sRNA109, sRNA110, sRNA64, sRNA25, sRNA20, sRNA31, sRNA55, sRNA10, sRNA59, sRNA106, sRNA5, newcandsRNA1, sRNA105, sRNA22, sRNA29, sRNA30, sRNA39, sRNA40, sRNA43, sRNA44, sRNA98, sRNA90, sRNA95, sRNA7, sRNA102, sRNA84, sRNA18, sRNA3, sRNA91, sRNA89, sRNA97, sRNA48, sRNA100, sRNA2, sRNA99

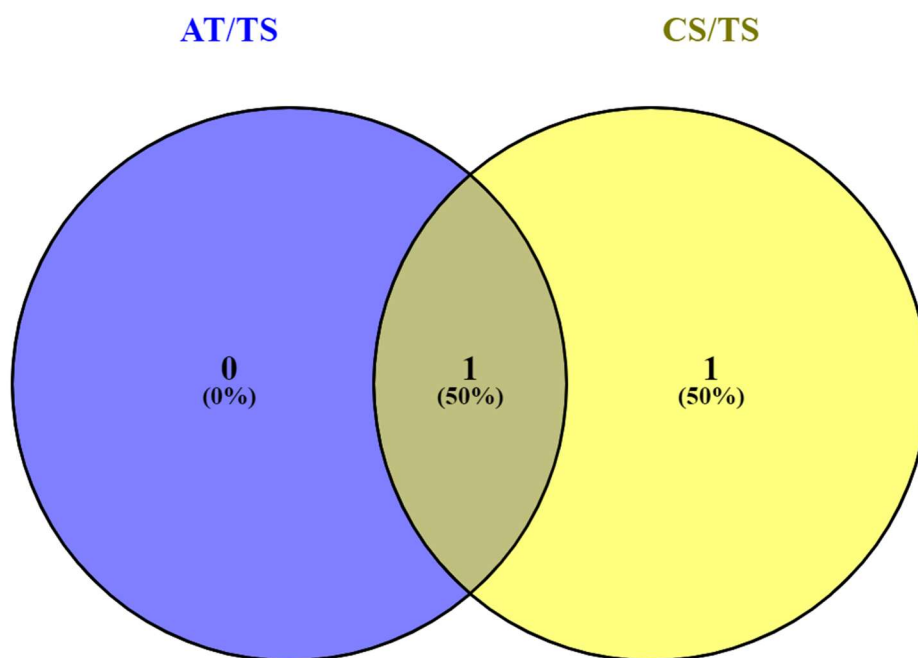


Figure 4.11: Venn diagram illustrate the numbers of 2-fold upregulated sRNAs overlaped between AT/TS and CS/TS

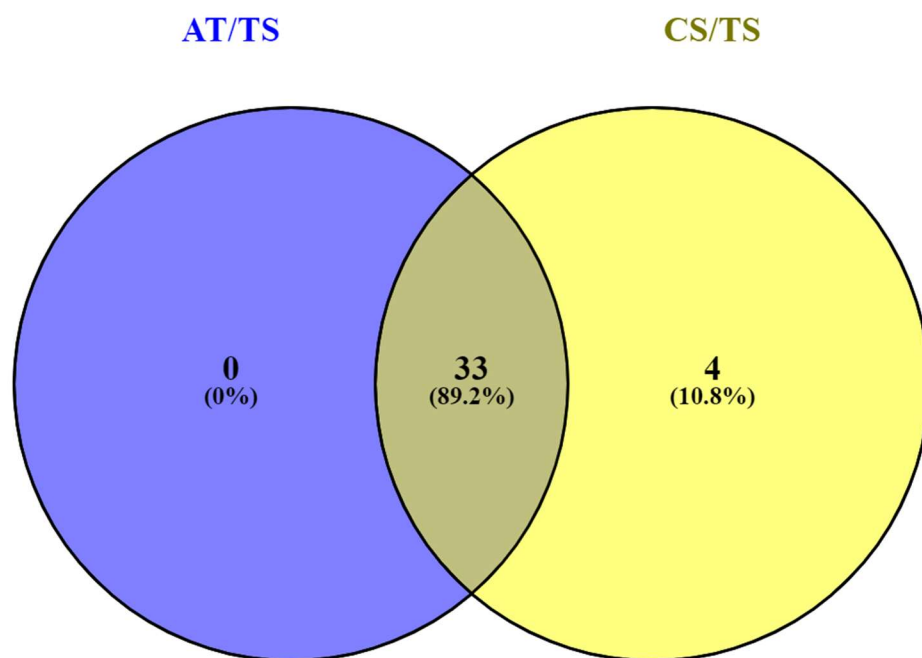


Figure 4.12: Venn diagram illustrate the numbers of 2-fold upregulated sRNAs overlaped between AT/TS and CS/TS

Table 4.8 shows the numbers and percentage of upregulated and downregulated sRNAs for heat shocks conditions (AT/TS and CS/TS) out of a total of 88 sRNAs. The results are very close for the response of two comparisons (Figure 4.13).

Table 4.8: Numbers of genes go up/down per comparison different heat shocks conditions.

Cut-off	No. of sRNAs > 2-fold up	No. of sRNAs unchanged	No. of sRNAs < 2-fold down
AT/TS	1 (1.15%)	54 (61.35%)	33 (37.5%)
CS/TS	2 (2.3%)	49 (55.7%)	37 (42%)

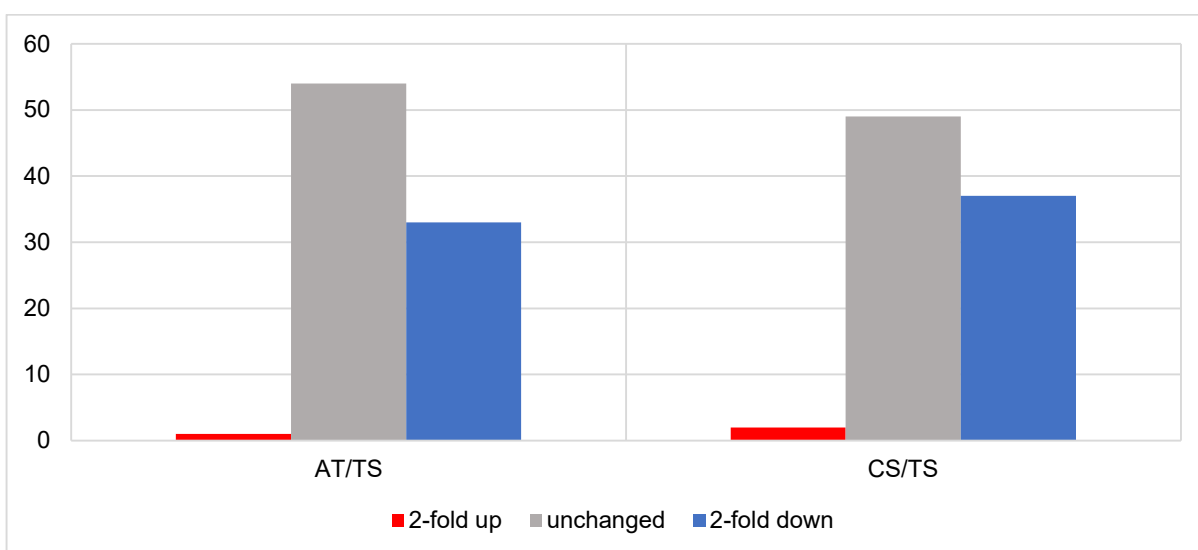


Figure 4.13: Using a cut-off value of 2-fold in difference of sRNAs expression, the bar chart shows the number of genes that is up- or downregulated or unchanged per comparison of different heat shocks conditions.

The abundance of each sRNAs in each heat shocks condition (AT/TS and CS/TS), can be seen from TPM values as shown in the heat map (Figure 4.14).

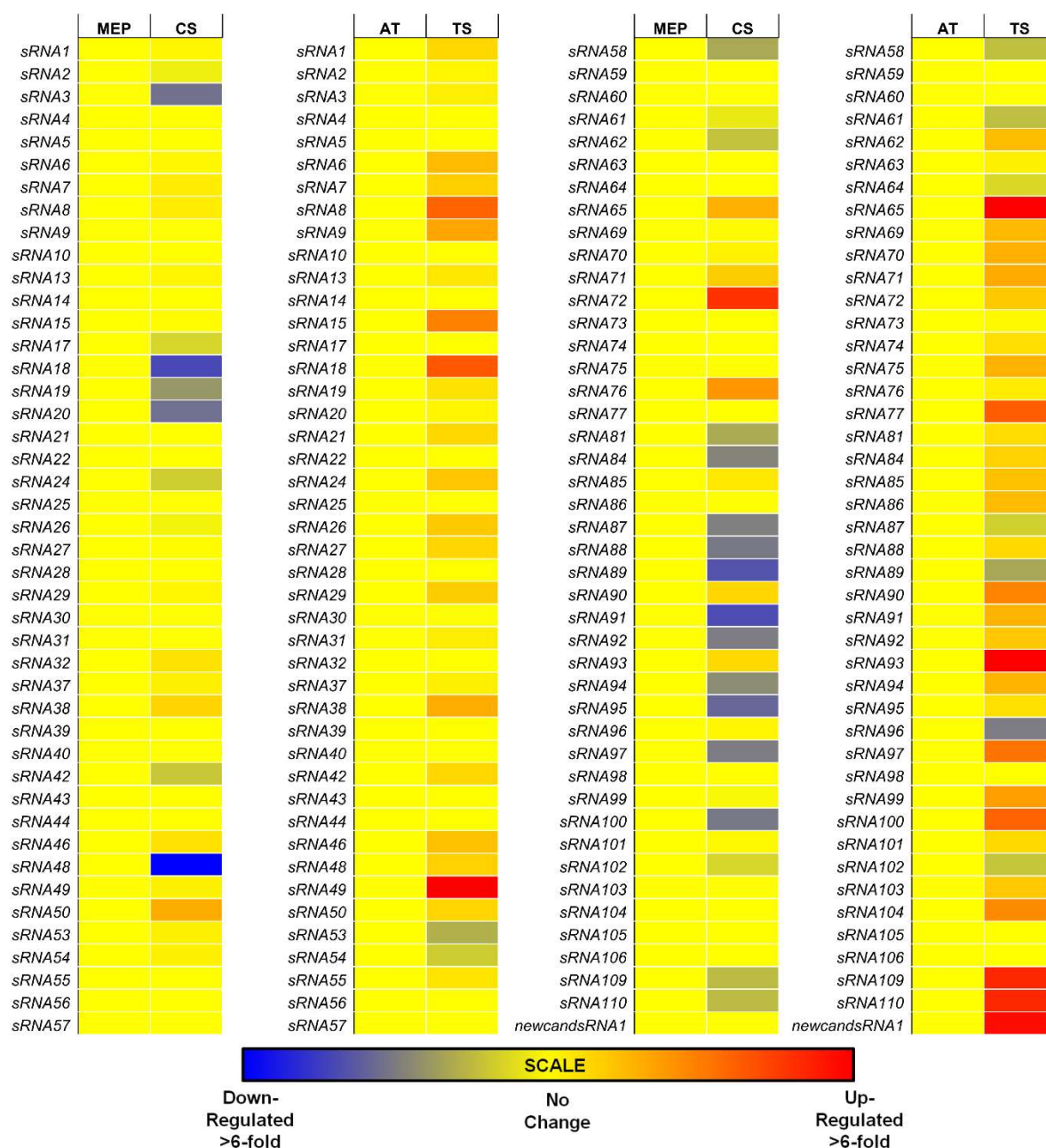


Figure 4.14: Heat map showing the relative gene expression of sRNAs at different temperatures (MEP, AT, TS and CS) based on TPM values.

Counting the most abundant sRNAs (the top 30), Table 4.9 shows the top 30 sRNAs, from the results, we see again that sRNA2 and sRNA89 were the most abundant at high levels compared to the rest of the other sRNAs in all heat shocks conditions (Figure 4.15).

Table 4.9: Ranked abundance of the Top 30 sRNAs at different temperatures based on TPM values.

Highlighted sRNAs that were further investigated are highlighted by colour.

	MEP	TPM	Col	TPM	AT	TPM	TS	TPM
1	sRNA2	21293	sRNA2	20280	sRNA89	35924	sRNA2	35006
2	sRNA89	15831	sRNA89	7035	sRNA2	29161	sRNA89	25738
3	sRNA99	1784	sRNA76	2340	sRNA76	3631	sRNA76	5003
4	sRNA37	1407	sRNA37	1861	sRNA37	2128	sRNA97	4450
5	sRNA76	755	sRNA99	1743	sRNA97	1199	sRNA99	2794
6	sRNA97	746	sRNA90	577	sRNA99	970	sRNA37	2793
7	sRNA3	619	sRNA15	549	sRNA3	642	sRNA15	1949
8	sRNA84	607	sRNA7	465	sRNA15	566	sRNA65	1870
9	sRNA15	504	sRNA97	429	sRNA84	535	sRNA90	1591
10	sRNA7	334	sRNA84	365	sRNA90	466	sRNA100	1148
11	sRNA90	318	sRNA96	338	sRNA96	413	sRNA84	1028
12	sRNA96	284	sRNA3	334	sRNA29	297	sRNA3	843
13	sRNA70	253	sRNA46	315	sRNA53	296	sRNA29	585
14	sRNA26	205	sRNA70	315	sRNA100	281	sRNA70	515
15	sRNA46	199	sRNA1	224	sRNA54	254	sRNA26	440
16	sRNA1	192	sRNA26	199	sRNA1	223	sRNA46	417
17	sRNA100	172	sRNA53	169	sRNA26	217	sRNA9	415
18	sRNA87	165	sRNA54	162	sRNA70	200	sRNA1	398
19	sRNA9	146	sRNA9	149	sRNA102	199	sRNA24	251
20	sRNA53	131	sRNA101	111	sRNA46	189	sRNA101	240
21	sRNA54	127	sRNA24	97	sRNA9	150	sRNA96	238
22	sRNA24	115	sRNA100	97	sRNA101	138	sRNA53	222
23	sRNA102	104	sRNA87	97	sRNA87	128	sRNA54	213
24	sRNA101	99	sRNA72	91	sRNA24	119	sRNA93	191
25	sRNA48	89	sRNA102	90	sRNA65	84	sRNA92	174
26	sRNA94	86	sRNA62	64	sRNA92	83	sRNA62	163
27	sRNA62	80	sRNA94	54	sRNA62	70	sRNA102	162
28	sRNA92	69	sRNA93	49	sRNA7	55	sRNA8	148
29	sRNA81	65	sRNA81	47	sRNA88	52	sRNA87	109
30	sRNA95	65	sRNA92	40	sRNA85	48	sRNA7	109

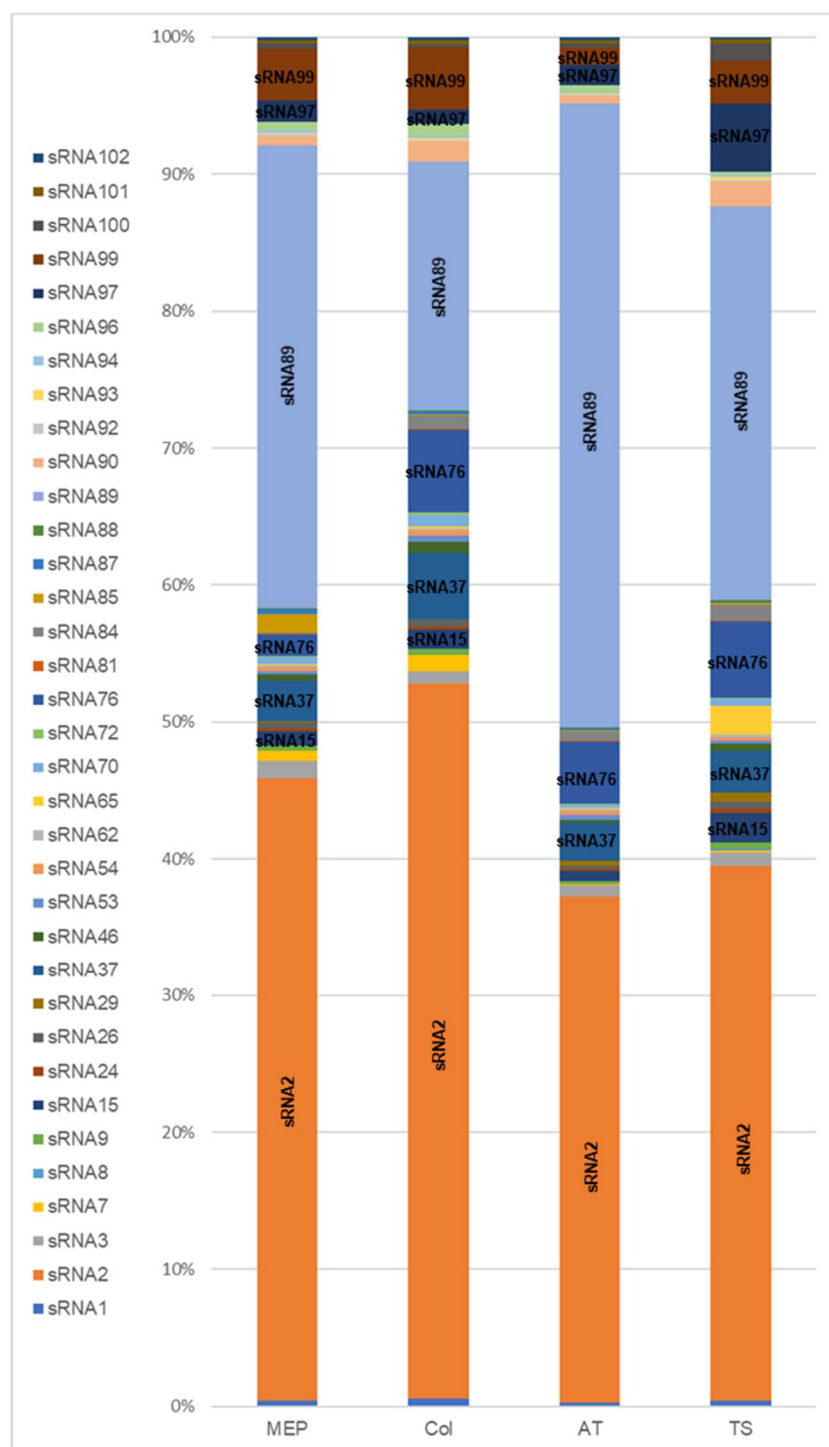


Figure 4.15: stacked column chart showing the most sRNAs that abundant in heat shocks conditions (AT, TS and CS) based on TPM values.

4.2 Investigation of sRNAs (44, 65, 75, 76, 99 and 100)

Eighty-eight sRNAs have been identified in *A. baumannii* AB5075. To narrow the selection of sRNAs to be studied in more detail, we selected sRNAs the following six sRNAs (sRNA44, sRNA65, sRNA75, sRNA76, sRNA99 and sRNA100) for further investigation because they showed a strong response to different growth phases and shocks conditions (Figure 4.16, 4.17). To confirm expression of sRNAs from the transcriptomic experiments in the different conditions, the expression level of sRNAs was analysed by Northern blotting in all different conditions (Figure 4.21, 4.22).

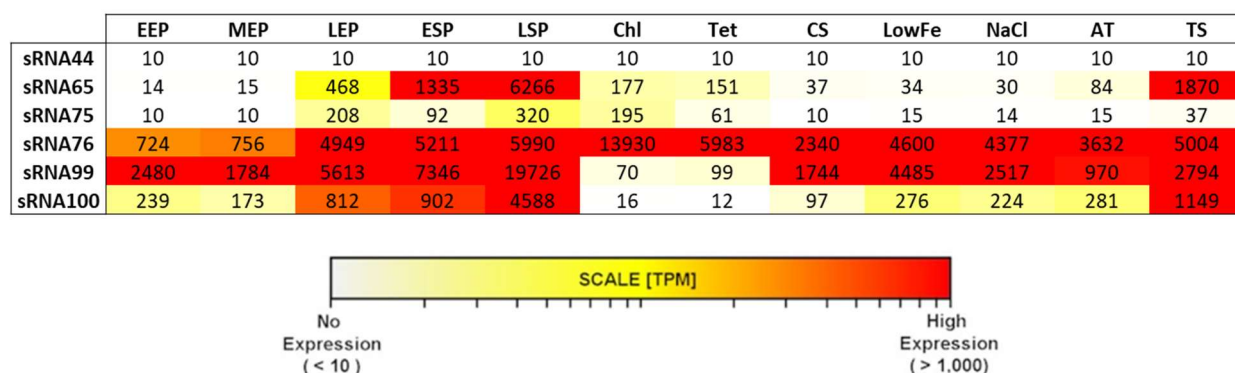


Figure 4.16: Heat map showing “absolute expression level” of sRNA44, sRNA 65, sRNA 75, sRNA 76, sRNA 99 and sRNA 100 across the environmental conditions based on TPM values.

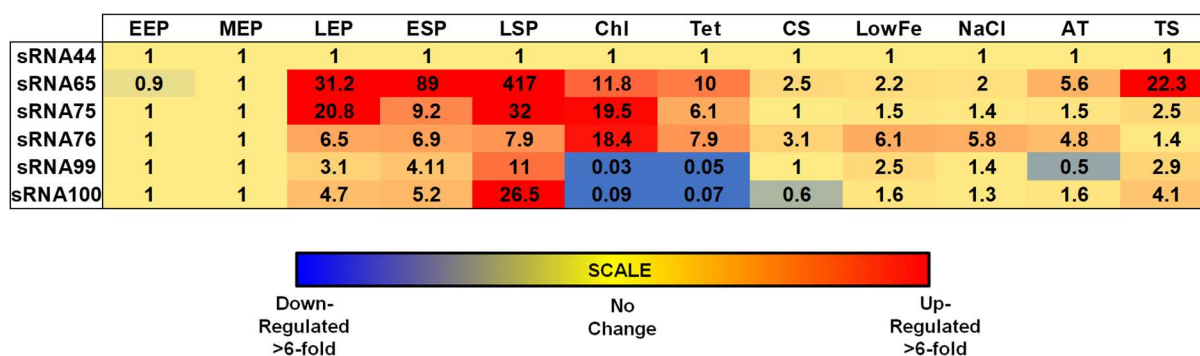


Figure 4.17: Heat map showing “relative gene expression” of sRNA44, sRNA 65, sRNA 75, sRNA 76, sRNA 99 and sRNA 100 conditions (MEP, LEP, ESP, LSP, Chl, Tet, CS, LowFe, NaCl) compared to MEP and TS compared to AT.

4.3 sRNAs deletion mutants (Δ sRNA44, Δ sRNA65, Δ sRNA75, Δ sRNA76, Δ sRNA99, Δ sRNA100)

In order to study the role of sRNAs (44, 65, 75, 76, 99 and 100) in *Acinetobacter baumannii*, we generated a deletion mutants using the gene replacement strategy as published by (Godeux *et al.*, 2020). Replacement of the sRNA gene with the *aacC4* and *sacB* selection genes, the insertion was confirmed by PCR (Figure 4.18). Subsequent removal of the selection was then again confirmed by PCR (Figure 4.19).

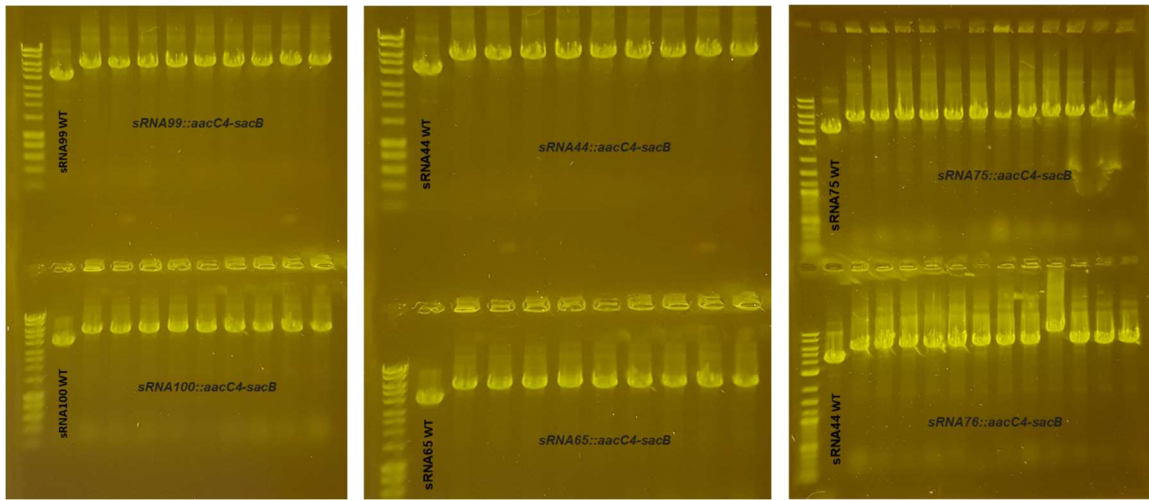


Figure 4.18: Agarose gel electrophoresis showing colony PCRs to check the insertion of *aacC4* and *sacB*, replacing sRNA99, sRNA100, sRNA44, sRNA65, sRNA75 and sRNA76. Genomic DNA of the WT was used as a control (first lane in each gel image).

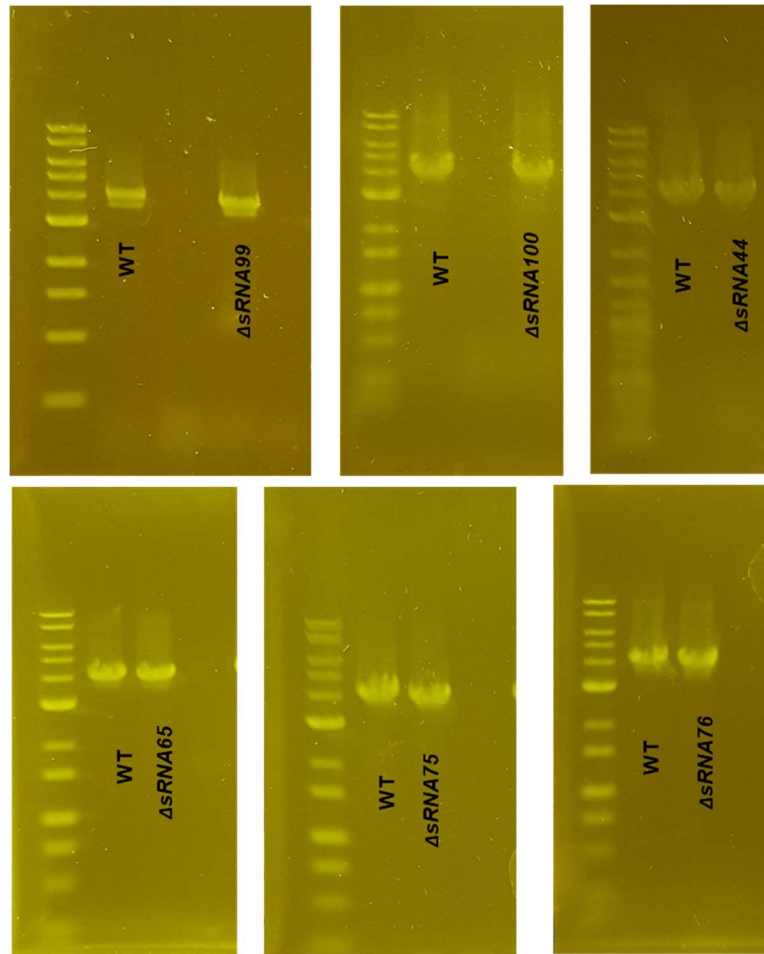


Figure 4.19: Agarose gel electrophoresis showing PCR for ($\Delta sRNA99$, $\Delta sRNA100$, $\Delta sRNA44$, $\Delta sRNA65$, $\Delta sRNA75$ and $\Delta sRNA76$) after removing the *aacC4* and *sacB* selection genes. The amplicon sizes are smaller comparing WT and sRNA deletions.

4.4 Investigation of sRNA99 and sRNA100

The sRNAs sRNA99 and sRNA100, which are located next to each other on the *A. baumannii* AB5075 chromosome (Figure 20) showed a similar expression pattern across conditions. The abundance of sRNA99 was typically overall higher than sRNA100 (Figures 4.16, 4.17 and 20). Most notably, the expression of both sRNAs dropped very strongly upon the antibiotic shocks (Chl and Tet, >10-fold down-regulation, Figures 4.16, 4.17 and 20). The reduced expression was independently confirmed by Northern blotting (Figure 4.21 (sRNA99), Figure 4.22 (sRNA100)). The band intensity for sRNA99 and sRNA100 was greatly reduced in the Chl and Tet shocks, while being visible throughout growth phases EEP-LSP (with an increase in

LSP) and in other tested shock conditions (LowFe and NaCl). This result broadly agreed with the obtained RNA-seq data (Figure 4.16, Figure 4.17).

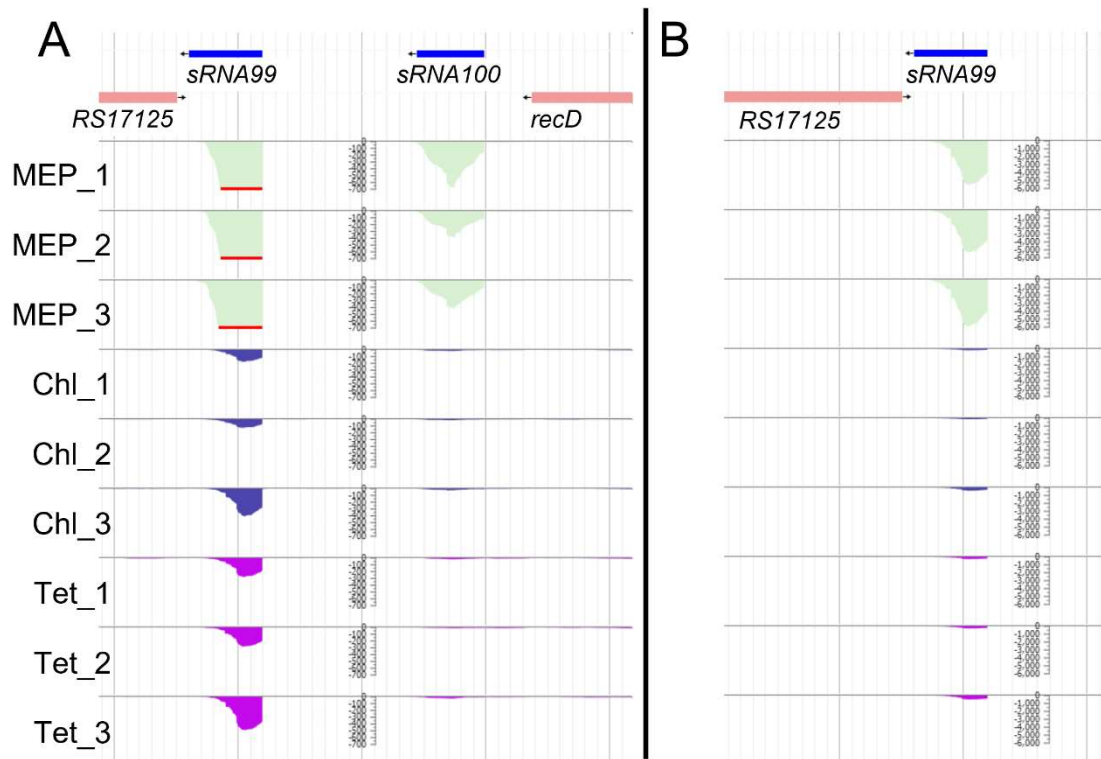


Figure 4.20: Expression pattern of sRNA99 and sRNA100 in MEP, Tet and Chl conditions generated by RNA-seq. Sequence reads have been mapped, normalized, and visualized in Jbrowse. The biological replicates are labelled with underscore and a number. The scale is 0-700 normalized reads for all tracks in (A) and 0-6000 in (B).

To investigate the impact on the transcriptome of sRNA99 and sRNA100, we carried out RNA-seq experiments comparing WT and $\Delta sRNA99$ and $\Delta sRNA100$ mutant strains in MEP. RNA-seq results confirmed the deletion and loss of expression of sRNA99 and sRNA100 (Figure 4.23) and that both deletions resulted in large transcriptomic changes. In the MEP condition, deletion of sRNA99 led to differential expression (fold-changes >2 -fold, $P_{adj} < 0.05$) of 577 genes (257 up-regulated, 320 down-regulated, Figure 4.24). Deletion of sRNA100 led to differential expression (fold-changes >2 -fold, $P_{adj} < 0.05$) of 430 genes (124 up-regulated, 306 down-regulated Figure 4.25). Overall,

the transcriptomic changes to deletion of sRNA99 and sRNA100 were similar with 46% (n=317) overlap of differentially expressed genes, which suggests that they are functionally connected but do not compensate for each other.

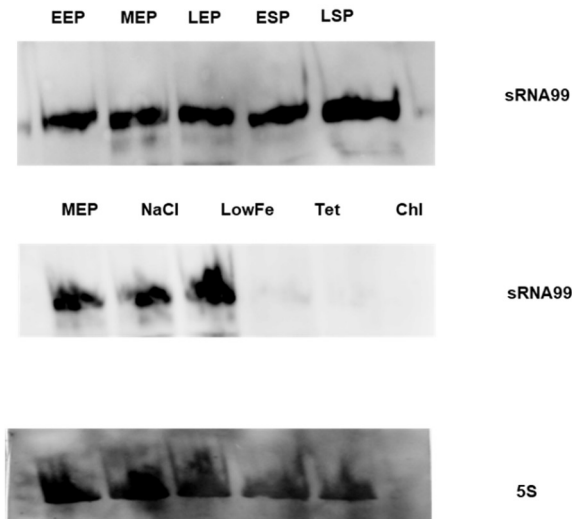


Figure 4.21: Expression of sRNA99 (149 bp size) in EEP, MEP, LEP, ESP, LSP conditions and NaCl, LowFe, Tet and Chl shocks confirmed by Northern blot with DIG-labelled sRNA99 riboprobe and 5s rRNA used as loading control.

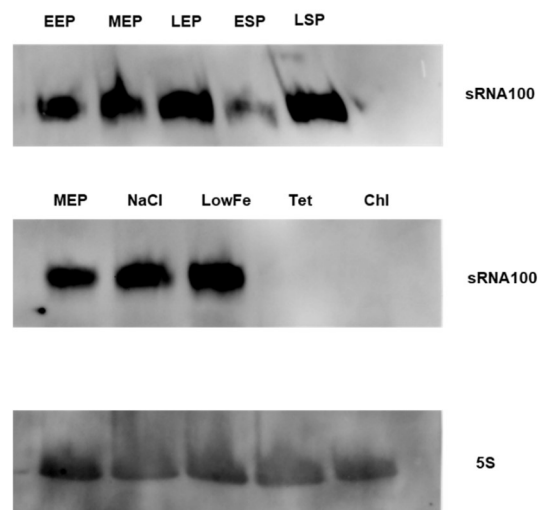


Figure 4.22: Expression of sRNA100 (136 bp size) in EEP, MEP, LEP, ESP, LSP conditions and NaCl, LowFe, Tet and Chl shocks confirmed by Northern blot with DIG-labelled sRNA100 riboprobe and 5s rRNA used as loading control.

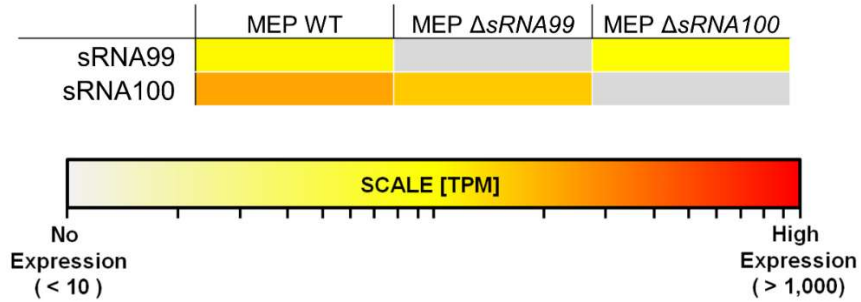


Figure 4.23: Heat map showing “absolute expression level” of sRNA99 and sRNA100 in WT, $\Delta sRNA99$ and $\Delta sRNA100$ in the MEP condition based on TPM values showing that there is no expression of sRNA99 and sRNA100 in the respective mutant strains confirming their deletion.

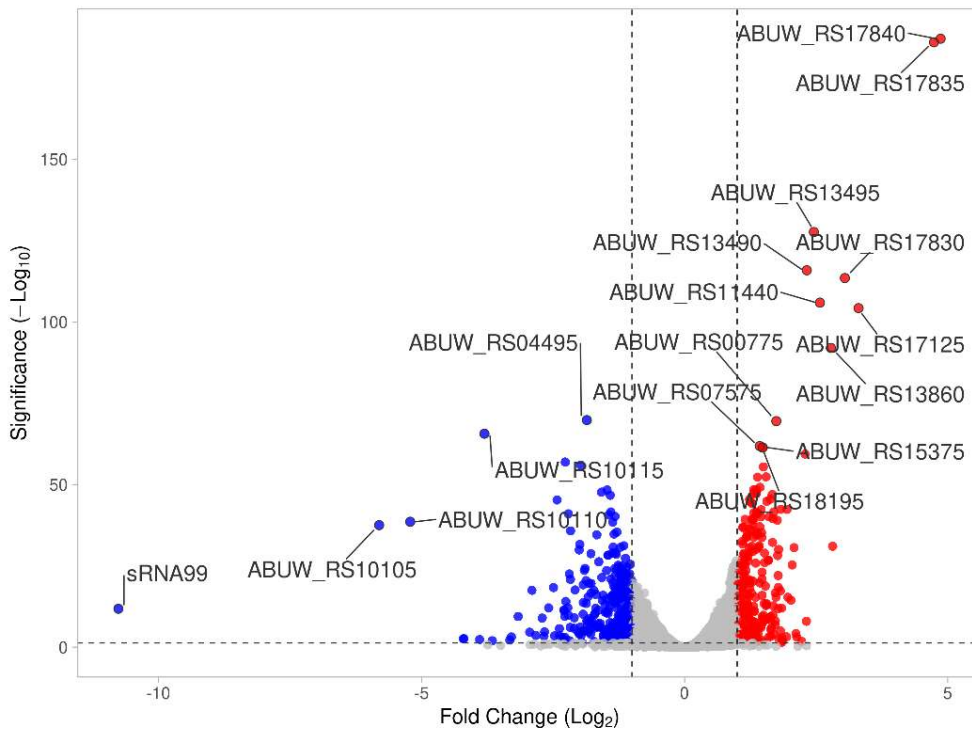


Figure 4.24: Gene expression changes comparing WT and $\Delta sRNA99$ in the MEP condition. The vertical lines are at a fold change of 2 and the horizontal line indicates the significance cut-off (at P_{adj} value of 0.05). Red dots ($n=257$) show genes that are more than 2-fold up-regulated and a $P_{adj} < 0.05$ in the $\Delta sRNA99$ mutant and a $P_{adj} < 0.05$, blue dots ($n=320$) show genes that are more than 2-fold down-regulated and a $P_{adj} < 0.05$ in the $\Delta sRNA99$ mutant.

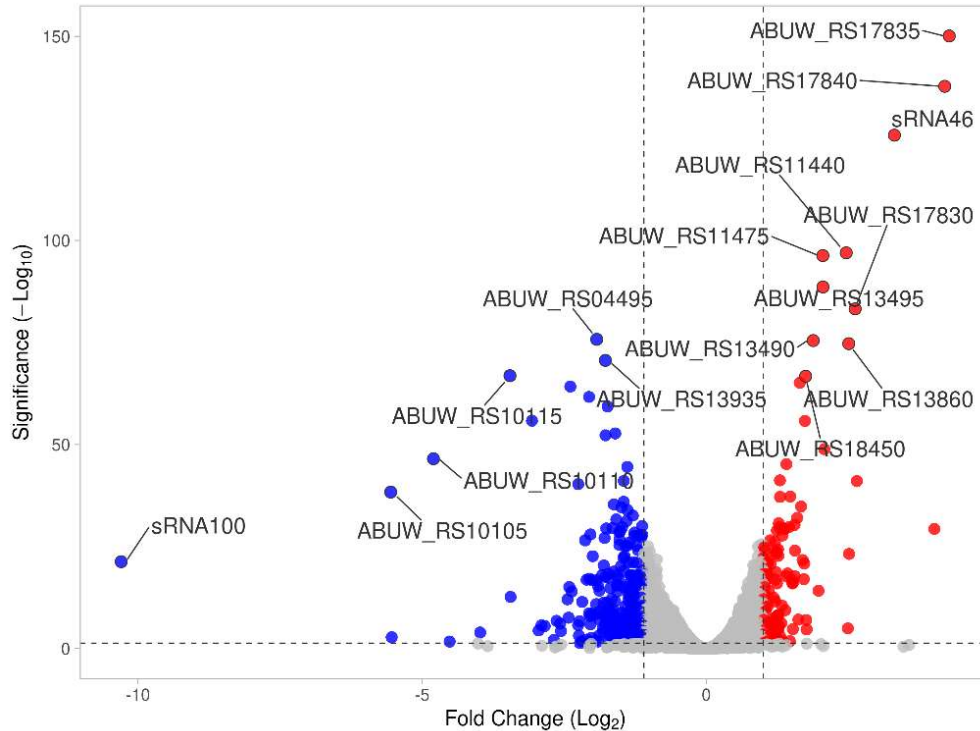


Figure 4.25: Gene expression changes comparing WT and $\Delta sRNA100$ in the MEP condition. The vertical lines are at a fold change of 2 and the horizontal line indicates the significance cut-off (at P_{adj} value of 0.05). Red dots ($n=124$) show genes that are more than 2-fold up-regulated and a $P_{adj} < 0.05$ in the $\Delta sRNA100$ mutant and a $P_{adj} < 0.05$, blue dots ($n=306$) show genes that are more than 2-fold down-regulated and a $P_{adj} < 0.05$ in the $\Delta sRNA100$ mutant.

The genes that showed the largest difference in expression were similarly expressed in $\Delta sRNA99$ and $\Delta sRNA100$ mutants. Three genes that showed strong up-regulation in both $\Delta sRNA99$ and $\Delta sRNA100$ mutants are in an operon: *ABUW_RS17830* (signal peptidase II, also annotated in uniparc as *ispA* that could remove signal peptides from prolipoproteins), *ABUW_RS17835* (cation transporter, also annotated in uniprot as *cadA*, heavy metal detoxification protein) and *ABUW_RS17840* (ISL3-like element ISPPu12 family transposase) (Figures 4.24, 4.25, 4.26, and 4.27). A second gene showing up-regulation is also annotated as a cation transporter (*ABUW_RS13860*, annotated in uniprot as a cadmium, cobalt and zinc/H(+)-K(+) antiporter). Therefore, differences in membrane transport could be expected in the sRNA mutants and further experiments would be required to dissect their roles. In both mutants, three genes of an operon showed very strong down-regulation: *antA*, *antB* and *antC* (*ABUW_RS10105*,

ABUW_RS10110 and *ABUW_RS10115*), which encode for anthranilate 1,2-dioxygenase large subunit, anthranilate 1,2-dioxygenase small subunit and anthranilate 1,2-dioxygenase electron transfer component (Figure 4.24, 4.25, 4.26 and 4.27).

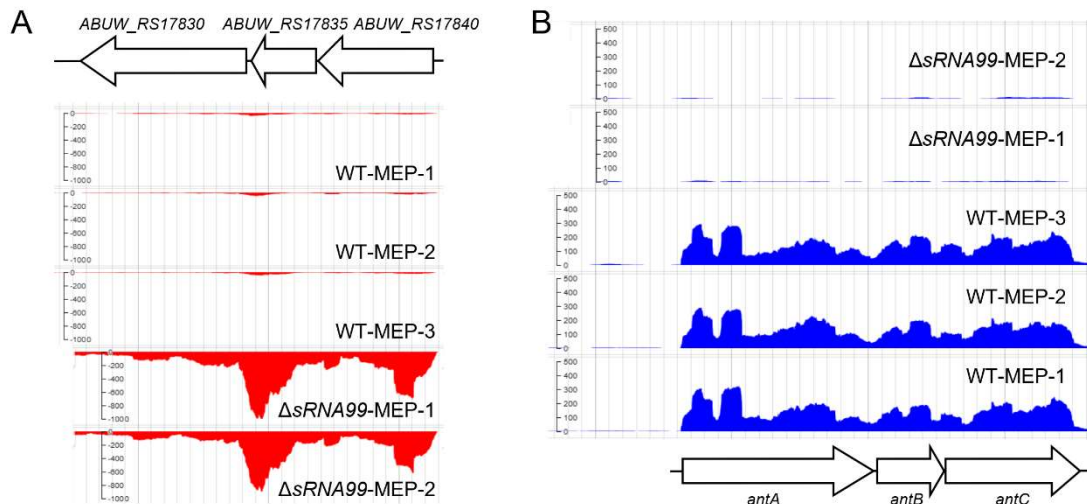


Figure 4.26: Differential expression of genes upon deletion of *sRNA99*. (A) The operon *ABUW_RS17830-40* is up-regulated in the $\Delta sRNA99$ mutant. (B) The *antA-C* operon is down-regulated in the $\Delta sRNA99$ mutant. Normalised sequence reads are plotted. The scale is 0-1000 reads in (A) and 0-500 reads in (B) visualised in Jbrowse.

The enzyme catalyses the reaction from anthranilate (2-aminobenzoate) to catechol (Eby *et al.*, 2001), which can be further metabolised. Therefore, anthranilate can be used as a carbon source by *Acinetobacter* spp., which was shown in *A. baylyi* ADP-1 (Eby *et al.*, 2001). Why these genes are expressed in the WT is unclear and is in contradiction with data from Chapter 3 (in Chapter 3 and for the RNA-seq experiments in this Chapter, two different companies were used, and new RNA samples were sent). Therefore, the difference in expression should be independently verified. Another interesting down-regulated gene is *lysM* (*ABUW_RS15080*), which encodes a peptidoglycan-binding protein (Figure 4.27). Typically, enzymes containing the LysM domain are peptidoglycan hydrolases and are widespread in bacteria (Buist *et al.*, 2008). LysM-domain containing proteins most likely recognize the N-acetylglucosamine moiety of peptidoglycan (Buist *et al.*, 2008).

Whether sRNA99 and sRNA100 are *trans*-acting regulatory RNAs is also not clear. IntaRNA prediction did not predict strong duplexes between sRNA99 and sRNA100 with the genes changing in expression above. The effects might also not be direct effects of regulation of the genes that change expression, but indirect effects of regulation. Further experiments will be required to characterise the biological roles of sRNA99 and sRNA100 in more detail.

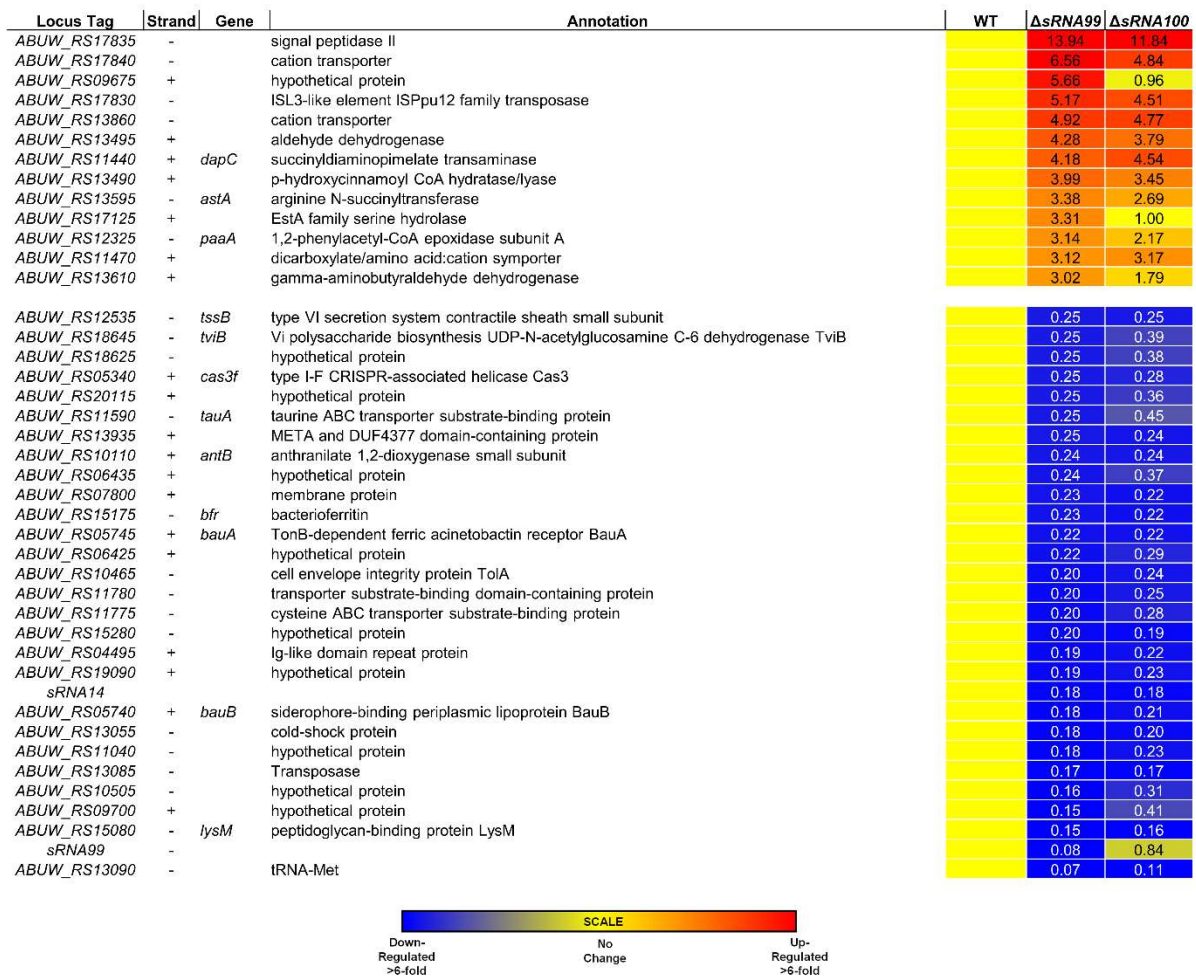


Figure 4.27: Heat map showing “relative gene expression” comparing WT with Δ sRNA99 and Δ sRNA100 in the MEP condition based on TPM values. The data are sorted by the fold-change in Δ sRNA99. Note that the fold-changes based on TPM data are slightly different to DESeq2 values, but overall trends are similar.

4.5 Target prediction of sRNA65, sRNA75 and sRNA76

sRNA65 showed low expression in response to LEP, Chl and Tet and showed high expression in ESP, LSP and TS, while showed almost no expression in other stresses. Therefore, a condition, where the function of sRNA65 should be studied could be the effect of temperature shift. Previous work from our group using the Hi-GRIL-seq method identified potential target molecules for sRNAs in *A. baumannii* AB5075 (Hamrock *et al.*, 2023) (Table 4.10). In Hi-GRIL experiment the sRNAs ligate onto other RNA molecules and this makes a chimera, all of these chimeras are sequenced and the number of actual sequences that detected for each sRNAs attached to molecules. Messenger RNAs that were ligated to sRNA65 included a DUF2171 domain-containing protein (*ABUW_RS07145*), also the peptidoglycan-binding protein (*lysM*, *ABUW_RS15080*) and an OmpA family protein (*ABUW_RS03195*). sRNA75 showed highest expression in LSP. Ligated RNA molecules from Hi-GRIL-seq include *ABUW_RS11870* (hypothetical protein) and *ABUW_RS12325* (1,2-phenylacetyl-CoA epoxidase subunit A). sRNA76 showed strong up-regulation in the antibiotic shock conditions, mild up-regulation in the NaCl and LowFe conditions and was more abundant towards stationary phase compared to early growth stages. This suggests that the sRNA could be involved in a more general stress response, because it is up-regulated in multiple shock conditions and would be an interesting sRNA to investigate further in the future.

4.6 Target prediction of sRNA44

In the data presented above, sRNA44 showed “no expression” in all conditions tested. Therefore, it seems counter-intuitive why this sRNA was selected for further analysis. Previous data suggested that the sRNA is expressed in a pooled sample of 16 conditions (Kröger *et al.*, 2018) and that was ligated to genes of biological relevance (e.g., the biofilm-associated protein *bap*, (*ABUW_RS19720*)). This sRNA will be investigated in more detail in Chapter 5.

Table 4.10: sRNAs as a target for sRNA analysis.

sRNA	Gene	Target	Number of ligations in Hi-GRIL-seq
44	ABUW_RS19720	<i>bap</i> , Ig-like domain-containing protein	28
	ABUW_RS10035	dipeptidase	22
	ABUW_RS05340	type I-F CRISPR-associated helicase Cas3	11
65	ABUW_RS07145	DUF2171 domain-containing protein	93
	ABUW_RS15080	peptidoglycan-binding protein LysM	54
	ABUW_RS03195	OmpA family protein	43
75	ABUW_RS11870	hypothetical protein	31
	ABUW_RS12325	1,2-phenylacetyl-CoA epoxidase subunit A	11
76	ABUW_RS11470	dicarboxylate/amino acid:cation symporter	1633
	ABUW_RS00325	4-hydroxyphenylpyruvate dioxygenase	427
	ABUW_RS03195	OmpA family protein	410
99	ABUW_RS05940	Superoxide dismutase	164
	ABUW_RS12330	Phenylacetic acid degradation difunctional protein PaaZ	48
	ABUW_RS02765	Carbapenem-hydrolysing class D beta- lactamase OXA-23	32
100	ABUW_RS11470	dicarboxylate/amino acid:cation symporter	1016
	ABUW_RS17415	DsbA family oxidoreductase	712
	ABUW_RS16775	endonuclease	665

Chapter 5

Mechanistic characterisation of small RNA44

5.1 Does sRNA44 exist in *A. baumannii* AB5075?

In our large-scale RNA-seq experiments outlined in Chapter 3 and Chapter 4, we do not see sRNA44 expressed at a level that would suggest a biological role (i.e., a TPM value higher than 10) or even presence of an sRNA gene at the annotated position. However, sRNA44 has been annotated based on (d)RNA-seq data generated previously in *A. baumannii* ATCC17978 and the expression from a pooled RNA sample from 16 different conditions shows transcriptional start site and expression of sRNA44 (Figure 5.1).

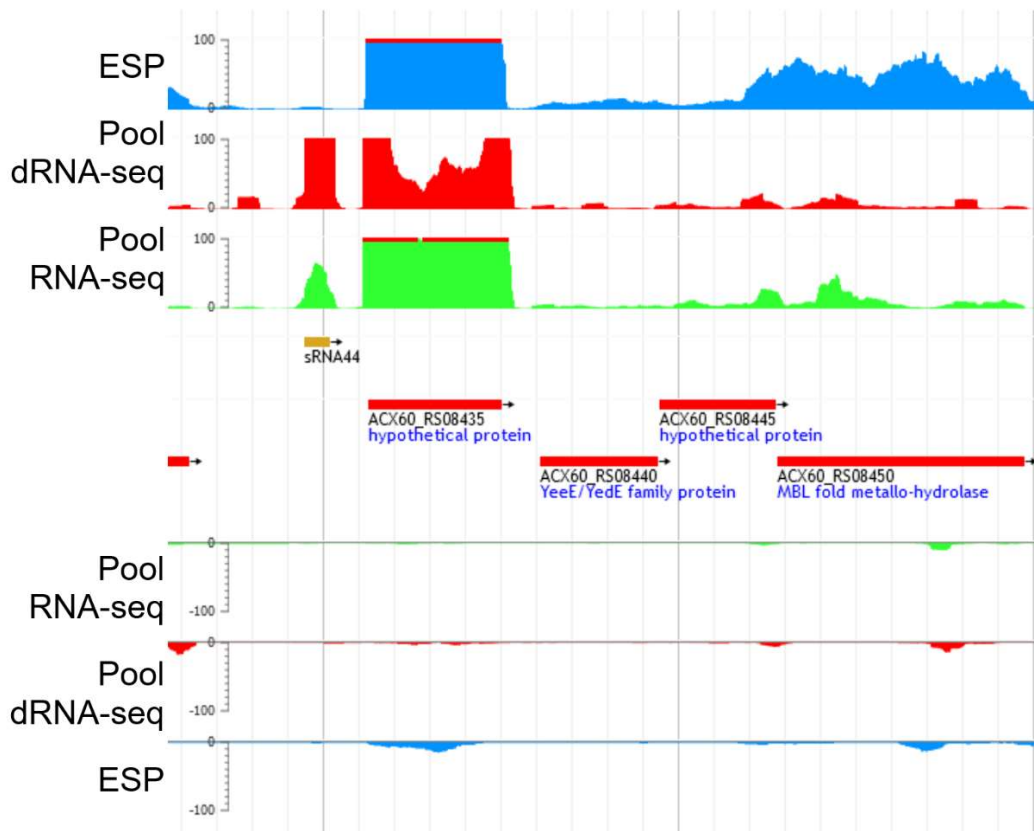


Figure 5.1: Expression of sRNA44 (orange annotation) in pooled RNA samples from 16 different environmental conditions (Kröger *et al.*, 2018a). The scale of normalized sequencing reads mapped to the *A. baumannii* ATCC17978 genome is 100 and illustrated in AcinetoCom.

The locus is conserved in *A. baumannii* AB5075 (Kröger *et al.*, 2018), therefore it was likely that sRNA44 is also expressed in AB5075. Previously, we have observed for *Salmonella enterica* that the commercial kits for RNA-seq library preparation sometimes do not recover small RNAs. The dRNA-seq data (Figure 5.2) was carried out by an in-house linker-ligation based method (by vertis Biotechnology, which has since closed for business) that results in better retention of small transcripts including sRNAs during library preparation for RNA-seq. This could also be negatively impacted by a large predicted loop at the 5'-end of sRNA44 (Figure 5.3). We detected sRNA44 in RNA-RNA ligation events generated by Hi-GRIL-seq (see below, and (Hamrock *et al.*, 2023)) which confirms that sRNA44 is present and expressed in AB5075 at least in the ESP condition.

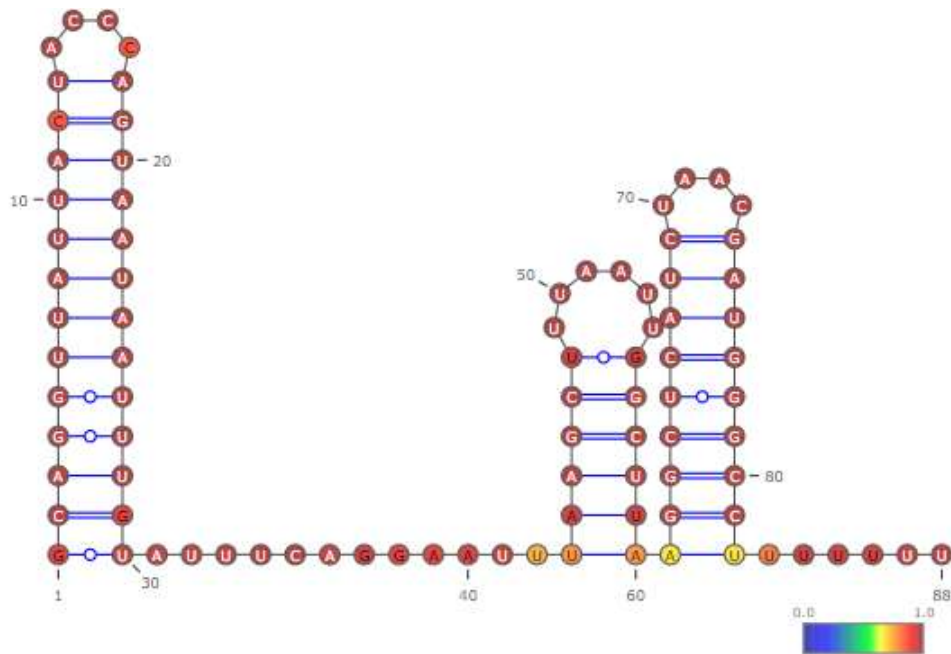


Figure 5.2: Predicted secondary structure of sRNA44 Made by RNAfold webserver and VARNA used to visualise the sRNA. RNAfold minimum free energy (MFE) prediction was used. The scale bar and colour of the nucleotides reflects the base-pair probability where the more certain nucleotides are closer to red (=1) and the less certain ones are closer to blue (=0).

5.2 Identification of sRNA-mRNA interaction pairs

Two lines of investigation were pursued to identify mRNA target molecules of sRNA44: the Hi-GRIL-seq experiment by Hamrock *et al.* (Hamrock *et al.*, 2023) and bioinformatic predictions, and a “target hunt” experiment through transient overexpression of sRNA44 using the plasmid constructed above followed by RNA-seq. The two processes are outlined below.

5.3 Target molecule identification of sRNA44 with Hi-GRIL-seq.

Data from a proximity ligation experiment was used to identify possible target molecules of sRNA44 (Hamrock *et al.*, 2023). The Hi-GRIL-seq experiment relies on the inducible expression of T4 RNA ligase that ligates RNAs in proximity including sRNA-mRNA duplexes that might be functionally relevant interactions. The experiment was carried out in four different conditions (**Table 5.1**): “NI” (T4 RNA ligase non-induced), “IND” (T4 RNA ligase induced), “DIP” (T4 ligase induced and addition of iron chelator 2,2'-dipyridyl) and “IMIP” (T4 RNA ligase induced and addition of sub-inhibitory concentrations of imipenem). Three mRNAs were ligated to sRNA44: ABUW_RS20195 (encoding a hypothetical protein), ABUW_RS19720 (annotated as encoding a “Ig-like domain-containing protein”, a.k.a. biofilm-associated protein *bap*) and ABUW_RS05340 (annotated as encoding a Type I-F CRISPR-associated helicase Cas3).

Table 5.1: Number of the three most abundant ligation events of sRNA44 from Hi-GRIL-seq (Hamrock *et al.*, 2023).

Gene	Function	Number of ligation events				% reads of Hi-GRIL-seq-mapping to IntaRNA prediction
		NI	IND	DIP	IMIP	
ABUW_RS19720	Ig-like domain-containing protein (<i>bap</i>)	0	8	14	6	100%
ABUW_RS20195	Hypothetical protein	0	12	4	6	22.72%
ABUW_RS05340	Type I-F CRISPR-associated helicase Cas3	0	3	6	2	0%

To confirm sRNA-mRNA interactions in *A. baumannii* AB5075 from Hi GRIL-seq and CopraRNA the IntaRNA was used (Mann *et al.*, 2017). These results were then

compared to the previous data from the Kröger group (Hamrock, 2021) to find the percentage chimera mapping to the Hi-GRIL-seq data (Table 5.1). While over 30 interactions were investigated in this manner, only one interaction pair was identified with over 50% chimera mapping. Because this interaction pair mapped 100% of its chimeras to the Hi-GRIL-seq data, we consider it to be an extremely promising interaction partner. The data predicted that sRNA44 interacts with *bap* (*ABUW_RS19720*) mRNA. This interaction pair had 100% chimera mapping to the Hi-GRIL-seq data making it a very promising interaction pair. The Bap protein (Penesyan *et al.*, 2019) which may be secreted from the cell and may be involved in cellular adhesion and biofilm maturation (Loehfelm *et al.*, 2008; Law and Tan, 2022). Therefore, secondary structures often play a role in base-pairing, for instance aiding the binding of target molecules. To determine the secondary structure of sRNA44, the programme VARNA was employed (Figure 5.2). This structure showed that the predicted seed sequence, which is a short, typically conserved sequence in sRNAs with complementarity in the target mRNA facilitating the interaction between the two (Bandyra *et al.*, 2012), of sRNA44 is located in a single stranded region of the molecule. The single stranded nature of this region aids its accessibility for interaction with another molecule, supporting the assumption that this is where the sRNA-mRNA interaction is occurring. Even though the sRNA44-bap interaction pair had been found, it still needed to go through the process of being experimentally verified, and all of the subsequent research centred on this interaction pair.

5.4 Investigation of sRNA44-*bap* mRNA interaction

To validate sRNA44 as post-transcriptional regulator of *bap* mRNA in *A. baumannii*, IntaRNA was used to predict a possible RNA-RNA duplex formation of sRNA44 with *bap* mRNA. The prediction showed a long 20 nucleotide duplexes followed by a shorter six nucleotide duplex (**Figure 5.3**). The longer duplex formed directly after the start codon of *bap* mRNA therefore the possible mechanism of regulation is not straightforward to predict and whether this interaction could have an influence on translation initiation.

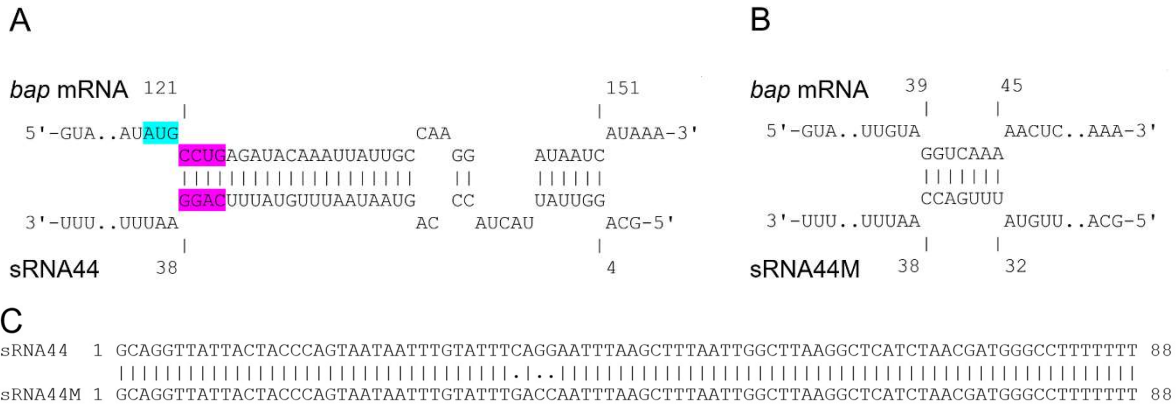


Figure 5.3: Prediction of sRNA44-*bap* mRNA interaction with IntaRNA (Mann *et al.*, 2017). (A) Predicted RNA-RNA duplex of sRNA44 and *bap* mRNA. The numbers refer to location relative to the transcriptional start sites. The start codon (AUG) of *bap* is highlighted in light blue. The nucleotide sequence (5'-CAGG-3') mutated for sRNA44M is shown in pink. (B) Predicted remaining RNA-RNA interaction between sRNA44M (5'-CAGG-3' -> 5'-GACC-3') and *bap* mRNA showing that the interaction in (A) is disrupted. (C) Sequence alignment of sRNA44 (WT) and sRNA44M.

To experimentally validate this interaction, we used the established two-plasmid system in *E. coli*, because we do not have two compatible plasmids that replicate in *A. baumannii* AB5075 (Figure 5.4). The plasmids for these experiments were created as part of the MSc thesis by Jessica White (Kröger Lab). In this system, the regulation by an sRNA of a target mRNA is analysed through a constitutive expression of the sRNA and a translational fusion of the target gene with sfGFP. For the plasmid pXG10sf-*bap*-sfGFP, the sequence from the transcriptional start site of *bap* and the first 13 codons were cloned in frame with a start codon-less sfGFP gene, which includes the predicted interaction site of sRNA44 with *bap* mRNA. As a control, a short non-sense RNA expressing plasmid (pJV300) is combined with pXG10sf-*bap*-sfGFP.

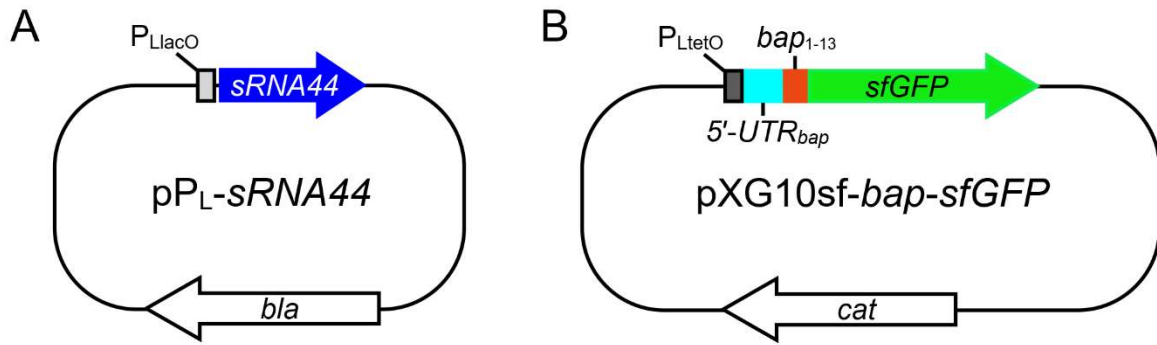


Figure 5.4. Plasmids to investigate *sRNA44-bap* sRNA-mRNA interaction in *E. coli* (Urban and Vogel, 2007; Corcoran *et al.*, 2012). (A) The pPL-sRNA44 expresses sRNA44 (dark blue) constitutively from the P_{LlacO} promoter (light grey box) and possesses a beta-lactamase (*bla*, empty arrow) gene for selection with ampicillin. (B) A translational fusion encoding the 5' untranslated region (UTR, light blue) and the first 13 codons of *bap* (brown) fused to a translational start codon-less sfGFP (green). Constitutive expression is achieved by the P_{LtetO} promoter (dark grey box). The plasmid encodes a chloramphenicol acetyltransferase (*cat*, empty arrow) for selection with chloramphenicol. The plasmids were generated by Jessica White (White, 2022).

The plasmids are capable of co-replicating in *E. coli* TOP10 cells. The strains equipped with the two plasmids were grown in L-broth and on L-agar overnight and the abundance of Bap-sfGFP was visualised on a blue light table (Figure 5.5). The level of Bap-sfGFP in the strain expressing the WT version of sRNA44 was markedly reduced compared to the control plasmid pJV300 suggesting that sRNA44 inhibits translation of Bap-sfGFP. Expressing the mutant version sRNA44M abrogated the effect on translation of Bap-sfGFP showing that sRNA44M was no longer able to repress translation. This suggests that the three mutated nucleotides in sRNA44M are involved in base-pairing with *bap-sfGFP* mRNA. To quantify the level of translational repression, the same strains as above were grown overnight and the Bap-sfGFP abundance was measured in a plate reader. Measuring 100 μ L from an overnight culture confirmed a statistically significant lower abundance of Bap-sfGFP when co-expressed with WT sRNA44 compared to the empty plasmid pJV300 and the mutated sRNA44M (Figure 5.6).

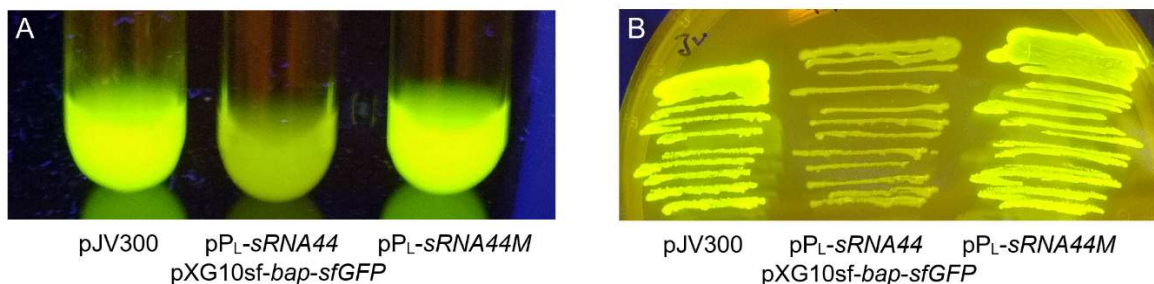


Figure 5.5: Expression of sRNA44 down-regulates translation of Bap-sfGFP in *E. coli*. (A) Visualisation of Bap-sfGFP abundance of *E. coli* overnight cultures carrying pXG10sf-bap-sfGFP and pJV300 (left), pPL-sRNA44 (middle) and pPL-sRNA44M (right) on a blue light table. (B) Visualisation of Bap-sfGFP abundance of *E. coli* cultures streaked on L-agar carrying pXG10sf-bap-sfGFP and pJV300 (left), pPL-sRNA44 (middle) and pPL-sRNA44M (right) on a blue light table.

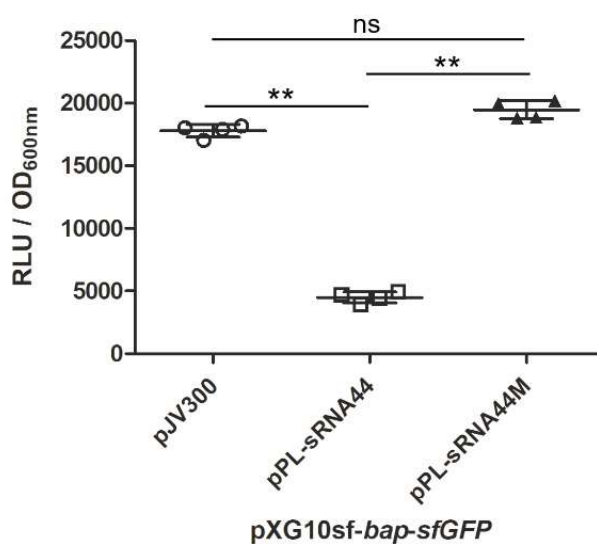


Figure 5.6: Quantification of Bap-sfGFP abundance in *E. coli*. All strains carry the pXG10sf-bap-sfGFP plasmid. Cells are co-transformed with pJV300, pPL-sRNA44 and pPL-sRNA44M respectively. Samples taken from overnight cultures grown in L-broth and were measured in a plate reader (100 μ L). Statistical analysis was carried out with the Kruskal–Wallis test with post hoc analysis via Dunn’s multiple comparison test with statistical significance set at a P value of 0.05 (*P<0.05, **P<0.01, ***P<0.001).

5.5 Expression of *bap* in *A. baumannii* in WT and sRNA44 mutant strains

To test the expression of *bap* upon deletion and complementation of sRNA44 in *A. baumannii*, qRT-PCR was performed to measure *bap* mRNA abundance. RNA was isolated at ESP and expression was compared to *lptB* mRNA, which encodes an LPS export ABC transporter ATP-binding protein and which little changes to environmental

changes. Deletion of sRNA44 resulted in a mild up-regulation (~1.6-fold) of *bap*, whereas overexpression of sRNA44 resulted in mild down-regulation of *bap* (~2-fold) (Figure 5.7). This could indicate that sRNA44 is important for optimal gene expression of *bap* in *A. baumannii*.

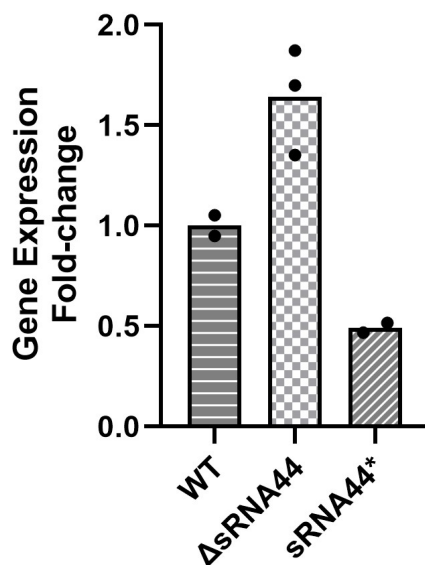


Figure 5.7: Gene expression of *bap* compared to *lptE* measured by qRT-PCR ($2^{-\Delta\Delta C_t}$ method). Deletion of sRNA44 (Δ sRNA44) led to higher level of *bap* mRNA, while overexpression of sRNA44 resulted in lower level of *bap* mRNA (sRNA44*). No statistical analysis was performed, because for WT and sRNA44*, only biological replicates were obtained.

5.6 Impact of sRNA44 on biofilm formation

It was discovered that sRNA44 represses translation of *bap* in *E. coli*. As this interaction was carried out in a heterologous host, it remained unexplored whether sRNA44 influences *bap* expression in *A. baumannii* AB5075. Since Bap is a biofilm associated protein, we tested the effect of sRNA44 deletion on biofilm formation. As a control, the *bap* gene was deleted (Figure 5.8) and used in biofilm formation assays. If sRNA44 reduces the production Bap in the cell, the expectation would be that sRNA44 deletion would result in a higher level of Bap production and potentially a quicker biofilm formation as compared to the WT.

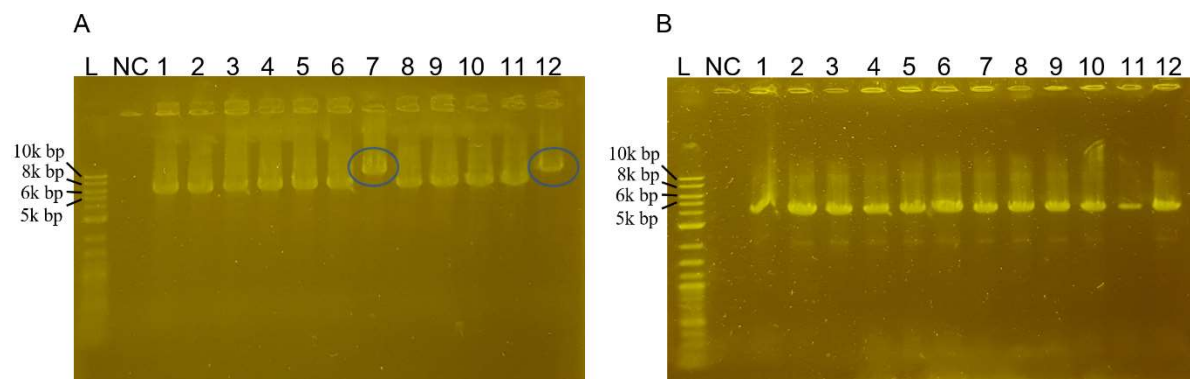


Figure 5.8: Deletion of the *bap* gene. (A) Colony PCR confirming insertion of *aacC4* and *sacB* genes into *bap* locus (highlighted by circle, lanes 7 and 12, expected size: 8000 bp). All other colonies were WT (expected size: 5455 bp). (B) PCR confirmation after removal of *aacC4* and *sacB* genes after counterselection. All colonies were correct (expected size: 4000 bp) and suggested successful deletion of the *bap* gene. NC: Negative control (no cells added to PCR) L: “Ladder”, DNA size standard.

Biofilm formation was measured over the periods of 24, 48 and 72 hours (Figure 5.9, wild-type AB5075, AB5075 $\Delta sRNA44$ and AB5075 Δbap). Wells were stained with crystal violet and biofilm formation was measured by absorbance at 570 nm. The experiment showed that the $\Delta sRNA44$ strain had significantly more biofilm formation compared to WT and that the Δbap strain produced less biofilm formation after 24h. Longer incubation (48 and 72 h) led to saturation of biofilm production showing that the kinetics of biofilm formation were different at earlier stages of biofilm formation between the different strains. It also shows that the Δbap mutant is still capable of biofilm formation and that *bap* may not be essential for this process. However, this result does not offer evidence of a significant impact upon biofilm formation in the $\Delta sRNA44$ mutant. (Figure 5.9).

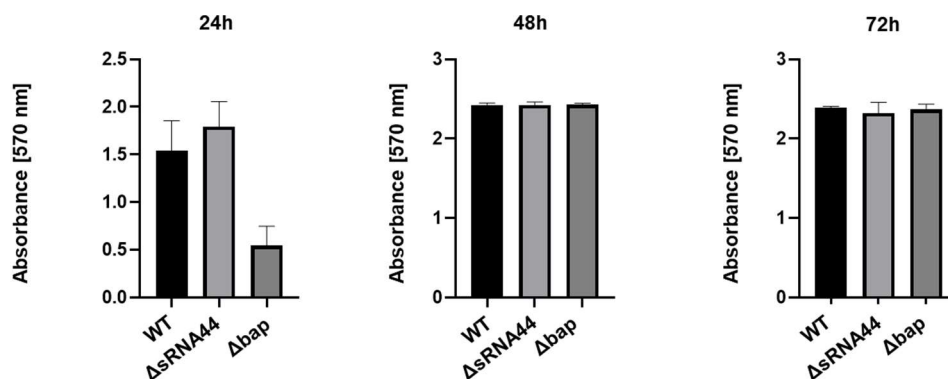


Figure 5.9: Impact of *sRNA44* and *bap* on biofilm formation in *A. baumannii* strain AB5075. Biofilm formation was compared in *A. baumannii* strains WT, $\Delta sRNA44$ and Δbap after 24, 48 and 72 h incubated at 37°C. Biofilm formation was measured as absorbance at 570 nm.

5.7 Identification of additional mRNA target molecules through transient overexpression of sRNA44

Because the expression sRNA44 could be potentially low, and to identify target molecules of sRNA44 apart from the Hi-GRIL-seq data produced in Hamrock *et al.*, we constructed an sRNA44 overexpression plasmid based on the published pVRL2Z plasmid that replicates in *A. baumannii* AB5075 and possesses a zeocin resistance gene for selection (Lucidi *et al.*, 2018). To only obtain sRNA44 expression from the plasmid and not the chromosomal locus, an sRNA44 deletion mutant ($\Delta sRNA44$) was constructed (Godeux *et al.*, 2020). The sRNA44 gene was then cloned into pVRL2Z (pVRL2Z-sRNA44), which contains an L-arabinose-inducible promoter and the *araC* gene (Lucidi *et al.*, 2018). This plasmid, and the control “empty” plasmid (pVRL2Z), were transformed into the *A. baumannii* AB5075 $\Delta sRNA44$ mutant strain. The concentration of L-arabinose needed to induce high expression of sRNA44 was assessed from pVRL2Z-sRNA44 in $\Delta sRNA44$ mutant strain with Northern blotting (Figure 5.10). This strain was grown to ESP and sRNA44 expression was induced for 0 min, 15 min, 30 min and 1 h with varying concentrations of L-arabinose (0 mM, 50 mM and 100 mM). We observe a dose-dependent induction of full length sRNA44, with high expression in 100 mM L-arabinose from 30 mins. Because the Northern blot was not very clear (Figure 5.10), the induction (30 min, 100 mM L-arabinose) of sRNA44

expression was independently replicated and showed clear albeit weak expression of sRNA44 only when induced (Figure 5.11).

To identify additional sRNA44 target genes, gene expression of cells harbouring pVLR2Z-sRNA44 were grown to ESP after which the expression of sRNA44 was induced for 30 min was compared with non-induced cells. RNA-seq results identified 50 genes that showed significant changes (>2 -fold-change, $P_{adj} < 0.05$) in gene expression (Figure 5.10, Table 5.2, Table 5.3). The sRNA44 was shown to be over-expressed confirming the results seen on the Northern blot (Figure 5.11, Table 5.2). Overall, fold-changes were comparably mild. The up-regulated genes contain many genes that are annotated as hypothetical genes and none of the genes had a common gene name. Therefore, it was hard to select genes that could be test for phenotypes. In the list of down-regulated genes, there were a few genes with a clearer annotation. The most down-regulated gene (6.7-fold) is annotated as a DEAD/DEAH box helicase.

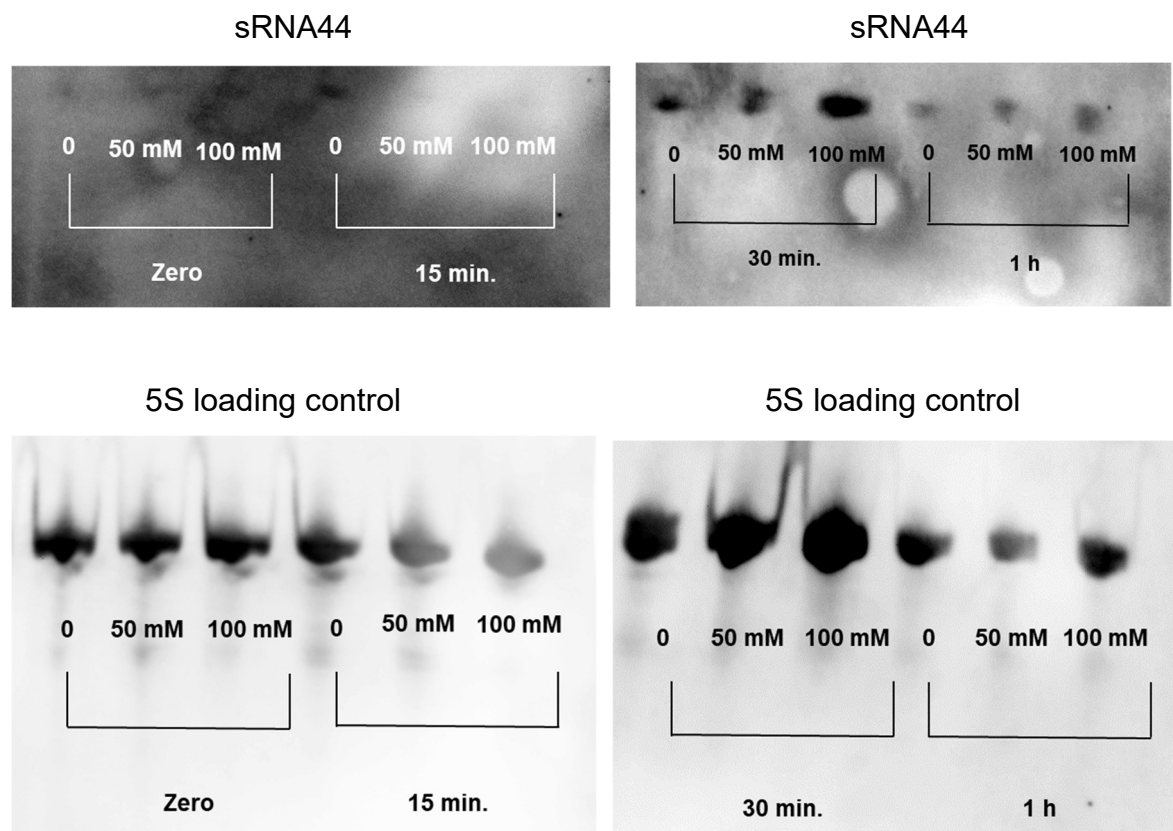


Figure 5.10: Determination of L-arabinose concentration and induction times for sRNA44 expressed from pVRL2Z. Northern blotting was carried out for induced expression of sRNA44 with different doses of L-arabinose (0 mM, 50 mM and 100 mM) and different induction times (0 min, 15 min, 30 min, 1 h). Blots were probed with a riboprobe for sRNA44 (two top panels) and for 5S rRNA (two bottom panels, loading control).

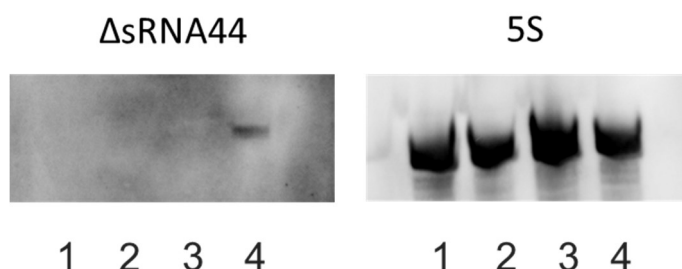


Figure 5.11: Confirmation of sRNA44 overexpression from pVRL2Z by Northern blotting. Cells were grown to ESP in L-broth and expression of sRNA44 was uninduced or induced with 100 mM L-arabinose for 30 min. Left panel: AB5075 Δ sRNA44 pVRL2Z (lane 1, uninduced), AB5075 Δ sRNA44 pVRL2Z (lane 2, induced), AB5075 Δ sRNA44 pVRL2-sRNA44 (lane 3, uninduced). AB5075 Δ sRNA44 pVRL2Z-sRNA44 (lane 4, induced). Right panel: Loading control probed with 5S rRNA riboprobe.

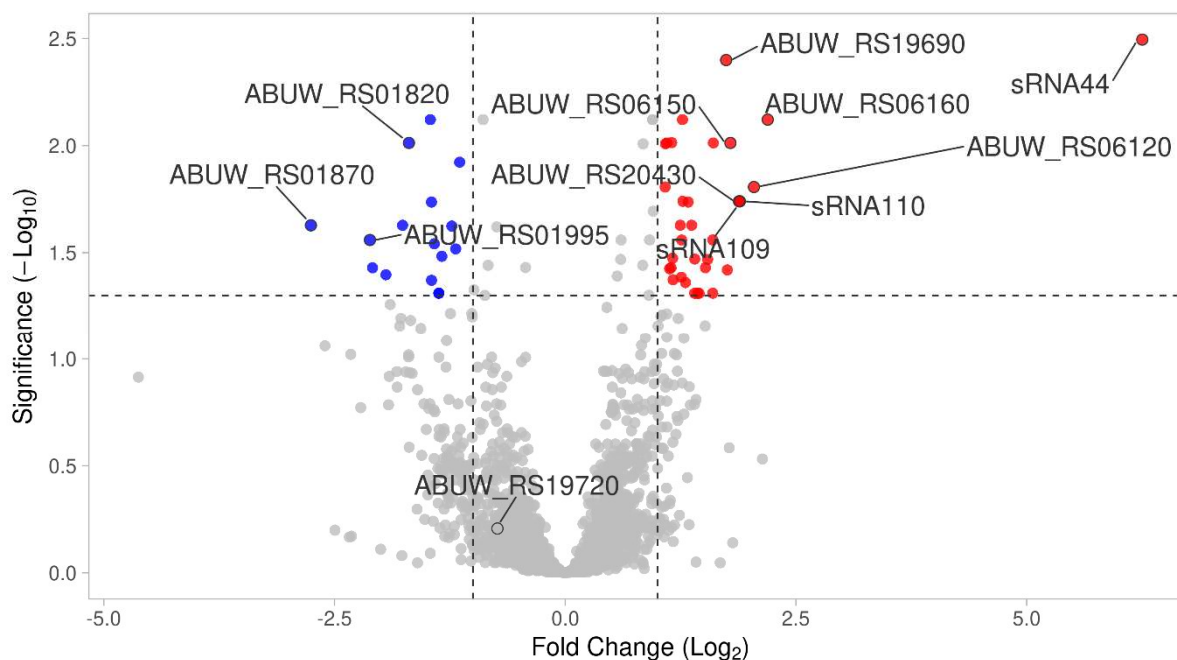


Figure 5.12: Changes in gene expression upon induction of sRNA44 expression from pVRL2Z. Compared are changes in expression (Log₂ fold-change) and significance (-Log₁₀ P_{adj}) of AB5075

pVRL2Z-sRNA44 with and without addition of L-arabinose (induced vs. non-induced) calculated with DESeq2. The dashed horizontal line is at $P_{adj} = 0.05$ and the two vertical dashed lines are at fold-changes of 2 (2-fold up-regulated and 2-fold down-regulated). Red dots are genes that are >2-fold up-regulated with a P_{adj} value <0.05 and blue dots are genes that are >2-fold down-regulated with a P_{adj} value <0.05 in the strain overexpressing sRNA44. The plot was generated with VolcanoR (Goedhart and Luijsterburg, 2020).

IntaRNA predicted two regions of potential interaction, however, they appear quite AT-rich and might therefore weak. They are predicted to occur in the coding region of ABUW_RS01870 mRNA. Potentially, they might attract RNaseE that would degrade the mRNA before complete translation. These interactions could be further validated experimentally (Figure 5.13). Seven down-regulated genes are annotated as ribosomal proteins. It is curious but might be a questionable effect given the typically very high expression of ribosomal proteins, which could mean that this is an artifact. Independent experimental validation would be required.

A more promising result could be the down-regulation of a three-gene operon (ABUW_RS16090, ABUW_RS16095, ABUW_RS16100) encoding for subunits of a NAD(P)(+) transhydrogenase, which is responsible transhydrogenation between NADH and NADP, is coupled to respiration, ATP hydrolysis and functions as a proton pump across the membrane. The highest expression of these three genes is at ESP, which could make it a target for binding of sRNA44, however, IntaRNA prediction did not identify a duplex between sRNA44 and any of the three mRNAs of ABUW_RS16090, ABUW_RS16095, ABUW_RS16100. Therefore, the result could be questionable and would need further experimentation. The *bap* gene (ABUW_RS19720) was slightly down-regulated, but not significantly. This could hint towards a mechanism where sRNA44 might repress translation of *bap* mRNA as seen in the heterologous 2-plasmid system experiment, but not induce the degradation of *bap* mRNA as seen in the RNA-seq experiment. Because of time constraints, none of the genes could be experimentally investigated, but a list of genes was nevertheless produced that could be further analysed in detail in the future.

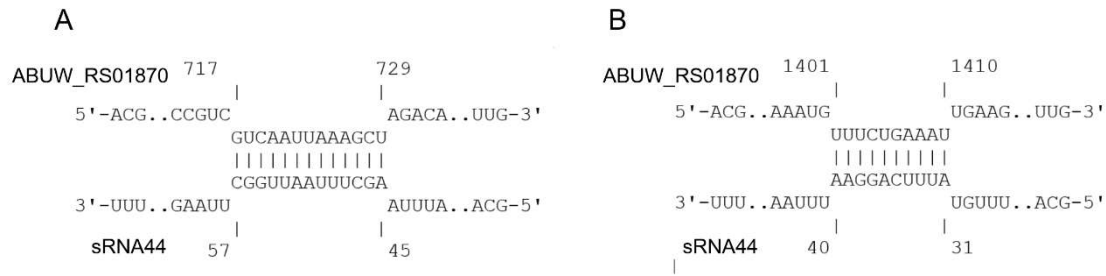


Figure 5.13: Predicted interactions of sRNA44 and ABUW_RS1870 mRNA. The duplexes were predicted with IntaRNA. For both predicted interactions, sRNA44 would bind within the coding region of ABUW_RS01870 mRNA.

Table 5.2: Up-regulated genes (>2-fold, $P_{adj} < 0.05$) upon transient overexpression of sRNA44

Gene ID	Fold-Change (log2)	P_{adj}	Function
sRNA44	6.25	0.003	sRNA44
ABUW_RS06160	2.19	0.007	hypothetical protein
ABUW_RS06120	2.04	0.015	hypothetical protein
sRNA109	1.89	0.018	sRNA109
sRNA110	1.89	0.018	sRNA110
ABUW_RS20430	1.88	0.018	hypothetical protein
ABUW_RS06150	1.79	0.009	hypothetical protein
ABUW_RS06155	1.75	0.038	hypothetical protein
ABUW_RS19690	1.74	0.003	hypothetical protein
ABUW_RS03625	1.60	0.009	hypothetical protein
ABUW_RS06130	1.59	0.027	hypothetical protein
ABUW_RS06135	1.59	0.048	hypothetical protein
ABUW_RS06145	1.54	0.034	PD-(D/E)XK nuclease-like domain-containing protein
ABUW_RS03660	1.51	0.037	hypothetical protein
sRNA97	1.44	0.048	sRNA97
ABUW_RS06125	1.43	0.048	hypothetical protein
ABUW_RS03685	1.40	0.033	hypothetical protein
ABUW_RS09905	1.40	0.048	hypothetical protein
ABUW_RS03630	1.37	0.023	hypothetical protein
ABUW_RS06835	1.33	0.018	hypothetical protein
ABUW_RS06140	1.30	0.043	hypothetical protein
ABUW_RS06855	1.27	0.018	hypothetical protein
ABUW_RS01810	1.27	0.007	putative DNA modification/repair radical SAM protein
ABUW_RS06850	1.26	0.027	hypothetical protein
ABUW_RS06190	1.25	0.041	hypothetical protein
ABUW_RS05685	1.24	0.023	hypothetical protein
ABUW_RS06840	1.16	0.042	"ribbon-helix-helix protein, CopG family"

ABUW_RS06890	1.16	0.033	hypothetical protein
ABUW_RS09645	1.15	0.009	hypothetical protein
ABUW_RS06845	1.14	0.037	hypothetical protein
ABUW_RS03690	1.13	0.037	GntR family transcriptional regulator
ABUW_RS11800	1.1	0.009	N-acetyltransferase
ABUW_RS00690	1.08	0.009	DUF2147 domain-containing protein
ABUW_RS09650	1.08	0.015	helix-turn-helix transcriptional regulator

Table 5.3: Down-regulated genes (>2-fold, $P_{adj} < 0.05$) upon transient overexpression of sRNA44.

Gene ID	Name	Fold-Change (log2)	P_{adj}	Function
ABUW_RS01870		-2.75	0.023	DEAD/DEAH box helicase
ABUW_RS01995	<i>rplC</i>	-2.11	0.027	50S ribosomal protein L3
ABUW_RS02000	<i>rplD</i>	-2.08	0.037	50S ribosomal protein L4
ABUW_RS01990	<i>rpsJ</i>	-1.94	0.04	30S ribosomal protein S10
ABUW_RS01585	<i>trmD</i>	-1.76	0.023	tRNA (guanosine(37)-N1)-methyltransferase TrmD
ABUW_RS01820		-1.69	0.009	HPP family protein
ABUW_RS16090		-1.46	0.007	NAD(P)(+) transhydrogenase (Re/Si-specific) subunit beta
ABUW_RS16095		-1.44	0.018	NAD(P) transhydrogenase subunit alpha
ABUW_RS01575	<i>rpsP</i>	-1.44	0.042	30S ribosomal protein S16
ABUW_RS16100		-1.41	0.028	Re/Si-specific NAD(P)(+) transhydrogenase subunit alpha
ABUW_RS17490	<i>rplA</i>	-1.37	0.048	50S ribosomal protein L1
ABUW_RS06035	<i>rpsB</i>	-1.36	0.048	30S ribosomal protein S2
ABUW_RS20425		-1.33	0.032	hypothetical protein
ABUW_RS01590	<i>rplS</i>	-1.22	0.023	50S ribosomal protein L19
ABUW_RS17500	<i>nusG</i>	-1.18	0.030	transcription termination/antitermination protein NusG
ABUW_RS02780		-1.14	0.011	phage major tail tube protein

Chapter 6

Discussion

6.1 Gene expression throughout growth phases of AB5075

Patterns of gene expression shed light on the regulatory networks that govern a variety of cellular functions, including differentiation, metabolism, cell division, and stress responses (Colgan *et al.*, 2017; Hör *et al.*, 2018). Through examining the variations in gene expression during distinct growth stages, intricate regulatory frameworks can be deciphered that oversee these functions (Hammarlöf *et al.*, 2013). It is possible to find new genes, non-coding RNAs, and regulatory elements that are selectively active or repressed at distinct stages of growth by tracking gene expression throughout the growth phases deepening our comprehension of how genes work and how cells function (Kröger *et al.*, 2013; Perez-Sepulveda and Hinton, 2018; Kröger *et al.*, 2018). In this study, a transcriptomic study of *A. baumannii* AB5075 was carried out from several different conditions, including growth stages and environmental “shock” conditions in nutrient rich broth. Transcriptomic studies have been performed in *A. baumannii* from different conditions, including several shock conditions, but were either done in the *A. baumannii* ATCC17978 (Kröger *et al.*, 2018) strain or in *A. baumannii* AB5075 on a very global level focusing on similarities with other pathogenic bacteria (Avican *et al.*, 2021). Here, I focused providing a more focused, in-depth analysis of *A. baumannii* AB5075 and to analyze not only protein-coding transcripts, but also expression of small, potentially regulatory RNAs.

Five stages of growth in nutrient rich L-broth were analyzed first ranging from early exponential growth phase to stationary phase. The MEP condition also served as a control for the shock conditions. No significant difference (FC two-fold, $P_{adj} < 0.05$) between gene expression in early and mid-exponential growth phase (EEP vs. MEP) of *A. baumannii* AB5075 was found. Gene expression changes may only occur gradually after cells have left exponential growth showing no difference the early and mid-exponential phases of the exponential phase. An earlier timepoint prior to EEP

could be interesting, because marked gene expression changes have been observed in other bacterial pathogens within the first four to eight minutes of being inoculated into fresh medium (Rolfe *et al.*, 2012). This could be an informative condition to investigate in the future because it would be a nutrient shock condition that could illustrate a quick change of environments for *A. baumannii* (e.g., being transferred from a nutrient poor hospital environment to a nutrient rich host). During exponential growth (EEP and MEP), cells are mainly focusing on synthesis of cellular components and the variations in gene expression between these two phases might not be as noticeable. This is highlighted by the high level of expression of ribosomal proteins (Rps: proteins of small ribosomal subunit, Rpl, Rpm: proteins of large ribosomal subunit) at EEP and MEP, which gradually declines from entering LEP towards LSP, when essential nutrients start to run out. As the growth stage progresses, we find that the extent in transcriptional responses increases. When comparing MEP vs LEP, MEP vs ESP, there a gradual increase in the number of differentially expressed genes, but the largest variation is between MEP and LSP. Using DNA microarrays and comparing exponential phase ($OD_{600} = 0.4$) or stationary phase ($OD_{600} = 2.2$), it was shown that 502 genes showed a differential expression in *A. baumannii* ATCC17978 (Jacobs *et al.*, 2012). Here, with RNA-seq and its much greater dynamic range of measurement, we see 3186 genes with a two-fold difference in gene expression.

Focusing on genes and pathways with annotated function of up-regulated genes, we saw a dramatic up-regulation of the virulence-associated (*paa*) pathway including *paaA*, *paaB*, *paaC*, *paaJ*, *paaK* and *paaZ* in LEP and ESP without the addition of any additional environmental stressors. The *paa* pathway was previously shown to be regulated by the sensor kinase GacS in *A. baumannii* ATCC17978 (Cerqueira *et al.*, 2014), therefore GacS appears to be activated in LEP and ESP conditions. Functional studies of GacS should therefore focus on these conditions. The environmental signal for GacS activation is unclear but its discovery could have important implications on understanding *A. baumannii* virulence as phenylacetate was shown to be a chemoattractant for neutrophils in a zebrafish model (Bhuiyan *et al.*, 2016). More recently, it was discovered that PAA levels influence antibiotic resistance and biofilm

formation (Hooppaw *et al.*, 2022). Therefore, this pathway is of utmost importance for *A. baumannii* biology.

It may be possible that *A. baumannii* experiences intracellular oxidative stress when entering stationary phase, because we see the katalase gene *katE* to be highly up-regulated in ESP and LSP. The catalase enzyme, which is encoded by the *KatE* gene, is essential for shielding bacterial cells from oxidative damage. Reactive oxygen species (ROS) are produced as consequences of the increased metabolic activity that bacterial cells experience during development stages. Hydrogen peroxide (H_2O_2) is one type of ROS that can harm lipids, proteins, and DNA in cells. The effective detoxification of H_2O_2 provided by *katE* upregulation shields the cells from oxidative damage. *Acinetobacter*'s significant overexpression of *katE* throughout growth stages is a calculated reaction to control oxidative stress brought on by elevated metabolic activity, guaranteeing cellular survival and protection during times of rapid growth and multiplication. It has been demonstrated that *katG* expression is rapidly induced during the rapid exponential growth phase in *E. coli* (Sun *et al.*, 2016). In the stationary phase, the *katE* gene was preferentially expressed. H_2O_2 stimulation boosted *katE* expression in *A. nosocomialis* cells during the stationary phase but had no effect during exponential growth (Sun *et al.*, 2016), this finding consist with our results.

The functions of *mdc* (malonate decarboxylase) and *mad* (malonate transporter) genes in malonate metabolism and adaptability to different carbon sources during active growth phases can account for the significant overexpression of these genes in *Acinetobacter* growth stages. Bacterial cells need a variety of carbon sources during growth stages in order to meet their metabolic needs for biomass generation and cell division. When other preferred carbon sources are scarce or exhausted, malonate is used as a backup source, as indicated by the upregulation of the *mdc* and *mad* genes. The utilization of malonate as an alternative carbon source, regulatory responses to carbon availability, and the bacterium's adaptability to thrive in a variety of environmental conditions by effectively utilizing available nutrients for growth and metabolism are all linked to the strong upregulation of *mdc* and *mad* genes in *Acinetobacter* growth stages.

6.2 Gene expression throughout shocks in AB5075

In this study, *A. baumannii* AB5075 was exposed to four different environmental “shocks”: Osmotic shock (NaCl), iron limitation (LowFe) and antibiotic shocks (sub-inhibitory concentrations of chloramphenicol and tetracycline). The data from the shocks were compared with MEP. The NaCl and LowFe conditions show similar number of genes changing with 301-307 up-regulated and 212-230 genes down-regulated out of 4034 genes and an overlap of 60% of genes showing differential gene expression (compared to MEP). This is in marked difference to the response to NaCl and LowFe in *Salmonella enterica*, which used the same conditions (Kröger *et al.*, 2013). Only 25 genes overlapped in gene expression in *Salmonella enterica*, illustrating that the two bacteria have evolved to deal with those stresses very differently. Genes encoding the uptake of iron via the siderophore Acinetobactin were up-regulated in both conditions. While this appears intuitive for LowFe and was in agreement with microarray data from *A. baumannii* ATCC17978 (Eijkelkamp *et al.*, 2011), this was less expected for the NaCl condition. When *A. baumannii* experiences high osmotic pressure it can cope with this stress by producing so-called compatible solutes (e.g., trehalose, glycine betaine, mannitol), which can be taken up or synthesised by *A. baumannii* to alleviate the osmotic pressure (Zeidler and Müller, 2019). In this short osmotic shock, we do not see induced expression of *otsAB* (producing trehalose) or the *bet* genes, involved in glycine betaine-mediated accumulation of compatible solutes, but a more detailed experimental analysis would be required to elucidate the immediate and long-term response in *A. baumannii* AB5075, as most work was done in the historical strains *A. baumannii* ATCC17978 and ATCC19606 (Zeidler and Müller, 2019; Breisch *et al.*, 2022).

The two antibiotic shocks show gene expression changes to a much larger extent with 1271-1556 genes up-regulated and 1046-1051 genes down-regulated out of 4034 genes. This illustrates that the protein synthesis stress that the cells are exposed to in the antibiotic shocks require a much larger transcriptomic response to cope with the stress compared to the osmotic and iron limitation stress. Protein synthesis stress is an urgent and serious danger to cell viability, especially when it is caused by antibiotics that target ribosomes or translation machinery. In order to mitigate the negative

consequences of protein synthesis suppression and preserve vital cellular activities, a greater transcriptome response is required. An immediate response to the antibiotic stress appears to be the down-regulation of the NADH-quinone oxidoreductase complex, which is encoded by the *nuo* genes, and a central protein complex in the respiratory chain (Brandt, 2006; Verkhovsky and Bogachev, 2010). This could indicate the antibiotics could influence the proton gradient across the membrane or that further growth and ATP synthesis should be immediately reduced.

6.3 Gene expression throughout different temperatures in AB5075

Temperature is an underappreciated environmental factor influencing gene expression in bacterial pathogens. In *A. baumannii*, temperature has been often viewed in the light of elevated temperature to the extremes where *A. baumannii* can grow (45°C) (Hubloher *et al.*, 2020). While this is of interest, it might be less important for the adaptation to a human host temperature. Overall, we show that there were large changes to the transcriptome in all temperature comparisons. The transcriptome signatures are distinct for each condition, however, AT and TS cluster more closely together, and likewise CS and MEP. Genes considered up-regulated represent genes at higher gene expression at ambient temperature compared to 37°C. The *otsAB* operon was strongly up-regulated upon temperature shift, as these genes are involved in virulence and when deleted impair growth at 45°C (Hubloher *et al.*, 2020). Interestingly, also the *paa* genes were up-regulated upon temperature upshift, which could mean that one signal for the induction of the *paa* pathway is temperature. Whether this is mediated via GacS as at 37°C remains to be investigated. The gene *pilA* was the most down-regulated gene when cells were experiencing a temperature upshift (TS), and *pilB*, *pilN*, *pilO*, *pilP* and *pilV* were also within the top10 down-regulated genes, which could mean that DNA uptake is at least transiently down-regulated when *A. baumannii* enters a warm-blooded host. Type IV pili may be found on a wide variety of bacterial species and have been extensively researched in Gram-negative infectious strains (Smedley *et al.*, 2005; Power *et al.*, 2006; Voisin *et al.*, 2007; Aas *et al.*, 2007; Allison *et al.*, 2015; Gault *et al.*, 2015). The *pilA* gene from *Acinetobacter* is quite variable, and there is evidence that it evolved similarly to other

type IV pilins from other species (Ronish *et al.*, 2019). It could be interesting to test whether DNA uptake has different efficiencies at different temperatures (ambient vs. body temperature).

The cold-shock induced the expression of the T6SS and surprisingly the resistance island genes that are located on plasmid p1AB5075 and encode multiple antibiotic resistance genes (e.g., against aminoglycosides, chloramphenicol and sulfamethoxazole and trimethoprim) (Jacobs *et al.*, 2014; Gallagher *et al.*, 2015; Kyriakidis *et al.*, 2021). These could be responses when *A. baumannii* returns to the environment and has to prepare for defense against other microorganisms. Firstly, the expression should be validated independently. T6SS activity could be assessed via killing assays of other microorganisms, e.g. *Candida albicans* (Luo *et al.*, 2023). Antibiotic sensitivity could be tested at lower temperature to determine which factors are involved in the down-regulation of resistance island genes. For both cases, T6SS and AMR genes, such a quick down-regulation could be a post-transcriptional effect.

6.4 The expression landscape of sRNAs

Small RNAs are now well-established as post-transcriptional regulators in complex regulatory networks in bacteria (Papenfort and Vogel, 2010; Barquist and Vogel, 2015; Nitzan *et al.*, 2017; Brosse and Guillier, 2018). Small RNAs are often involved in stress responses as they are not costly and quickly made in the cell as mediators of rapid adaptation to changing environments (Holmqvist and Wagner, 2017; Papenfort and Melamed, 2023). They typically balance gene expression and therefore deletion mutants rarely exhibit strong phenotypes. To understand their biological role in the cell, the timing and level of expression are valuable data because sRNA compete for binding at the RNA chaperone Hfq (Wagner, 2013).

Overall, the relative abundance of sRNAs increases across the growth phase in nutrient rich broth. This is similar to what has been observed in other bacteria such as *Salmonella enterica* (Kröger *et al.*, 2013). 39-50 sRNAs showed up-regulation in LEP to LSP compared to the MEP control condition illustrating an increased importance of sRNAs when cells start to enter stationary phase. This suggests that sRNAs play

important roles in the adaptation to an environment when less resources are available. Small RNAs that showed an increased abundance towards LSP include sRNA65, sRNA75, sRNA76, sRNA97, sRNA99 and sRNA100 among others. Only few sRNAs decreased in relative abundance, most notably sRNA2, which is the most abundant sRNA in EEP (~50% of all sRNA transcripts) and which decreased to ~5% of all sRNA transcripts. A constantly abundant sRNA is sRNA89, which, as sRNA2, is functionally uncharacterised. Given their high abundance, these are attractive sRNAs to study in the future as their abundance suggests an important biological role in *A. baumannii*.

In the shock conditions, up-regulation of sRNAs also dominated over down-regulation, which might illustrate that sRNAs tend to be not expressed and then their expression is induced when they are required to carry out their biological role. A larger number of sRNAs changed their expression in the Tet and Chl compared to NaCl and LowFe shocks. As discussed above, because the sub-inhibitory levels of antibiotics pose a significant stress on the cell resulting in slowed growth, this might call for much larger adaptation of gene expression and therefore a greater number of sRNAs are being induced. Few sRNAs showed a condition-specific high up-regulation in NaCl or LowFe conditions. However, the sRNA93 showed strong up-regulation in both NaCl and LowFe shocks, which would make it a prime target to investigate in these conditions.

One sRNA, sRNA76, was very strongly induced in all four shock conditions. This could make it a more global regulator of stress in *A. baumannii*. The Hi-GRIL-seq data suggest *ABUW_RS11470*, encoding a dicarboxylate/amino acid:cation symporter, as the predominant target with 1633 chimeras and as third most abundant target, *ABUW_RS03195*, encoding an OmpA family protein with 410 chimeras. As transporters, especially outer membrane proteins are often targeted by sRNAs (Vogel and Papenfort, 2006; Holmqvist and Wagner, 2017; Papenfort and Melamed, 2023), these appear promising targets for further studies.

In Chl and Tet conditions, several sRNAs were strongly up-regulated. Mostly, the patterns of expression were overlapping indicating a common response to the protein biosynthesis stress. Specific up-regulation was shown by sRNA101 and to a lesser extent sRNA46. One example of a condition-specific up-regulation was seen for

sRNA90, which was only highly up-regulation in the Chl shock. In this context, the sRNA90 should be assessed in their role for chloramphenicol resistance, which is a regulated feature in *A. baumannii* (Kröger *et al.*, 2018).

In the cold-shock condition, sRNAs typically showed a lower abundance as compared to MEP. Only sRNA72 showed higher abundance in the cold-shock condition. Moving cells to higher temperature increased the abundance of several sRNAs, including sRNA65 as the most prominent candidate. Those specific expression patterns would make them an attractive target for further studies.

Although most sRNAs showed upregulation upon environmental shocks, some sRNA showed rapid downregulation in Chl and Tet conditions. This included the sRNAs sRNA2, sRNA99 and sRNA100, which very quickly dropped in abundance when the cells experienced the Chl and Tet shocks. The downregulation was independently validated by Northern blotting for sRNA99 and sRNA100 confirming the rapidly dropped abundance. Deletion of sRNA99 and sRNA100, which are next to each other in the *A. baumannii* AB5075 genome, resulted in large expression changes in MEP in the mutants compared to the WT. Both genes showed a similar transcriptional response, which could suggest that they are involved in the same biological function. However, they do not appear to overly compensate for the loss of the other sRNA. Significantly down-regulated was the *antA-C* operon in both, the Δ sRNA99 and the mutant Δ sRNA100 mutants. *Acinetobacter* spp. can metabolise aromatic compounds such as anthranilate and convert it to catechol (Eby *et al.*, 2001). The biological role of this change is unclear, but growth with anthranilate as the sole carbon source would be a good starting point to investigate the roles of sRNA99 and sRNA100. Also, a peptidoglycan hydrolase as down-regulated (*lysM* (ABUW_RS15080)). These enzymes are widespread in bacteria and are predicted to recognize the N-acetylglucosamine moiety of peptidoglycan (Buist *et al.*, 2008). Because of this differential expression, the sRNA99 and sRNA100 mutants might possess differences in the cell wall, which could be microscopically investigated. Resistance to antibiotics such as beta-lactam antibiotics that target the cell wall could also be tested whether

they have modulated activity, which could be very interesting in the context of carbapenem-resistant *A. baumannii*.

Overall, many avenues of investigation have been opened with this large transcriptomic dataset. Future studies will be required to describe the roles of sRNAs in *A. baumannii*. This thesis provides a solid foundation that will boost discoveries in *A. baumannii* sRNA biology. In addition, the newly created gene expression database AcinetoCom2.0 will be a useful discovery tool to study gene expression in *A. baumannii* and will inform future discoveries by the *A. baumannii* research community.

6.5 Mechanistic characterization of small RNA44

One small RNA was investigated mechanistically in more detail (sRNA44). Previous data generated by Hi-GRIL-seq in *A. baumannii* AB5075 suggested that sRNA44 was ligated to the mRNA of the *bap* gene (Hamrock *et al.*, 2023). Many bacteria use biofilms as a major virulence factor, which helps them survive in unfavorable conditions, spreads across the reservoir, and creates a niche for the exchange of genetic material (Hall-Stoodley and Stoodley, 2005; Luo *et al.*, 2015). Biofilms are linked to 80% of persistent and recurrent microbial infections, which is a significant issue with nosocomial infections (Sharma *et al.*, 2019). Expression of *bap* is associated with biofilm maturation (Law and Tan, 2022) and it has been demonstrated to play a part in the biofilms' thickness. It may also be important for infection and biofilm persistence in hospital settings (Brossard and Campagnari, 2012). The virulence of *A. baumannii* species and the presence of genes that produce biofilms have been compared in numerous studies. 84% of environmental isolates and 87% of clinical isolates were found to encode the *bap* gene, which was linked to the production of biofilms (Bardbari *et al.*, 2017). In the transcriptomic data from this thesis, the sRNA44 was not detected above the TPM10 cut-off. However, sRNA44 was previously identified by RNA-seq in *A. baumannii* ATCC17978 (Kröger *et al.*, 2018). Overall, sRNA44 appears to be expressed at a low level as even in ATCC17978 the expression was low and Northern blotting in *A. baumannii* AB5075 did not show high expression. However, because ligation to *bap* mRNA was detected by Hi-GRIL-seq and because the chimera RNAs created by Hi-GRIL-seq included the predicted interaction (base-pairing) of sRNA44

and *bap* mRNA as mapped by IntaRNA, sRNA44 was considered an attractive sRNA to work on. The sRNA44-*bap* base-pairing was the sole interaction found to be a reasonable candidate, because it mapped 100% to the Hi-GRIL-seq data. Also, preliminary data from J. White (Kröger Lab), indicated that sRNA44 can act on *bap* mRNA. In *E. coli*, the interaction of sRNA44-*bap* mRNA base-pairing was verified with an established two-plasmid system, which detects interaction between sRNA and target mRNA on the basis of a translational fusion of the target and sfGFP (Urban and Vogel, 2007). Because we do not have two compatible plasmids in *A. baumannii*, this technique was adopted as a first mechanistic indication. The two-plasmid system also helped identifying the interaction between Aar (sRNA21) and *carO* mRNA in *A. baumannii* AB5075 (Hamrock *et al.*, 2023). Typically, productive sRNA-mRNA interactions require the RNA chaperone Hfq, which in *A. baumannii* is structurally somewhat different from *E. coli* Hfq, because it contains an additional glycine rich C-terminus (Sharma *et al.*, 2018). However, *A. baumannii* Hfq was able to mediate the *Salmonella* sRNA RhyB-*sodB* mRNA interaction, suggesting that Hfq could have a similar function in *A. baumannii* facilitating sRNA-mRNA interactions (Sharma *et al.*, 2018). Although an *hfq* deletion strain exists in the literature (Kuo *et al.*, 2017), our attempts to delete *hfq* in *A. baumannii* were not successful. The interaction between sRNA44 and *bap* mRNA was predicted to be just downstream of the start codon. Insertion three nucleotide exchanges into the sRNA44 disrupted the interaction in *E. coli* suggesting that these nucleotides are involved in base-pairing. Therefore, sRNA44 interacts with *bap* mRNA to inhibit translation, as the two-plasmid system showed. Whether translation itself is inhibited (e.g. binding of the 30S ribosomal subunit) or *bap* mRNA is degraded in an accelerated manner by endogenous RNases is unclear and could be addressed in the future. This interaction would have to be validated in the *A. baumannii* host, for example by introducing the same mutation into the sRNA44 gene on the chromosome as previously demonstrated for the *aar-carO* mRNA interaction (Hamrock *et al.*, 2023). Preliminary qRT-PCR data showed a trend of higher *bap* mRNA levels in the Δ sRNA44 mutant and reduced *bap* mRNA levels in a sRNA44 overexpression compared to the WT. *In vitro* binding studies such as EMSAs or in-line probing could further determine the nucleotides involved in base-pairing at a single

nucleotide resolution. To show a biological relevance of sRNA44 on biofilm formation, sRNA44 and *bap* were deleted and subjected to a biofilm formation assay. After 24h, the *bap* mutant showed reduced biofilm formation, but caught on to the WT after 48h and longer. The sRNA44 mutant showed a trend of increased biofilm formation after 24h. This should be repeated with earlier timepoints, where maybe there could be a larger difference in biofilm establishment and more biological replicates to determine whether this difference is statistically significant. In the future Bap protein levels should be measured in WT and sRNA44 mutants to determine whether and to what extent Bap levels are altered. In an attempt to find additional sRNA targets, transient overexpression of sRNA44 and subsequent RNA-seq was carried out. This method has been used widely to detect mRNA targets of sRNAs in other bacteria (Sharma and Vogel, 2009). The analysis revealed that *bap* was not differentially expressed upon expression of sRNA44 from a plasmid, which could indicate that translation of *bap* is reduced but that *bap* mRNA degradation might not be altered when sRNA44 binds to *bap* mRNA. The *ABUW_RS01870* mRNA encoding a DEAD/DEAH box helicase was the most promising mRNA to be downregulated when sRNA44 was overexpressed. If sRNA44 induces accelerated degradation of *ABUW_RS01870* mRNA the location of the binding deep within the coding region would fit with the mechanism of increased degradation of sRNA when binding to their targets within the coding regions as exemplified with sRNA MicC regulating *ompD* mRNA by attracting RNaseE-mediated degradation (Pfeiffer *et al.*, 2009). However, this would have to be tackled experimentally in the future. Overall, the role of sRNA44 was shown to reduce translation of Bap in *E. coli* by base-pairing to the region just downstream of the coding region potentially regulating the ability of *A. baumannii* to form biofilms. Through overexpression of sRNA44, *ABUW_RS01870* was identified as a potential additional target. If the suggested mechanisms of translational inhibition and induction of increased degradation would be independently validated, it would mean that sRNA44 can act by two different mechanisms of action to regulate expression in a post-transcriptional manner.

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Appendix I

Table S1. RNA-seq data: Absolute and relative expression (LEP/MEP > 2-fold up)

locus_tag	'old_locus_tag'	chrom	start	stop	strand	refseq_id	symbol	name	baseMean	log2FoldChange	fcSE	stat	pvalue	padj	-log10
ABUW_R007145	ABUW_1466	NZ_CP008706.1	155645	146678	-	WP_001094301.1		DUF2171 domain-containing protein	10507.06702	8.953125939	0.62841974	14.24722366	4.68E-46	1.33E-44	43.87616386
ABUW_R002475	ABUW_2443	NZ_CP008706.1	2430503	2430466	-	WP_00025935.1		hypothetical protein	1933.02491	8.593996103	0.884526485	9.7502859	2.58E-22	1.79E-21	20.74746697
ABUW_R007170	ABUW_1471	NZ_CP008706.1	1460237	1460599	+	WP_00072837.1		NiOY10YiWYd family stress tolerance e protein	9865.07839	8.471505048	0.509984411	9.61000779	5.80E-42	3.54E-40	59.45099674
ABUW_R007960	ABUW_1631	NZ_CP008706.1	1628562	1629002	+	WP_000750872.1		spore coat protein U domain-containing protein	7973.252085	8.306075706	0.47853355	9.8779682	6.31E-48	1.06E-45	84.97469413
ABUW_R007330	ABUW_2530	NZ_CP008706.1	252184	2522621	-	WP_001569442.1		enoyl-CoA hydratase/isomerase family protein	794.6383576	7.800696148	0.514930883	16.26549004	1.30E-52	4.83E-51	50.33414901
ABUW_R003035	ABUW_2311	NZ_CP008706.1	218658	217918	-	WP_001077519.1		thiamine pyrophosphate-dependent dehydrogenase E1c component subunit	638.3666658	7.837204251	0.589559177	19.29332926	2.03E-40	5.23E-39	38.28149851
ABUW_R001870	ABUW_2430	NZ_CP008706.1	242876	2428967	+	WP_000183865.1		hypothetical protein	10948.8858	7.732254365	0.624480798	12.3819021	3.28E-35	4.89E-34	33.3106914
ABUW_R005445	ABUW_1193	NZ_CP008706.1	101868	103389	+	WP_000469453.1		alpha-keto acid decarboxylase family protein	4938.377473	7.7107919	0.420868763	13.32165427	5.56E-35	5.09E-33	72.29328222
ABUW_R002295	ABUW_2520	NZ_CP008706.1	2521057	2521848	-	WP_000386201.1		2-(1,3-apoxy-1,2-dihydrophenylacetyl)-CoA isomerase	1400.627279	7.600958984	0.41890906	18.8724505	8.30E-78	8.80E-76	75.05557533
ABUW_R003030	ABUW_1310	NZ_CP008706.1	218583	218642	-	WP_00183050.1		alpha-ketocid dehydrogenase subunit beta	790.1459166	7.632069342	0.569932214	13.3918786	6.81E-41	1.46E-39	38.83664714
ABUW_R003030	ABUW_1317	NZ_CP008706.1	218396	218397	-	WP_001001666.1		mechanosensitive ion channel	1419.22788	7.61232001	0.30180839	25.2581977	9.21E-141	6.19E-138	107.200616
ABUW_R000260	ABUW_0053	NZ_CP008706.1	58824	58782	-	WP_000490267.1		DUF528 domain-containing protein	5808.425003	7.58067885	0.352767978	2150.55710	1.50E-102	5.05E-100	99.29670862
ABUW_R00005	ABUW_2060	NZ_CP008706.1	204577	204542	-	WP_001027338.1		hypothetical protein	3287.87935	7.562060775	0.475686865	16.89808266	6.53E-57	3.06E-55	54.51927857
ABUW_R002334	ABUW_2534	NZ_CP008706.1	2525000	2525290	-	WP_000389648.1	paab	1,2-phosphatyl-CoA epoxidase subunit B	2333.557698	7.524717951	0.600302881	12.53488897	4.81E-36	7.50E-35	34.0493874
ABUW_R002325	ABUW_2535	NZ_CP008706.1	2525233	2526261	-	WP_000431028.1	paaA	1,2-phosphatyl-CoA epoxidase subunit A	8269.755897	7.463103537	0.587591024	12.70103394	5.84E-37	9.60E-36	50.0772877
ABUW_R000025	ABUW_2064	NZ_CP008706.1	204577	204612	-	WP_000044010.1		hypothetical protein	365.3338908	7.43844195	0.69135286	17.563199	5.53E-27	5.06E-26	25.29584948
ABUW_R0018415	ABUW_3782	NZ_CP008706.1	3842938	3843628	-	WP_00107291.1	mmB	3-hydroxyisobutyrate dehydrogenase	414.5389476	7.386862435	0.464679404	15.89686568	6.68E-57	3.09E-55	54.51904152
ABUW_R0021315	ABUW_2533	NZ_CP008706.1	2524322	2524987	-	WP_00187691.1	paac	phenylacetate-CoA oxygenase subunit PaaC	2868.159042	7.37295019	0.67938963	12.7180884	4.25E-37	7.05E-36	35.1510188
ABUW_R002305	ABUW_2531	NZ_CP008706.1	2523260	2523651	-	WP_00077461.1	paak	phenylacetate-CoA oxygenase/reductase subunit PaaK	18.755354	7.336824595	0.588406659	13.1885584	1.07E-39	3.89E-38	37.4100504
ABUW_R0012725	ABUW_2532	NZ_CP008706.1	252376	2419007	-	WP_001073131.1		hypothetical protein	4941.499428	7.279551746	0.37070938	16.6537886	4.27E-46	6.16E-44	83.21180163
ABUW_R0018420	ABUW_3783	NZ_CP008706.1	3843840	3845357	-	WP_001092394.1		CoA-acylating methylmalonate-semialdehyde dehydrogenase	1649.02384	7.214286643	0.390877751	18.45632326	4.61E-76	4.42E-74	73.35457731
ABUW_R0021315	ABUW_2532	NZ_CP008706.1	252376	2523242	-	WP_001073936.1	paaJ	phenylacetate-CoA oxygenase subunit PaaJ	2571.070063	7.19428555	0.390377958	13.48735677	1.88E-41	4.10E-40	39.38404995
ABUW_R0018175	ABUW_2440	NZ_CP008706.1	2429004	2429411	-	WP_000102046.1		hypothetical protein	33008.55582	7.146588611	0.44857089	16.9468104	3.11E-57	1.46E-55	54.8356471
ABUW_R0030340	ABUW_2128	NZ_CP008706.1	212472	212475	-	WP_001087542.1	tpdA	dihydrologlycol dehydrogenase	665.6828746	7.04952714	0.455003599	15.49028033	4.04E-54	1.53E-52	51.81630857
ABUW_R001855	ABUW_2436	NZ_CP008706.1	242975	2429222	-	WP_001885865.1	katE	catalase HPI	40275.84516	6.994655196	0.38505882	16.165794	9.74E-74	8.53E-72	71.06800509
ABUW_R0007965	ABUW_1632	NZ_CP008706.1	1629165	1629889	+	WP_000739311.1		molecular chaperone	944.5360165	6.874552222	0.43342598	16.8265658	8.36E-57	3.81E-55	54.41907502
ABUW_R0030335	ABUW_1316	NZ_CP008706.1	2183500	2183527	-	WP_000543705.1		hypothetical protein	2521.945201	6.829312705	0.342608867	19.9332617	2.09E-48	3.67E-46	55.8333394
ABUW_R0030345	ABUW_1210	NZ_CP008706.1	214286	215821	-	WP_001089728.1		2-one-acyl dehydrogenase subunit E2	734.842135	6.818983763	0.442918976	14.0772707	5.93E-58	3.16E-56	55.50070735
ABUW_R0018410	ABUW_3781	NZ_CP008706.1	3841057	3842856	-	WP_000695676.1		AMP-binding protein	693.101288	6.75530613	0.38452527	17.5469564	5.98E-49	4.82E-47	66.3195206
ABUW_R0021320	ABUW_R008706.1	NZ_CP008706.1	271670	271875	-	WP_000026486.1		OmpA family protein	719.248195	6.712866977	0.203472833	32.99144166	1.08E-238	4.34E-235	234.362163
ABUW_R0019170	ABUW_2055	NZ_CP008706.1	274727	276916	+	WP_00101061.1		bifunctional Sulf1 family inorganic anion transporter/carbonic anhydrase	5543.887225	6.671729033	0.281827738	23.86318742	7.40E-56	3.73E-52	92.4282912
ABUW_R0018440	ABUW_2433	NZ_CP008706.1	2429850	2421104	-	WP_000024222.1		stress-induced protein	91647.252	6.675882363	0.527660347	12.65322001	1.07E-36	1.74E-35	34.75645075
ABUW_R0021320	ABUW_2536	NZ_CP008706.1	2526527	2526829	-	WP_000892952.1	paaZ	phenylacetate acid degradation bifunctional protein PaaZ	4627.007006	6.67543349	0.40147602	16.64084166	3.53E-42	2.19E-40	59.65558959
ABUW_R0018680	ABUW_2437	NZ_CP008706.1	2429727	2427686	-	WP_001145690.1		iron-containing redox enzyme family protein	6730.166542	6.67185644	0.41437243	16.09692603	2.68E-58	1.54E-56	54.84163751
ABUW_R0021320	ABUW_2673	NZ_CP008706.1	2668236	2668784	-	WP_001058419.1		hypothetical protein	4617.200979	6.648526405	0.384044469	17.27193094	7.73E-47	5.66E-45	64.24718357
ABUW_R0007900	ABUW_1787	NZ_CP008706.1	178248	1783605	+	WP_000165571.1		hypothetical protein	4077.391826	6.604069645	0.356592700	16.6687833	5.97E-77	6.01E-75	74.22102553
ABUW_R0005435	ABUW_1111	NZ_CP008706.1	102645	103075	-	WP_00183471.1		aldehyde dehydrogenase family protein	4291.19369	6.556303265	0.287562918	24.50379147	1.35E-52	7.75E-50	92.106693
ABUW_R0007500	ABUW_1636	NZ_CP008706.1	1629527	1629257	-	WP_000859008.1		hypothetical protein	54.818978	6.495048108	0.48375511	15.90459256	5.89E-57	2.79E-55	54.54395618
ABUW_R0019165	ABUW_1323	NZ_CP008706.1	214284	214471	-	WP_000404106.1		trehalase-6-phosphate synthase	9244.358405	6.468700597	0.41893241	16.62891594	4.63E-55	1.83E-53	52.73754891
ABUW_R0019160	ABUW_1322	NZ_CP008706.1	214284	2143296	+	WP_001064773.1	otsB	trehalase-phosphatase	9339.033028	6.412344635	0.576277046	11.06024588	1.40E-28	1.42E-27	26.84771196
ABUW_R0007165	ABUW_1468	NZ_CP008706.1	145739	1458733	+	WP_000356984.1		PGD-1 family deacetylase	1665.10356	6.382190918	0.439301731	14.52894551	7.94E-48	2.44E-46	45.61281017
ABUW_R0021305	ABUW_1657	NZ_CP008706.1	162977	161908	+	WP_000161254.1		hypothetical protein	513.5381643	6.220713908	0.601909568	10.347319	4.30E-25	3.66E-24	24.4485
ABUW_R0007160	ABUW_1469	NZ_CP008706.1	1458708	1459307	+	WP_000581927.1		class I SAM-dependent methyltransferase	1136.371545	6.214533175	0.43071842	14.428363	3.43E-47	1.03E-45	44.9871827
ABUW_R0007165	ABUW_1470	NZ_CP008706.1	1459304	1459948	+	WP_000690470.1		glycosyltransferase	1075.619586	6.21082229	0.40510984	16.33431598	4.15E-53	1.65E-51	50.78251066
ABUW_R001845	ABUW_2455	NZ_CP008706.1	2446627	2444658	-	WP_000481820.1		acetyltransferase/methyltransferase	3873.508829	6.181555764	0.2950539	21.204594502	8.60E-100	2.66E-97	96.57518356
ABUW_R0021320	ABUW_2456	NZ_CP008706.1	252158	2521554	-	WP_000102574.1		3-hydroxyacyl-CoA dehydrogenase	16.1510049	6.18579088	0.239487568	25.5402781	7.04E-144	5.67E-141	104.2464169
ABUW_R0030330	ABUW_0887	NZ_CP008706.1	691949	696092	-	WP_001884626.1		entericidin A family lipoprotein	6928.695798	6.086596971	0.31733931	19.8009198	5.43E-82	6.43E-80	79.9187803
ABUW_R0005450	ABUW_1114	NZ_CP008706.1	115330	115409	-	WP_000383013.1		amino acid permease	1596.508443	6.063690301	0.278683601	17.74426909	7.63E-105	1.51E-102	101.542181
ABUW_R0007970	ABUW_1633	NZ_CP008706.1	1629879	1632338	-	WP_000873962.1		ribitol biosynthetic outer membrane usher protein	26.9172232	6.054485899	0.349885612	17.30419652	4.37E-47	3.26E-45	64.8872164
ABUW_R0018245	ABUW_2603	NZ_CP008706.1	2558261	2559739	-	WP_001091900.1		ATP-gase domain-containing protein	22.01223466	6.045809583	0.51253338	19.29205744	6.26E-43	8.79E-41	80.92023
ABUW_R001865	ABUW_2438	NZ_CP008706.1	2428002	2428481	-	WP_000482091.1		CNA family protein	165.3707082	6.031733004	0.776280739	7.769888571	7.86E-6	3.41E-4	81.04724562
ABUW_R0021390	ABUW_2674	NZ_CP008706.1	2667054	2667332	-	WP_00072985.1		hypothetical protein	324.4144914	5.992028627	0.457008794	11.1140772	2.83E-39	5.52E-38	37.25680062
ABUW_R0018440	ABUW_2454	NZ_CP008706.1	2441852	2442655	+	WP_000107229.1		enoyl-CoA hydratase/isomerase family protein	1274.638723	5.98679514	0.321842768	18.59237142	3.70E-77	3.83E-75	74.41880123
ABUW_R0019160	ABUW_2456	NZ_CP008706.1	2446557	2445557	+	WP_001088910.1		hydroxymethylglutaryl-CoA lyase	1690.797706	5.979364479	0.285710308	20.9287702	2.93E-57	7.38E-55	94.194364
ABUW_R00191615	ABUW_2448	NZ_CP008706.1	2433753	2438406	-	WP_000296021.1		class I SAM-dependent methyltransferase	158.580408	5.96857184	0.291954697	20.5067044	1.88E-93	3.78E-91	90.4225082
ABUW_R0007980	ABUW_3898	NZ_CP008706.1	3965532	3965783	-	WP_000269732.1	GidB/YeaQ/YmgJ family stress response membrane protein	1865.08856	5.957996727						

ABUW_RS08045	ABUW_RS08045	ABUW_649	NZ_CP008706.1	1723523	1724800	+	WP_031005296.1		D- amino acid dehydrogenase	5169.893825	5.01410985	0.25575421	19.60519431	1405E-83	1.94E-83	82.71026827
ABUW_RS08045	ABUW_649	NZ_CP008706.1	1723523	1724800	+	WP_031005296.1		hypothetical protein	1723.980466	5.00584884	0.323756803	15.4618516	6.305E-54	2.37E-52	516.025185	
ABUW_RS14240	ABUW_2933	NZ_CP008706.1	12947306	2948451	+	WP_000371256.1		galactose mutarotase	4310.177044	4.987919981	0.273646237	19.22702128	3.12E-74	2.78E-72	71.5043598	
ABUW_RS1845	ABUW_2434	NZ_CP008706.1	14223589	2423002	+	WP_000893536.1			38.6320481	8.80036506	1.050422291	4.16401943	3.38E-06	7.68E-06	51.63431878	
ABUW_RS09050	ABUW_859	NZ_CP008706.1	8564269	8566828	+	WP_000387590.1		hypothetical protein	559.554375	4.860946921	0.524486128	9.268025195	1.90E-20	1.18E-19	19.5281799	
ABUW_RS07975	ABUW_934	NZ_CP008706.1	933239	933348	+	WP_000555766.1		spore coat protein U domain-containing protein	1453.5572	4.852180211	0.28534016	17.00487612	7.55E-05	5.25E-63	82.2798407	
ABUW_RS09995	ABUW_2058	NZ_CP008706.1	2038281	2040162	-	WP_000632243.1			2580.471981	4.795195327	0.289232105	16.59282625	7.85E-62	4.72E-60	59.326588	
ABUW_RS00325	ABUW_0066	NZ_CP008706.1	70383	71438	+	WP_000353163.1	hpdD	4-hydroxyphenylpyruvate dioxygenase	9314.533216	4.773882884	0.325356098	17.8737366	9.63E-49	3.05E-47	46.5107010	
ABUW_RS12280	ABUW_2526	NZ_CP008706.1	2519665	2518254	-	WP_000037856.1	paaf	phenylacetate-CoA ligase	3739.377241	4.746833289	0.183677888	25.84324838	2.90E-47	2.62E-44	14.5341071	
ABUW_RS11885	ABUW_2442	NZ_CP008706.1	2429805	2430233	-	WP_01016759.1		hypothetical protein	263.3190753	4.734708176	0.508854448	9.304641432	1.34E-20	8.44E-20	10.07365755	
ABUW_RS10330	ABUW_2126	NZ_CP008706.1	2110972	2110203	-	WP_000642316.1		2,3-butanediol dehydrogenase	837.2140566	4.710202789	0.237639102	19.84951443	1.11E-87	1.79E-85	84.74718697	
ABUW_RS07925	ABUW_924	NZ_CP008706.1	1619019	1620191	+	WP_000874704.1		iron-containing alcohol dehydrogenase	2045.830793	4.710864454	0.289844526	16.26342414	1.79E-59	1.02E-57	56.99193983	
ABUW_RS06270	ABUW_0286	NZ_CP008706.1	1006188	1006451	+	WP_001039306.1		hypothetical protein	504.7519217	4.703050405	0.574994674	11.92903857	2.86E-16	1.35E-16	14.86066623	
ABUW_RS18405	ABUW_3780	NZ_CP008706.1	3840508	3841195	-	WP_01080766.1		acyl-CoA dehydrogenase family protein	643.9599498	4.691670742	0.329318897	11.24676192	4.70E-46	1.33E-44	43.67618836	
ABUW_RS11910	ABUW_2448	NZ_CP008706.1	2434209	2435492	-	WP_001991886.1		hypothetical protein	362.5669837	4.674420123	0.297210856	15.72751959	9.80E-56	4.18E-54	53.38619518	
ABUW_RS10180	ABUW_2088	NZ_CP008706.1	2080105	2081624	+	WP_000418629.1		short-chain fatty acid transporter	1402.812259	4.669051474	0.356238463	13.9484011	3.09E-39	5.98E-38	37.22323982	
ABUW_RS10475	ABUW_2156	NZ_CP008706.1	2158335	2159194	-	WP_000564581.1		hypothetical protein	2839.365429	4.657370439	0.338128877	13.00495093	1.15E-38	2.16E-37	36.69596623	
ABUW_RS10205	ABUW_2523	NZ_CP008706.1	2514993	2516276	-	WP_010171641.1		Paal family histonease	68.5166519	4.650796192	0.394945231	11.66713481	1.87E-31	2.28E-30	29.4206915	
ABUW_RS18430	ABUW_3779	NZ_CP008706.1	3839273	3840046	-	WP_001898091.1		enoyl-CoA hydratase	234.409076	4.650287145	0.322627777	11.22702068	6.23E-46	1.73E-44	43.7819539	
ABUW_RS11630	ABUW_2452	NZ_CP008706.1	2439044	2440216	+	WP_001053639.1		isovaleryl-CoA dehydrogenase	234.015086	4.549345234	0.359073987	12.66965975	8.7E-37	1.41E-35	34.80078089	
ABUW_RS10500	ABUW_2658	NZ_CP008706.1	2654223	2654996	-	WP_002039934.1		DUF4882 family protein	375.181851	4.516354191	0.21751599	20.78718953	1.02E-95	2.29E-93	92.64016452	
ABUW_RS05995	ABUW_0227	NZ_CP008706.1	1027210	10269675	-	WP_000576848.1		acyl-CoA dehydrogenase	2404.047217	4.465295909	0.334201911	13.35299933	1.14E-40	2.40E-39	38.91871687	
ABUW_RS03295	ABUW_2922	NZ_CP008706.1	2919108	2932162	+	WP_000854552.1		hypothetical protein	944.8374549	4.455289487	0.372906708	11.9405493	7.23E-33	1.68E-32	31.0141464	
ABUW_RS02955	ABUW_903	NZ_CP008706.1	9030508	9036933	+	WP_000706933.1		hypothetical protein	18.6996649	4.452351937	0.468617846	15.93028975	2.08E-21	3.97E-20	19.80372984	
ABUW_RS05220	ABUW_063	NZ_CP008706.1	1072881	1074525	-	WP_000705598.1		hypothetical protein	1709.88461	4.44166231	0.21418415	11.40454582	1.04E-75	9.75E-74	73.01099538	
ABUW_RS08000	ABUW_951	NZ_CP008706.1	1645792	1646262	+	WP_010132411.1		hypothetical protein	984.5032291	4.354161	0.509540725	11.545252396	1.28E-17	6.78E-17	11.8810223	
ABUW_RS10005	ABUW_2678	NZ_CP008706.1	2669697	2670336	+	WP_000247196.1		hypothetical protein	272.7938274	4.305692333	0.393535669	10.9417211	7.33E-28	7.07E-27	26.10505899	
ABUW_RS09045	ABUW_858	NZ_CP008706.1	8550592	8550240	+	WP_000896623.1		acyl-CoA dehydrogenase family protein	206.195171	4.28252106	0.607365710	10.94047109	2.25E-12	0.34E-12	10.7883395	
ABUW_RS14025	ABUW_2887	NZ_CP008706.1	2884092	2884571	+	WP_000749178.1		copper-resistance protein NtrE	12285.46824	4.26227389	0.329234593	12.94005965	2.47E-38	4.55E-37	34.164906	
ABUW_RS08050	ABUW_1761	NZ_CP008706.1	1758355	1758993	-	WP_000322547.1		SDS response-associated peptidase family protein	561.7360635	4.210022405	0.359419894	11.76533992	1.05E-31	1.29E-30	29.8894129	
ABUW_RS16445	ABUW_2149	NZ_CP008706.1	2143917	2140453	+	WP_000191725.1		hypothetical protein	249.4369006	4.211940232	0.333095959	12.64307204	1.22E-36	1.95E-35	34.70174393	
ABUW_RS07905	ABUW_920	NZ_CP008706.1	1613356	1614792	+	WP_001075439.1	eat	ethanolamine permease	85.25975536	4.89101676	0.351924612	11.90653362	1.09E-32	1.45E-31	30.838832	
ABUW_RS09260	ABUW_902	NZ_CP008706.1	902188	9003495	+	WP_000848751.1		sorbose dehydrogenase family protein	1369.888758	4.16654107	0.261953108	11.90557242	5.88E-57	2.78E-55	54.5659552	
ABUW_RS09055	ABUW_960	NZ_CP008706.1	956639	957186	+	WP_001050502.1		nucleosyl transfer factor 2 family protein	479.0793038	4.1638161	0.426312386	11.7673406	1.56E-22	1.10E-21	20.5880731	
ABUW_RS19395	ABUW_3778	NZ_CP008706.1	3838235	3839260	-	WP_001091033.1		enoyl-CoA hydratase/isomerase family protein	1119.231698	4.166883706	0.24268841	17.9284501	9.10E-66	6.44E-64	63.191110	
sRNA27	no	no	no	no	no	no	no	no	240.0879651	4.148847727	0.2640662	15.7139225	1.26E-55	5.24E-54	53.28068871	
ABUW_RS09040	ABUW_957	NZ_CP008706.1	953946	955055	+	WP_01021599.1		amidase	4.18391482	4.12431007	0.51097364	10.77421083	6.62E-16	3.07E-16	14.5129862	
ABUW_RS16280	ABUW_3351	NZ_CP008706.1	3387175	3388300	-	WP_000037364.1		hypothetical protein	980.1742542	4.086537105	0.425246468	10.69080585	7.27E-22	4.9E-21	20.30891551	
ABUW_RS05225	ABUW_064	NZ_CP008706.1	1074526	1075776	+	WP_000033256.1		glycosyltransferase family 2 protein	1291489325	0.702230308	0.258485653	15.79338229	6.51E-66	2.79E-54	53.5543568	
ABUW_RS09270	ABUW_904	NZ_CP008706.1	904447	904743	+	WP_001277236.1		antibiotic biosynthesis monooxygenase	3.16651789	4.062303495	0.255810897	11.88226265	8.41E-97	3.81E-95	45.19077052	
newcardinalNA1	no	no	no	no	no	no	no	no	238.6279859	0.440338875	0.668467034	10.64970738	1.45E-09	4.35E-09	8.35852589	
ABUW_RS09005	ABUW_962	NZ_CP008706.1	955484	955969	+	WP_001056337.1		aromatic-mg-hydroxylating dioxygenase subunit beta	714.8232945	4.032541629	0.426780874	11.948794326	3.43E-21	2.25E-20	19.64781748	
sRNA55	no	no	no	no	no	no	no	no	3728.887349	4.005471521	0.440991893	9.02837724	1.05E-19	6.30E-19	8.20065945	
ABUW_RS07985	ABUW_936	NZ_CP008706.1	934289	935030	+	WP_000165428.1		SDR family NAD(P)-dependent oxidoreductase	210.9334479	3.998757869	0.312855064	12.78967727	1.87E-37	3.16E-36	35.50031932	
ABUW_RS16425	ABUW_2145	NZ_CP008706.1	210417	210683	+	WP_001937021.1		hypothetical protein	1494.49286	3.998021645	0.286280863	13.96540586	2.53E-44	6.59E-43	42.1837587	
ABUW_RS17165	ABUW_3516	NZ_CP008706.1	3564335	3564664	+	WP_000207459.1		MerR family transcriptional regulator	924.2330037	3.977109368	0.342461916	12.505853	1.39E-34	3.26E-33	32.69250396	
ABUW_RS20105	no	NZ_CP008706.1	1488830	1488964	+	WP_000891873.1		hypothetical protein	15.9345802	3.91686636	0.91722585	4.26923461	1.96E-05	4.13E-05	4.380440948	
ABUW_RS14030	ABUW_2888	NZ_CP008706.1	2894635	2896239	+	WP_000214787.1		isocitrate lyase	10548.13035	3.916343031	0.255469786	15.26207186	5.12E-53	1.86E-51	50.73044706	
ABUW_RS05235	ABUW_066	NZ_CP008706.1	1076559	1077399	+	WP_010186266.1		hypothetical protein	389.360916	3.895398728	0.307373367	12.67301472	8.34E-37	1.36E-35	34.86645109	
ABUW_RS16140	ABUW_3322	NZ_CP008706.1	3357519	3357882	+	WP_000885013.1		hypothetical protein	526.52006	3.891674294	0.4018186	11.698494301	3.7E-22	2.18E-21	20.65164351	
ABUW_RS05910	ABUW_010	NZ_CP008706.1	1050283	1051740	+	WP_000830596.1		hypothetical protein	10727.00405	3.881027332	0.170458384	22.7681809	9.48E-16	4.24E-102	111.372341	
ABUW_RS12750	ABUW_2628	NZ_CP008706.1	2624476	2625780	+	WP_000659371.1		MFS transporter	181193458	3.875729847	0.286777555	15.9476005	1.28E-41	2.90E-40	39.537002	
ABUW_RS05230	ABUW_065	NZ_CP008706.1	1075763	1076659	+	WP_000607479.1		hypothetical protein	495.8730488	3.870052408	0.26491973	11.60872912	2.47E-48	7.66E-47	46.1677123	
ABUW_RS03285	ABUW_0667	NZ_CP008706.1	673231	673680	+	WP_000190594.1		SRPB/C family protein	1667.195335	3.851646697	0.27158315	11.8005019	1.09E-45	2.96E-44	43.52870829	
ABUW_RS19790	ABUW_3252	NZ_CP008706.1	3281966	3282304	+	WP_011874611.1	aaIA	ribosome-associated translation inhibitor RaaI	3509.359416	3.84638271	0.21814334	11.6284437	1.08E-58	5.99E-57	54.5002749	
ABUW_RS02300	ABUW_0468	NZ_CP008706.1	481071	481116	+	WP_000462894.1		DUF2789 domain-containing protein	2297.893528	3.832770432	0.302230972	12.6819385	7.48E-37	1.23E-35	44.62291849	
ABUW_RS09275	ABUW_905	NZ_CP008706.1	904783	905424	+	WP_000200064.1		hydrolase	833.8009455	3.832572694	0.201023807	19.03685788	8.44E-81	9.12E-79	78.0132374	
ABUW_RS01620	ABUW_0206	NZ_CP008706.1	213911	2132327	+	WP_000406166.1		hydrolase	412.509722	3.80218898	0.21834592	17.41594189	6.1E-68	6.05E-66	55.29702862	
ABUW_RS20160	no	NZ_CP008706.1	1897127	1897621	+	WP_000000000.1		hypothetical protein</								

ABLW_RS09525	ABLW_1658	NZ_CP008706.1	1959711	1662767	+	WP_000162636.1		DEAD/DEAH box helicase family protein	1472.424893	3.243.54262	0.19229847	16.86579181	8.035E-64	5.22E-62	6.18223295
ABLW_RS08175	ABLW_1720	NZ_CP008706.1	178319	178685	-	WP_000105078.1	tusD	sulfatransferase complex subunit TusD	3942.661732	3.243025553	0.324454808	9.995307424	1.60E-23	1.2E-22	2.191971463
ABLW_RS01740	ABLW_1622	NZ_CP008706.1	167940	1608392	+	WP_011865574.1		ONAT family N-acetyltransferase	306.488597	3.240901829	0.319466402	0.28967473	7.84E-25	6.36E-24	23.19654288
ABLW_RS00995	ABLW_1981	NZ_CP008706.1	199427	200184	-	WP_001026735.1		hypothetical protein	555.1797251	3.239212708	0.306029751	0.34653334	3.5E-26	3.08E-25	24.5184928
ABLW_RS01760	ABLW_1237	NZ_CP008706.1	215242	225931	-	WP_00194986.1	argZ	aquaporin Z	93712.19277	3.234704941	0.287019301	11.26999193	1.85E-29	2.01E-28	27.69800304
ABLW_RS00110	ABLW_1022	NZ_CP008706.1	25865	27183	+	WP_00102725.1		sodium-dependent transporter	9886.94454	3.231980997	0.180870006	9.22998693	2.08E-82	2.54E-80	75.95519628
ABLW_RS16475	ABLW_3186	NZ_CP008706.1	3215372	3218296	+	WP_00471023.1		hypothetical protein	171.6776206	3.197961441	0.241019874	0.126185248	3.85E-40	7.88E-39	8.10347378
ABLW_RS16440	ABLW_3179	NZ_CP008706.1	3206785	3207108	+	WP_001047855.1		hypothetical protein	501.8515851	3.170507351	0.325176055	9.75012552	1.84E-22	1.29E-21	20.88941629
sRNA44	no	no	no	no	no	no	no	no	4.738178039	3.16988675	1328204273	2.386455229	0.07012141	0.025070196	1.600842271
ABLW_RS00825	ABLW_1166	NZ_CP008706.1	195359	195105	-	WP_00071729.1		putative porin	57522.15981	3.160720051	0.237406871	0.31051545	1.93E-40	4.03E-39	38.39469495
ABLW_RS01575	ABLW_1540	NZ_CP008706.1	1526290	1527840	+	WP_0010295009.1		circularlypermuted type 2 ATP-grasp protein	880.190564	3.157464773	0.247142079	0.277590526	2.24E-37	3.74E-36	35.4271284
ABLW_RS1030	ABLW_2330	NZ_CP008706.1	231406	231419	-	WP_010132006.1		amino acid ABC transporter ATP-binding protein	1680.359521	3.165201494	0.23491066	0.43558093	3.74E-41	8.16E-40	39.08884239
ABLW_RS10610	ABLW_2802	NZ_CP008706.1	2800244	2801874	+	WP_010140777.1		gamma-aminobutyraldehyde dehydrogenase	663.7003967	3.150456666	0.359163269	8.534046934	1.4E-17	7.45E-17	16.12784373
ABLW_RS17480	ABLW_3587	NZ_CP008706.1	3645893	3645249	-	WP_001034851.1		hypothetical protein	928.7108039	3.145739356	0.302840272	0.38745389	2.83E-25	2.36E-24	23.827088
ABLW_RS17420	ABLW_3579	NZ_CP008706.1	3637107	3638266	+	WP_000846679.1		hypothetical protein	4553.25095	3.19483888	0.232841634	0.48334416	1.96E-41	4.32E-40	39.36451925
ABLW_RS017425	ABLW_1521	NZ_CP008706.1	150545	1507192	+	WP_000901778.1		sotobosome dehydrogenase family protein	781.4867356	3.158558628	0.243190251	0.218914207	4.55E-38	8.22E-37	36.08512818
ABLW_RS01675	ABLW_1159	NZ_CP008706.1	1186580	1187407	+	WP_001017886.1		TeiR/AcrI family transcriptional regulator	967.4533435	3.127368755	0.358390286	8.72615751	5.63E-19	1.44E-17	15.8413771
ABLW_RS17575	ABLW_2795	NZ_CP008706.1	2782499	2793937	-	WP_000671021.1		hypothetical protein	37.71235294	3.12644465	0.586328699	5.332239823	9.70E-08	2.54E-07	6.59516263
ABLW_RS10365	ABLW_1703	NZ_CP008706.1	2119327	2100489	+	WP_0001067591.1		transcriptional regulator	796.4408741	3.12503516	0.222960532	14.01609193	1.24E-44	3.25E-43	42.48811664
ABLW_RS01725	ABLW_1488	NZ_CP008706.1	1474973	1475521	+	WP_000577009.1	cusA	Cus fibrinolyticogenesis protein CusA	288.616321	3.12400695	0.127620624	2.448357979	0.014305092	0.021990967	1.669715562
ABLW_RS10280	ABLW_2736	NZ_CP008706.1	2724274	2724762	+	WP_000941916.1		CrkA family protein	165.684475	3.109536921	0.293833642	0.5387629	5.66E-26	4.90E-25	24.30580392
ABLW_RS01605	ABLW_0306	NZ_CP008706.1	3330212	3330676	-	WP_00067853.1	bfr	bacterioferritin	5792.399281	3.08981102	0.429116628	7.200416223	6.00E-13	2.33E-12	13.32644408
ABLW_RS04485	ABLW_0914	NZ_CP008706.1	910874	911812	+	WP_0101247651.1		NAD(+)-NADH kinase	725.0380992	3.088587201	0.206433523	14.96151205	1.30E-15	4.32E-14	48.36451925
ABLW_RS00885	ABLW_2056	NZ_CP008706.1	2013597	2013684	+	WP_000718470.1		DUF4882 family protein	429.0684263	3.08460206	0.209631221	0.28419587	8.30E-25	6.72E-24	23.12784373
ABLW_RS1165	ABLW_2093	NZ_CP008706.1	2074919	2075340	-	WP_000263726.1		GndP family permease	788.2046339	3.072273926	0.266168018	11.54216113	0.04E-31	9.48E-30	20.0231966
ABLW_RS00300	ABLW_1645	NZ_CP008706.1	1642557	1640811	-	WP_010130116.1		TeiR/AcrI family transcriptional regulator	10.2416457	3.053883038	0.991537419	0.380848186	0.002068971	0.003480261	1.866495952
ABLW_RS10035	ABLW_2685	NZ_CP008706.1	2675287	2675631	-	WP_0100104676.1		hypothetical protein	78.18102582	3.050045354	0.489797377	0.227167391	4.75E-10	1.48E-09	8.826819732
ABLW_RS001490	ABLW_1951	NZ_CP008706.1	1952288	1953076	+	WP_075874782.1		hypothetical protein	92.77109314	3.045386201	0.278002028	0.165454669	6.32E-28	6.15E-27	26.2142488
ABLW_RS00975	ABLW_2504	NZ_CP008706.1	2512229	2513747	+	WP_010104963.1		fibrinolyticogenesis outer membrane usher protein	242.003872	3.044590642	0.61534857	3.73169956	2.28E-13	9.16E-13	12.03810453
ABLW_RS00840	ABLW_1753	NZ_CP008706.1	1749233	1749526	+	WP_000689660.1		hypothetical protein	493.58747	3.043589302	0.312603239	9.783292949	2.1E-22	1.47E-21	20.73256267
ABLW_RS00845	ABLW_1775	NZ_CP008706.1	1774456	1774701	-	WP_000104968.1		hypothetical protein	2649.477444	3.042092787	0.262953624	11.56993272	5.92E-31	7.00E-30	29.15490196
ABLW_RS01750	ABLW_0357	NZ_CP008706.1	380432	380740	+	WP_004571608.1		hypothetical protein	96.23606246	3.023693691	0.396443011	7.620955861	2.40E-14	1.01E-13	12.95957681
ABLW_RS10270	ABLW_2524	NZ_CP008706.1	2513534	2513659	-	WP_01012269.1		carbonic anhydrase	309.64431	3.021836525	0.218935761	0.202238894	2.47E-43	6.71E-42	16.201971464
ABLW_RS1033	ABLW_2331	NZ_CP008706.1	2314163	2314840	-	WP_000347804.1		amino acid ABC transporter permease	107.859138	3.004716702	0.245022156	0.28324488	1.43E-34	2.07E-33	32.68429585
ABLW_RS10380	ABLW_2756	NZ_CP008706.1	2746479	2747006	-	WP_000608974.1		hypothetical protein	837.5659352	3.003872892	0.276162101	0.877799679	1.47E-27	1.39E-26	5.85899582
ABLW_RS00075	ABLW_1864	NZ_CP008706.1	1819752	1807705	+	WP_000219290.1		oxodolase	306.7263758	3.008601383	0.385012811	7.76434051	8.17E-15	3.54E-14	11.45099674
ABLW_RS01740	ABLW_0233	NZ_CP008706.1	2522711	2522714	+	WP_000581866.1		hypothetical protein	1082.890022	3.002856526	0.341248155	8.733396939	4.97E-17	1.36E-17	16.8664669
ABLW_RS1830	ABLW_3807	NZ_CP008706.1	3880842	3889199	-	WP_000089751.1	ppcC	2-methylerythritol synthase	3781.352569	2.973423039	0.274393611	0.83789487	2.28E-27	2.12E-26	27.67366414
ABLW_RS00605	ABLW_1241	NZ_CP008706.1	1237738	1237739	-	WP_000835608.1		DUF962 domain-containing protein	639.0061619	2.957986473	0.26898026	11.0305023	1.27E-29	1.40E-28	27.8587196
ABLW_RS20105	ABLW_0382	NZ_CP008706.1	405290	409475	+	WP_000471151.1		hypothetical protein	122.10632	2.95198881	0.428632458	6.885100094	5.77E-12	2.09E-11	16.67985371
ABLW_RS04475	ABLW_0912	NZ_CP008706.1	9107091	9108058	+	WP_000868053.1	gldD	glycerol-3-phosphate dehydrogenase	1006.051678	2.925532688	0.208252272	14.04934562	7.71E-45	2.04E-44	42.69035993
ABLW_RS01760	ABLW_2531	NZ_CP008706.1	2517325	2542124	-	WP_002017455.1		RMS repeat protein	6937.879138	2.920722166	0.162491476	0.100475055	1.8E-57	5.69E-56	55.22984771
ABLW_RS11755	ABLW_2293	NZ_CP008706.1	2279975	2290465	-	WP_000550341.1		polysaccharide-binding protein	2145.45552	2.914726399	0.224162384	0.00622663	1.9E-38	2.1E-37	36.87571754
ABLW_RS00855	ABLW_1782	NZ_CP008706.1	1795948	1796790	+	WP_001033284.1		PQQ-dependent sugar dehydrogenase	2276.90416	2.909342323	0.185364172	16.69527858	1.83E-55	6.63E-54	53.17648647
ABLW_RS00380	ABLW_0077	NZ_CP008706.1	82180	83827	+	WP_000208426.1	hufU	uracanine hydratase	7983.6429	2.90001654	0.447803814	8.476076284	9.46E-11	3.18E-10	9.507239611
ABLW_RS11075	ABLW_3105	NZ_CP008706.1	3146270	3146734	-	WP_001021465.1	bfr	bacterioferritin	5269.31849	2.877089198	0.402807181	0.176256523	9.16E-13	3.52E-12	14.45345734
ABLW_RS00970	ABLW_1863	NZ_CP008706.1	1815880	1819717	+	WP_000819505.1		SDR family oxidoreductase	355.5863172	2.837600889	0.426027987	6.605097375	2.73E-11	9.33E-11	10.03018336
sRNA77	no	no	no	no	no	no	no	no	229.3661001	2.834912884	0.37357548	1.588594872	3.23E-14	1.36E-13	12.86646199
ABLW_RS01720	ABLW_3875	NZ_CP008706.1	3842924	3843154	-	WP_0007133016.1		hypothetical protein	2956.819631	2.82618821	0.344263705	16.19471878	3.30E-16	1.05E-15	14.8008781
ABLW_RS00820	ABLW_1192	NZ_CP008706.1	1224268	1224738	+	WP_000914201.1		DUF3015 family protein	1792.05204	2.821974208	0.220838664	0.278444269	2.16E-37	3.63E-36	35.44009337
ABLW_RS00970	ABLW_2053	NZ_CP008706.1	2013437	2023271	+	WP_000774086.1		molecular chaperone	928.755828	2.808631839	0.606099935	4.633841824	3.59E-06	8.11E-06	5.09097798
ABLW_RS1730	ABLW_2411	NZ_CP008706.1	2398444	2398304	+	WP_001028523.1	yghU	glutathione-dependent disulfide-bond oxidoreductase	191.166473	2.805683965	0.252819511	11.09708875	1.28E-28	1.31E-27	26.8827287
ABLW_RS1640	ABLW_2372	NZ_CP008706.1	2318457	2318816	-	WP_000718479.1		DUF427 family protein	58.8948507	2.800547829	0.440297389	6.361016823	2.00E-10	6.46E-10	9.189787482
ABLW_RS10270	ABLW_1561	NZ_CP008706.1	1549554	1550417	-	WP_000102077.1		hypothetical protein	311.9448929	2.79442512	0.215210592	15.1645665	1.7E-39	3.42E-38	27.40597389
ABLW_RS1885	ABLW_3291	NZ_CP008706.1	3334185	3337993	+	WP_000353062.1	acpC	CoxA synthetase	358.519198	2.789993509	0.316479374	8.803080827	1.33E-19	7.47E-19	17.026794
ABLW_RS00520	ABLW_1062	NZ_CP008706.1	1071798	1072703	-	WP_000714421.1		hypothetical protein	573.6837546	2.78138668	0.19080787	14.31623975	1.04E-48	3.06E-45	4.51627857
ABLW_RS17145	ABLW_3524	NZ_CP008706.1	3580483	3580969	+	WP_000687235.1		hypothetical protein	336.22511	2.780546488	0.325823781	8.533896692	1.4E-17	7.45E-17	16.12784373
ABLW_RS17395	ABLW_3574	NZ_CP008706.1	3613292	3613783	-	WP_010101211.1		hypothetical protein	788.0260994	2.775233295	0.222977332	0.446257331	1.47E-35	2.25E-34	33.64719748
ABLW_RS01720	ABLW_1487	NZ_CP008706.1	1474362	1474898	+	WP_000790104.1	cusAB	Cus fibrinolyticogenesis							

ABIUW_RS02025	ABIUW_0449	NZ_CP008706.1	461097	463520	-	WP_000479308.1		hypothetical protein	15463.97897	2.520672669	0.267083501	9.437770057	3.8 E-21	2.48E-20	9.60554832
ABIUW_RS18880	ABIUW_2441	NZ_CP008706.1	14249496	2429717	-	WP_000498474.1		hypothetical protein	84.922427	2.59449732	0.423194264	5.964256006	2.6 E-09	7.75E-09	8.16068297
uRNA5	no	no	no	no	no	no	no	no	3.947.95952	2.519.90251	1.427004274	1.763204425	0.077866076	0.937447409	0.936405655
ABIUW_RS09965	ABIUW_2052	NZ_CP008706.1	2030185	2031048	+	WP_00073191.1		type I fibrillar protein	6554.754857	2.50954865	0.590355999	4.253320303	2.18E-05	4.4 E-05	4.88440111
ABIUW_RS12775	ABIUW_2834	NZ_CP008706.1	2843199	2843508	+	WP_000474506.1		hypothetical protein	388.7433293	2.48593873	0.297674597	8.34871975	6.93E-17	3.46E-16	5.4602039
ABIUW_RS08320	ABIUW_1709	NZ_CP008706.1	1710241	1710281	+	WP_010305979.1	msaA	GTP 3'-beta-cyclase MsaA	4915445099	2.479764809	0.363622039	9.40635557	5.0E-21	3.3 E-20	9.48017201
ABIUW_RS03090	ABIUW_0628	NZ_CP008706.1	629273	629914	-	WP_000175332.1		peroxiredoxin	1619.451623	2.470073604	0.369495684	6.684986343	2.3 E-11	7.94E-11	10.007795
ABIUW_RS02975	ABIUW_0605	NZ_CP008706.1	603670	605451	-	WP_001213422.1		acyl-CoA dehydrogenase C-terminal domain-containing protein	4097.43123	2.466550044	0.92589836	0.8066909	1.50E-37	2.57E-36	55.99066808
ABIUW_RS1895	ABIUW_2465	NZ_CP008706.1	2457318	2457986	-	WP_000668703.1		3-oxoacyl-CoA-transferase subunit A	34.94069804	2.405497684	0.477872263	5.6932686	2.48E-07	6.29E-07	6.201549355
ABIUW_RS18520	no	NZ_CP008706.1	386516	386534	-	WP_000350168.1		hypothetical protein	69.2614191	2.455695187	0.397249768	6.187410229	6.34E-10	1.96E-09	8.707743929
ABIUW_RS18685	ABIUW_2402	NZ_CP008706.1	2388349	2390028	-	WP_000399235.1	mdcA	malonate decarboxylase subunit alpha	169.6201832	2.45160022	0.357810545	6.850999939	7.33E-12	2.6 E-11	10.58335949
ABIUW_RS00516	ABIUW_0164	NZ_CP008706.1	105413	106809	+	WP_000619878.1		alpha/beta fold hydrolase	928.8868829	2.448579027	0.173658101	14.099664	3.80E-45	1.02E-43	42.91939983
ABIUW_RS00385	ABIUW_0078	NZ_CP008706.1	83915	85453	+	WP_000421900.1	hufH	histidine ammonia-lyase	47.61879973	2.445704606	0.360806316	6.778441985	12.8 E-11	4.26E-11	10.3705904
ABIUW_RS10770	ABIUW_2216	NZ_CP008706.1	2201452	2202107	-	WP_000156085.1		nucleoside-diphosphate sugar epimerase	303.4214736	2.444549771	0.2161416	11.58328117	5.01E-31	5.94E-30	29.22821056
ABIUW_RS18835	ABIUW_2432	NZ_CP008706.1	2420572	2423088	+	WP_000795916.1		hypothetical protein	217.5339958	2.449222505	0.297481982	8.21001587	2.18E-16	1.05E-15	14.9788107
ABIUW_RS05195	ABIUW_0642	NZ_CP008706.1	6505072	6505482	+	WP_001014257.1		GFA family protein	393.7299252	2.440628092	0.249926421	9.783304049	1.59E-22	1.0E-21	20.9507198
ABIUW_RS19475	ABIUW_3794	NZ_CP008706.1	3857039	3857416	-	WP_001079191.1		ribonuclease E inhibitor RseB	947.514358	2.440588447	0.793056631	3.077445358	0.002087831	0.003060407	2.51071676
uRNA23	no	no	no	no	no	no	no	no	394.2856283	2.433646171	0.526406496	4.823100964	3.78E-06	8.53E-06	5.089509959
ABIUW_RS10450	ABIUW_2770	NZ_CP008706.1	2761888	2763558	+	WP_000164593.1		GMC family oxidoreductase	568.2770896	2.430060509	0.206858688	11.76288485	6.06E-32	7.55E-31	30.1203505
ABIUW_RS09980	ABIUW_0655	NZ_CP008706.1	660751	661107	+	WP_000182767.1		flavin reductase family protein	276.7643261	2.41016729	0.38746587	6.248335447	4.15E-10	1.3 E-09	8.882727074
ABIUW_RS00270	ABIUW_0055	NZ_CP008706.1	59548	60717	+	WP_001099830.1		PQQ-dependent sugar dehydrogenase	379.176379	2.415757661	0.340212671	7.10712807	1.24E-12	4.72E-12	11.326058
ABIUW_RS13520	ABIUW_2784	NZ_CP008706.1	2779143	2779532	+	WP_000372413.1		Paal family thioesterase	33.1812834	2.4100034	0.56568977	4.268482394	2.00E-05	4.2 E-05	4.37571904
ABIUW_RS11860	ABIUW_2294	NZ_CP008706.1	2280380	2281687	+	WP_000442820.1		OsmC family protein	341.705182	2.40781563	0.328342055	7.33323383	2.25E-13	9.02E-13	10.04470346
ABIUW_RS10590	ABIUW_2798	NZ_CP008706.1	2791578	2796641	-	WP_000424089.1		amino acid permease	986.0880092	2.406222573	0.358145963	6.7185283	1.84E-11	1.0 E-10	9.954288
ABIUW_RS12385	ABIUW_2737	NZ_CP008706.1	2724189	2727398	+	WP_001021000.1	cpbB	ATP-dependent thioesterase CpbB	14167.99903	2.39179340	0.206817229	11.60288032	3.98E-31	4.78E-30	29.3202711
ABIUW_RS12230	ABIUW_2514	NZ_CP008706.1	2507164	25107484	-	WP_000338517.1		hypothetical protein	200.4946675	2.39587192	0.674419099	3.552650636	0.000381096	0.000701642	3.96425962
ABIUW_RS00690	ABIUW_0199	NZ_CP008706.1	163753	164190	+	WP_000719702.1		DUF2147 domain-containing protein	4566.10107	2.39454792	0.202633006	11.8171024	3.18E-32	4.07E-31	30.39040599
ABIUW_RS00285	ABIUW_0058	NZ_CP008706.1	63229	63432	-	WP_000419560.1		hypothetical protein	925.3951735	2.390790655	0.373282064	6.404875943	15.1 E-10	4.90E-10	9.30880392
ABIUW_RS1100	ABIUW_3320	NZ_CP008706.1	3354427	3355329	+	WP_001026877.1		copper resistance protein B	633.9744303	2.38481573	0.302104369	7.893357282	2.94E-15	1.3 E-14	13.8277827
ABIUW_RS09610	ABIUW_1555	NZ_CP008706.1	156893	1568323	-	WP_000193415.1		hematin lyase hemH	362.5923692	2.37218573	0.441064433	5.379316268	7.52E-08	1.99E-07	6.70146524
ABIUW_RS10970	ABIUW_2672	NZ_CP008706.1	2656673	2666017	-	WP_001004672.1		hypothetical protein	70.76522331	2.370310934	0.555191448	4.269357026	1.96E-05	4.13E-05	4.340409948
ABIUW_RS11800	ABIUW_2425	NZ_CP008706.1	241866	241850	+	WP_001025680.1		N-acetyltransferase	284.1577172	2.353707384	0.239886884	9.810711243	1.00E-22	7.23E-22	21.14086197
ABIUW_RS18865	ABIUW_3874	NZ_CP008706.1	3942434	3942750	+	WP_001024778.1		hypothetical protein	941807449	2.33570948	0.301089266	7.787531643	8.66E-15	3.75E-14	4.12598873
ABIUW_RS05480	ABIUW_1100	NZ_CP008706.1	114171	1143757	+	WP_001096831.1		BapA prefix-like domain-containing protein	4525.440612	2.335327738	0.205025887	11.39044027	4.67E-30	5.27E-29	28.2781939
ABIUW_RS18385	ABIUW_3776	NZ_CP008706.1	3836104	3836367	+	WP_000381787.1	abaI	acyl-homoserine-lactone synthase AbaI	45.91664997	2.37336815	0.34840948	6.65282692	2.88E-11	9.8 E-11	10.063982
ABIUW_RS09300	ABIUW_0190	NZ_CP008706.1	911194	912576	+	WP_000340497.1		amidohydrolase	280.5165212	2.313149488	0.372250706	6.209679596	5.3 E-10	1.65E-09	8.78251656
ABIUW_RS1405	ABIUW_2345	NZ_CP008706.1	2326031	2328676	+	WP_000183693.1		hypothetical protein	284.6057243	2.31490473	0.255474524	9.047831616	1.46E-19	8.63E-19	10.063982
ABIUW_RS04190	ABIUW_0303	NZ_CP008706.1	326919	327477	+	WP_000258946.1		TPM domain-containing protein	925.810824	2.30919268	0.37864994	13.2814689	2.97E-40	6.10E-39	38.21467016
ABIUW_RS1610	ABIUW_3216	NZ_CP008706.1	3247773	3248848	-	WP_000843791.1		zinc-binding dehydrogenase	107.1621519	2.307206084	0.298029758	7.714710429	9.8 E-15	4.24E-14	13.72623414
ABIUW_RS09285	ABIUW_0607	NZ_CP008706.1	606091	606103	+	WP_000383070.1		acyl-coA-acylating methyltransferase	1705.062847	2.306469176	0.619620793	13.59717399	4.15E-42	9.72E-41	40.0123374
ABIUW_RS07105	ABIUW_1464	NZ_CP008706.1	1453227	1454795	+	WP_0010018127.1		CoA-acylating pyridinolactone-semialdehyde dehydrogenase	524.0297573	2.305705197	0.276051091	8.352448808	6.69E-17	3.35E-16	14.9405519
ABIUW_RS02070	ABIUW_2365	NZ_CP008706.1	2871422	2871635	-	WP_001186305.1		hypothetical protein	953.3494449	2.304749594	0.294088906	7.930461428	4.62E-15	2.04E-14	13.9030693
ABIUW_RS11450	ABIUW_2354	NZ_CP008706.1	2336883	2337728	-	WP_000336318.1		AnsC family transcriptional regulator	632.444155	2.310716022	0.234881162	9.79947946	1.0E-22	8.10E-22	21.08990945
ABIUW_RS08530	ABIUW_1751	NZ_CP008706.1	1748425	1748784	+	WP_000798370.1		hypothetical protein	109.7445939	2.310527332	0.37016815	6.210716881	5.07E-10	1.58E-09	8.801642910
ABIUW_RS02380	ABIUW_0485	NZ_CP008706.1	496585	497496	+	WP_0001021938.1		SDR family oxidoreductase	154.9988263	2.297886239	0.370502928	6.209615064	5.3 E-10	1.65E-09	8.78251656
ABIUW_RS04495	ABIUW_0916	NZ_CP008706.1	92597	925945	+	WP_000250932.1		lyp-like domain repeat protein	22636.85735	2.284783957	0.18539905	0.323261023	6.76E-35	9.90E-34	10.04348481
ABIUW_RS04930	ABIUW_0303	NZ_CP008706.1	181036	1910341	+	WP_000383695.1		multidrug efflux MFS transporter	768.1810367	2.274983326	0.150190911	15.1727693	7.90E-52	2.77E-50	49.5570223
ABIUW_RS01640	ABIUW_0333	NZ_CP008706.1	356034	356402	+	WP_000181930.1		hypothetical protein	1649.178822	2.273472877	0.24503517	9.27921106	1.7 E-20	1.07E-19	19.87061822
ABIUW_RS16860	ABIUW_2234	NZ_CP008706.1	2221720	2223385	+	WP_000102661.1		maleate synthase G	92.51426337	2.262223349	0.177844503	0.720233023	4.57E-37	7.54E-36	15.1262865
ABIUW_RS16755	ABIUW_3245	NZ_CP008706.1	3274482	3275398	+	WP_000781688.1		hypothetical protein	3251798804	2.2621491	0.203609516	1.10232373	1.12E-28	1.6E-27	26.93554201
ABIUW_RS00910	ABIUW_0184	NZ_CP008706.1	204064	206319	+	WP_000807185.1		cation acetate symporter	3826.315546	2.261887698	0.386955631	5.840341917	5.06E-09	1.47E-08	17.82062665
ABIUW_RS12755	ABIUW_2830	NZ_CP008706.1	2836204	2837310	-	WP_001085954.1		RHS repeat-associated core domain-containing protein	1451584968	2.255336452	0.216868279	10.69547519	1.07E-26	6.86E-26	25.9145464
ABIUW_RS07285	ABIUW_1490	NZ_CP008706.1	1476039	1476872	+	WP_0001986519.1	csuC	Csu fibrin-like biogenesis chaperone CsuC	246.6660512	2.24184282	1.03821982	1.994838022	0.046005549	0.063810352	1.99508025
ABIUW_RS02005	ABIUW_3156	NZ_CP008706.1	3163997	3163927	+	WP_000742683.1		hypothetical protein	226.3425618	2.24105146	0.31931741	7.042783137	1.90E-12	7.10E-12	11.9871605
ABIUW_RS10560	ABIUW_3102	NZ_CP008706.1	3193141	3193922	-	WP_000188568.1		DUF2157 domain-containing protein	1210.049405	2.239409505	0.373632336	0.21971332	4.67E-38	8.40E-37	1.975712071
ABIUW_RS14490	ABIUW_2084	NZ_CP008706.1	2090533	2091034	-	WP_001091018.1		transform-binding protein-like solute binding protein	7114889999	2.233033888	0.446337291	5.003243058	5.64E-07	1.39E-06	5.86998752
ABIUW_RS16095	ABIUW_3310	NZ_CP008706.1	3347544	3347858	+	WP_000233043.1		NAD(P)transhydrogenase subunit alpha	263.9247905	2.231890071	0.298468419	7.477801981	7.56E-14	3.0E-13	0.30584541
ABIUW_RS16245	ABIUW_3140	NZ_CP008706.1	3164714	3166807	+	WP_000209696.1		hypothetical protein	1619.458006	2.221647773	0.222104148	10.00227594	1.49E-23	1.0E-22	21.94692166
ABIUW_RS07530	ABIUW_0														

ABLW_RS0480	ABLW_0301	NZ_CP008706.1	325229	325819	+	WP_000846931.1				LemA family protein	2088.037787	2.068570867	0.184243047	10.64939464	1.76E-26	1.56E-25	24.8068754
ABLW_RS1773	ABLW_0773	NZ_CP008706.1	172969	173829	-	WP_00036794.1				alpha-beta fold hydrolase	180.278196	2.064199787	0.246054538	8.389196242	4.89E-17	2.47E-16	15.60730305
ABLW_RS0390	ABLW_1349	NZ_CP008706.1	3176284	3176422	-	WP_000735804.1				NF382 beta family lipoprotein	102.945047	2.05589256	0.360959083	5.695609546	1.23E-08	3.46E-08	7.460923901
ABLW_RS0960	ABLW_2072	NZ_CP008706.1	205977	2059852	-	WP_000202696.1	pgk1			phosphoglycerate kinase 1	1655.564746	2.049364962	0.223823061	9.63799993	5.26E-20	3.19E-19	18.4982932
ABLW_RS0505	ABLW_3398	NZ_CP008706.1	3439482	3441626	+	WP_001892925.1	pta			phosphate acetyltransferase	106.973529	2.043098829	0.268257739	7.61618706	2.61E-14	1.91E-13	12.95650731
srNA74	no	no	no	no	no	no	no			no	67.0640898	2.039869255	0.317377253	6.427208973	1.30E-17	4.25E-16	9.3716187
ABLW_RS1180	ABLW_2298	NZ_CP008706.1	228540	228636	+	WP_000162618.1				hypothetical protein	225.7903063	2.035502042	0.287479371	7.060508892	1.44E-12	5.42E-12	11.26000771
ABLW_RS0720	ABLW_1491	NZ_CP008706.1	147869	1479367	+	WP_000603294.1	csuD			Csu fibrinol usher CsuD	970.571689	2.03510567	1.029159595	1.802483796	NA	NA	#VALUE!
ABLW_RS0360	ABLW_0360	NZ_CP008706.1	382756	383175	-	WP_000644154.1				hypothetical protein	5415244468	2.029467452	0.229670778	8.836459573	9.88E-19	5.08E-18	17.2533658
ABLW_RS0370	ABLW_0685	NZ_CP008706.1	693671	694552	+	WP_000022126.1				alpha-beta fold hydrolase	287.6001099	2.02695876	0.42137496	4.870772311	1.50E-06	3.54E-06	5.450996738
ABLW_RS1295	no	NZ_CP008706.1	266492	2665616	-					transposase	93.4438502	2.025478822	0.390767036	5.93341057	2.16E-07	5.55E-07	6.255707017
srNA50	no	no	no	no	no	no	no			no	67.5167563	2.024877502	0.197555429	0.24966773	1.91E-24	9.93E-24	23.0209071
ABLW_RS0585	ABLW_4122	NZ_CP008706.1	82889	83192	-	WP_000719166.1				hypothetical protein	5745.22151	2.023864537	0.185533346	0.90836002	1.05E-27	1.00E-26	26
ABLW_RS0500	ABLW_3395	NZ_CP008706.1	3438237	3439439	+	WP_000236000.1				acetate kinase	893.129219	2.019488198	0.272788808	7.395787879	1.41E-11	5.70E-13	12.24410514
ABLW_RS0580	ABLW_1996	NZ_CP008706.1	122881	1230380	+	WP_000893677.1	xthA			xanthine dehydrogenase small subunit	308.411944	2.016445855	0.206678672	9.756429338	1.73E-22	1.22E-21	20.91964017
ABLW_RS0875	ABLW_1790	NZ_CP008706.1	1785435	1786331	+	WP_000102943.1				nifuroxazole family protein	1911206567	2.013195191	0.21642456	9.30187503	1.38E-20	8.65E-20	19.0623983
ABLW_RS0190	ABLW_0343	NZ_CP008706.1	365274	365937	+	WP_000744750.1				hypothetical protein	729.9584919	2.011529213	0.207475008	6.984320449	9.16E-22	2.19E-21	20.659555589
ABLW_RS04935	ABLW_1006	NZ_CP008706.1	820050	820850	-	WP_000775546.1				enoyl-CoA hydratase/isomerase family protein	714.2674083	2.019532585	0.227772028	8.828197382	1.05E-18	5.97E-19	17.22402567
ABLW_RS0585	ABLW_1862	NZ_CP008706.1	188482	189510	-	WP_000168443.1				hypothetical protein	418.9595034	2.010229917	0.229989687	8.739552381	2.34E-17	1.29E-17	16.88941029
ABLW_RS0079	ABLW_0079	NZ_CP008706.1	85518	86930	+	WP_000081467.1				amino acid permease	2574.016251	2.007387985	0.355670251	5.643956873	1.66E-08	4.63E-08	7.334419009
ABLW_RS0685	ABLW_0175	NZ_CP008706.1	91311	915260	+	WP_001002965.1	acs			acetyl-CoA ligase	803.180253	2.00413426	0.21773274	9.204419354	3.44E-20	2.11E-19	16.67571954
ABLW_RS1405	ABLW_4082	NZ_CP008706.1	51428	51880	-	WP_000776261.1				hypothetical protein	326.010842	2.003889347	0.333806558	5.633799329	1.48E-08	4.15E-08	7.38951903
ABLW_RS1650	ABLW_2810	NZ_CP008706.1	2809373	281009	-	WP_000368993.1				ATP-binding protein	4191430525	2.002454934	0.164091664	0.20327036	2.99E-34	4.24E-33	32.37263414
ABLW_RS1900	ABLW_3314	NZ_CP008706.1	3348730	3348997	+	WP_001854048.1				Re/Sr specific NAD(P)(+)-transhydrogenase subunit alpha	1445.827742	1.996479605	0.321834926	6.2034276	5.52E-10	1.72E-09	8.76441753
ABLW_RS20235	ABLW_2515	NZ_CP008706.1	2507870	2508022	+	WP_00279184.1				hypothetical protein	1148609751	1.99361642	0.71654828	2.61942449	0.000848765	0.0159713	1.8662575
ABLW_RS1485	ABLW_3026	NZ_CP008706.1	305974	3052521	+	WP_001059437.1				VOC family protein	65.848317	1.992403252	0.37483238	5.316451274	1.06E-07	2.78E-07	6.55555204
srNA85	no	no	no	no	no	no	no			no	377.1631004	1.98573108	0.270756269	7.16309898	8.49E-13	3.27E-12	11.84545225
ABLW_RS0500	ABLW_1964	NZ_CP008706.1	1966695	1967213	+	WP_000651913.1				GINAT family N-acetyltransferase	229.899271	1.984595856	0.18381553	0.79609884	3.56E-27	2.45E-26	25.4528041
ABLW_RS1940	ABLW_2356	NZ_CP008706.1	233820	2338629	-	WP_000102180.1	msrB			peptide-methionine (R)-S-oxide reductase MsrB	1429.630212	1.976057457	0.25041637	9.604752279	7.63E-22	5.15E-21	20.2881927
ABLW_RS1495	ABLW_0448	NZ_CP008706.1	105688	1057475	+	WP_000885644.1				lipocalin family protein	1924.444737	1.9746610	0.21973268	8.986645191	2.55E-19	1.94E-18	34.46597339
ABLW_RS0650	ABLW_063	NZ_CP008706.1	379942	379987	+	WP_000681868.1				acyl-CoA dehydrogenase family protein	648.841903	1.974570485	0.16788275	0.506607016	6.87E-36	1.06E-34	33.97469410
ABLW_RS0019	ABLW_0185	NZ_CP008706.1	204489	207181	+	WP_001256565.1				hypothetical protein	196.420462	1.970592106	0.279177503	7.058563001	1.68E-12	6.31E-12	11.89970764
ABLW_RS1210	no	NZ_CP008706.1	2504687	2505388	-					TerR/Acr family transcriptional regulator	134.5420897	1.970421917	0.500690976	3.935403497	8.31E-05	0.000930557	17.66833084
ABLW_RS1810	ABLW_2223	NZ_CP008706.1	2208964	2209632	+	WP_000881924.1				ABC transporter permease	1084.628047	1.969886159	0.1962198	0.03819124	1.03E-23	7.87E-23	12.6402527
ABLW_RS1470	ABLW_3793	NZ_CP008706.1	3836633	3837910	-	WP_001054359.1				nuclear transport factor 2 family protein	720.8643934	1.963065679	0.734403282	2.873007771	0.007517451	0.01064498	19.33861253
ABLW_RS1820	ABLW_3865	NZ_CP008706.1	3938339	3934181	+	WP_000864180.1				NAD(P)+-dependent oxidoreductase	7811028805	1.959751626	0.252623705	7.647401821	2.05E-14	8.68E-14	10.848027
ABLW_RS0445	ABLW_1987	NZ_CP008706.1	1910362	1910327	+	WP_001076822.1	xthB			xanthine dehydrogenase myeloperoxidase binding subunit	356.271951	1.95910221	0.20873188	9.385859095	6.24E-21	4.02E-20	19.39773395
ABLW_RS0890	ABLW_1847	NZ_CP008706.1	1843497	1843363	+	WP_001187028.1				MBL fold metallo-hydrolase	316.535403	1.952791648	0.241092452	8.09976226	5.51E-16	2.08E-15	14.58838029
ABLW_RS0720	ABLW_1623	NZ_CP008706.1	1617856	161824	-	WP_001098105.1				alpha-beta hydrolase	587.641659	1.939453057	0.170435464	11.37399848	5.30E-30	5.94E-29	28.2221056
ABLW_RS1910	ABLW_2862	NZ_CP008706.1	2871643	2871894	-	WP_000768231.1				hypothetical protein	242.0235909	1.938875426	0.33008203	5.87389908	4.26E-09	1.24E-08	7.906578316
ABLW_RS1035	ABLW_3321	NZ_CP008706.1	3355516	3357433	+	WP_004571011				copper resistance system multicopper oxidase	1475.050001	1.93600305	0.301739708	6.41616841	1.40E-10	4.05E-10	9.341886603
ABLW_RS0500	ABLW_0332	NZ_CP008706.1	142532	1437361	+	WP_000782587.1				alpha-beta fold hydrolase	284.0019271	1.937582579	0.27607678	8.565850005	3.29E-19	1.95E-19	17.7896663
ABLW_RS1075	ABLW_2619	NZ_CP008706.1	261733	2619980	+	WP_002016766.1				serine hydrolase	411.0148039	1.934371062	0.16364221	0.59830284	2.16E-36	3.42E-35	34.46597339
ABLW_RS0040	ABLW_0081	NZ_CP008706.1	88198	89118	+	WP_001018986.1	hutG			formylglyoxylate	3818671938	1.931098712	0.31010491	6.412241801	1.43E-10	4.47E-10	9.330883119
srNA91	no	no	no	no	no	no	no			no	305.2828071	1.929054571	0.178936148	0.79067053	4.25E-27	3.90E-26	25.46939339
ABLW_RS05275	ABLW_0174	NZ_CP008706.1	9180805	9189341	+	WP_000542107.1	icd			NADP-dependent isocitrate dehydrogenase	2006.382013	1.918086317	0.1809414	0.58800005	3.39E-26	2.98E-25	34.25218374
ABLW_RS1035	ABLW_2700	NZ_CP008706.1	2684897	2685121	-	WP_000825869.1				hypothetical protein	704.1876478	1.915041969	0.223325317	8.575122116	9.90E-18	5.28E-17	16.27360068
ABLW_RS0140	ABLW_2474	NZ_CP008706.1	2467451	2468422	-	WP_000810508.1				ribonase monooxygenase	226.607258	1.910207919	0.253786305	7.533928663	4.92E-14	2.04E-13	12.69036983
ABLW_RS1470	ABLW_2358	NZ_CP008706.1	2340767	2342074	+	WP_000810505.1				dicarboxylate/amine acid cation symporter	3210.976507	1.911964755	0.365681978	5.22631081	1.73E-07	4.44E-07	6.35261703
ABLW_RS0330	ABLW_0576	NZ_CP008706.1	573257	57326	+	WP_000574911.1				phage holin family protein	12.80805996	1.908551218	0.56669085	0.248520228	0.000006881	0.001092611	2.96175302
ABLW_RS0200	ABLW_1918	NZ_CP008706.1	191241	1917381	+	WP_000770264.1				hypothetical protein	87.01932737	1.903106446	0.453965225	4.162251611	2.76E-05	5.67E-05	4.26419641
ABLW_RS0550	ABLW_2477	NZ_CP008706.1	2471770	2471770	+	WP_000501011.1				CoA transferase	225.8935151	1.902923369	0.211916799	8.979577715	7.72E-19	1.59E-18	17.79860288
ABLW_RS1935	ABLW_2783	NZ_CP008706.1	277856	2779102	+	WP_000758290.1				DUF3237 domain-containing protein	23.86190691	1.902856231	0.584198575	3.256885581	0.00102498	0.001958006	2.708195892
ABLW_RS1070	ABLW_2623	NZ_CP008706.1	2619612	2620562	+	WP_000384845.1				3-hydroxyacyl-CoA dehydrogenase	448.3122468	1.902462014	0.199893	9.517040881	1.78E-21	1.16E-20	9.32819759
ABLW_RS1925	ABLW_2683	NZ_CP008706.1	2672874	2674088	+	WP_000648003.1				MF5 transporter	64.17278191	1.901913389	0.403309983	4.70526874	2.43E-08	5.24E-08	5.24949105
ABLW_RS1660	ABLW_1793	NZ_CP008706.1	1719563	1719946	+	WP_01018611				acyl-CoA dehydrogenase family protein	300.2371846	1.90077119	0.186819536	0.17416547	2.59E-24	2.24E-23	22.69099883
ABLW_RS1855	ABLW_2811	NZ_CP008706.1	2818201	2819241	+	WP_000773509.1					438.0043061	1.899630285	0.325094629	5.843310296	5.10E-09	1.48E-08	7.82978285
ABLW_RS0240	ABLW_0489	NZ_CP008706.1	50193	50313	+	WP_000607540.1		</									

ABLW_RS09195	ABLW_1888	NZ_CP008706.1	1885950	1890657	+	WP_000180179.1		sacchampane dehydrogenase NADP- binding domain- containing protein	397.5036773	1.765532617	0.288607915	6.096285791	1.096-09	3.30E-09	8.48146606
ABLW_RS04745	ABLW_0967	NZ_CP008706.1	977483	978604	-	WP_001070874.1		Hyd family secretion protein	967.0319775	1.764848781	0.17820795	13.80721074	2.3E-43	5.8E-42	41.23582387
ABLW_RS1295	ABLW_2739	NZ_CP008706.1	2728502	2728927	-	WP_00126236.1		GNAT family N- acetyltransferase	23.1618286	1.764583094	0.219668279	8.032845447	9.52E-16	4.36E-15	14.36051501
ABLW_RS1660	ABLW_3214	NZ_CP008706.1	3245266	3246486	-	WP_001884166.1		acyl- CoA dehydrogenase	403.7460432	1.76327121	0.32618942	5.641090957	1.69E-08	4.7E-08	7.32697993
ABLW_RS1690	ABLW_3433	NZ_CP008706.1	3417821	3478799	-	WP_000271403.1		hypothetical protein	2965.488317	1.760657352	0.340494194	5.17088935	2.33E-07	5.93E-07	6.22634507
ABLW_RS20195	no	NZ_CP008706.1	1731521	1731537	+	WP_002012156.1		hypothetical protein	611.250589	1.760441809	0.373708193	4.7173884	2.47E-06	5.70E-06	5.24412514
ABLW_RS03470	ABLW_0705	NZ_CP008706.1	710624	711955	+	WP_000181534.1		palatin- like phospholipase family protein	575.5789825	1.751652917	0.1853888	9.446838813	3.43E-21	2.25E-20	6.9478194
ABLW_RS09355	ABLW_1921	NZ_CP008706.1	918920	9202060	-	WP_000786731.1		MFS transporter	224.8587641	1.747580985	0.210024589	8.242350185	1.69E-16	8.18E-16	15.0872467
ABLW_RS07275	ABLW_1492	NZ_CP008706.1	1479304	1480383	+	WP_002017500.1	csuE	Csu fibrinolytic adhesin CsuE	254.4310251	1.737501488	1.106090938	1.56432904	NA	NA	15.0872467
ABLW_RS19515	ABLW_4107	NZ_CP008707.1	67345	67845	+	WP_001058570.1	lepB	signal peptidase I	84.35772922	1.731942657	0.269823825	6.418790706	1.37E-10	4.48E-10	9.348721986
ABLW_RS04355	ABLW_0888	NZ_CP008706.1	884968	885684	-	WP_000722324.1		metalloprotease	338.4125986	1.717501142	0.175833989	9.76631679	1.07E-22	1.1E-21	20.55467702
ABLW_RS09785	ABLW_2015	NZ_CP008706.1	2007107	2007411	-	WP_000050492.1		DUF2523 domain- containing protein	9.52870962	1.719660705	0.17526451	3.003268495	0.002670967	0.004343003	2.353024017
ABLW_RS05680	ABLW_1161	NZ_CP008706.1	1187482	1188457	+	WP_000725511.1		hypothetical protein	90.43343304	1.72556031	0.321916164	5.319874647	1.04E-07	2.7E-07	6.567030709
ABLW_RS03190	ABLW_0648	NZ_CP008706.1	653328	653843	-	WP_000477151.1		GspHFM family pseudopilin	798.0289907	1.703267904	0.212125547	8.029527438	9.78E-16	4.46E-15	14.35066514
ABLW_RS16800	ABLW_2221	NZ_CP008706.1	2205801	2207331	-	WP_001950318.1		ABC transporter/ATP- binding protein	1077.883096	1.70111185	0.142356654	11.92254587	4.28E-32	5.40E-31	30.26760824
ABLW_RS16730	ABLW_3240	NZ_CP008706.1	326719	3269044	-	WP_001933109.1		hypothetical protein	2343.956208	1.69985376	0.12557424	16.16212056	1.07E-51	5.3E-50	49.27490548
ABLW_RS12895	no	NZ_CP008706.1	2053604	2054148	-			hypothetical protein	34.27594609	1.698240578	0.400767979	4.237465745	2.26E-05	4.7E-05	6.32697993
ABLW_RS01935	ABLW_0394	NZ_CP008706.1	418673	418699	+	WP_000712907.1	adeT2	putative multidrug efflux protein AdeT2	244.552092	1.690919578	0.184047187	8.710914625	2.94E-18	1.6E-17	6.79317412
ABLW_RS02980	ABLW_0606	NZ_CP008706.1	605619	607421	-	WP_00156747.1		acyl- CoA dehydrogenase C- terminal domain- containing protein	7167.932858	1.688260292	0.220680921	7.650780732	2.00E-14	8.40E-14	10.07262964
sRNA57	no	no	no	no	no	no	no	no	33.85.63499	1.68770751	0.328047791	5.14470019	2.68E-07	6.79E-07	16.98100226
ABLW_RS19140	ABLW_4023	NZ_CP008707.1	1251	12524	+	WP_000274905.1		ParA family protein	3454.018065	1.685032691	0.19934236	4.52958476	2.84E-17	1.45E-16	15.838332
ABLW_RS04830	ABLW_0885	NZ_CP008706.1	979795	9800436	+	WP_000080799.1		CSLREA domain- containing protein	1770.04582	1.675380277	0.208190541	8.045007394	8.38E-16	3.84E-15	14.4184127
ABLW_RS11870	ABLW_2460	NZ_CP008706.1	2451498	2453300	-	WP_001191921.1		acyl- CoA dehydrogenase C- terminal domain- containing protein	94.7320181	1.674423497	0.201639655	6.39973118	1.56E-10	5.05E-10	9.296708822
ABLW_RS02495	ABLW_5011	NZ_CP008706.1	5011	7151	-	WP_001284284.1		hypothetical protein	219.615106	1.67396628	0.246730857	6.784584222	1.96E-11	4.06E-10	10.3872156
ABLW_RS01850	ABLW_1776	NZ_CP008706.1	1774901	1775330	-	WP_000838063.1		heme- binding protein	546.9363457	1.67357556	0.21402891	6.944214041	3.8E-12	1.39E-11	10.8958562
ABLW_RS10580	ABLW_2796	NZ_CP008706.1	2794084	2794488	-	WP_001095968.1		DUF4265 domain- containing protein	59.2880051	1.67372386	0.367723867	4.544819519	5.50E-06	1.22E-05	4.91040169
ABLW_RS10765	ABLW_2832	NZ_CP008706.1	2843323	2843655	+	WP_000725505.1		hypothetical protein	261.0859851	1.667891488	0.307936734	5.834346663	6.08E-08	1.62E-07	6.79044885
ABLW_RS10800	ABLW_1885	NZ_CP008706.1	1886100	188710	-	WP_001922559.1		hypothetical protein	147.7267189	1.66711847	0.20745192	8.044294857	8.87E-16	3.98E-15	14.4018993
ABLW_RS08175	ABLW_1678	NZ_CP008706.1	167339	1672107	-	WP_000333807.1		TerR family transcriptional regulator	909.4294683	1.66639907	0.230546575	7.226035856	4.90E-13	1.92E-12	17.6696877
ABLW_RS01975	ABLW_0402	NZ_CP008706.1	428321	429778	-	WP_000537103.1		DUF2523 domain- containing protein	887.7287171	1.665509253	0.19742181	8.44161042	3.1E-17	1.59E-16	5.79960358
ABLW_RS09495	ABLW_1952	NZ_CP008706.1	195373	1954659	+	WP_000841603.1		Gh3 auxin- responsive promoter family protein	86.49374677	1.659653304	0.215588533	8.599599438	4.20E-11	1.4E-10	9.950750887
ABLW_RS14775	ABLW_3045	NZ_CP008706.1	3071489	3071022	-	WP_001024151.1		OrnA family protein	37602.89175	1.657683294	0.239232124	6.929175183	4.23E-12	1.54E-11	10.8147328
ABLW_RS1465	ABLW_3388	NZ_CP008706.1	342811	3429424	-	WP_00184480.1		alpha beta hydrolase	1650.712899	1.65552842	0.166625796	8.421710067	3.7E-17	1.88E-16	15.72584215
sRNA33	no	no	no	no	no	no	no	no	1.755571931	1.647888612	1.482710768	1.114027141	0.266395033	0.318866782	0.49033071
ABLW_RS20125	no	NZ_CP008706.1	186120	186103	-			hypothetical protein	238.068481	1.644192705	0.303988025	5.408741688	6.35E-08	1.09E-07	6.772110295
ABLW_RS01200	ABLW_1059	NZ_CP008706.1	1068477	1069178	-	WP_000853860.1		Vif family protein	5153438777	1.643780731	0.28692475	5.728959959	10.1E-08	2.87E-08	7.54211813
sRNA75	no	no	no	no	no	no	no	no	2018.99062	1.6391719	0.298359515	5.943946428	3.93E-08	1.06E-07	6.97494015
ABLW_RS18460	ABLW_2772	NZ_CP008706.1	2774830	2786272	-	WP_001886531.1		MFS transporter	243.5147894	1.637402056	0.287765702	5.89036561	1.27E-08	3.56E-08	7.448550002
ABLW_RS18440	ABLW_3787	NZ_CP008706.1	3784665	3805024	-	WP_000071347.1		RfxA family protein	1056.617113	1.634948205	0.237919558	6.87190344	6.35E-12	2.9E-11	10.64016452
ABLW_RS19005	ABLW_2860	NZ_CP008706.1	2871632	2871949	-	WP_000663963.1		hypothetical protein	74.33741065	1.633367124	0.375730208	4.34715969	1.38E-05	2.94E-05	4.53162527
ABLW_RS02090	no	NZ_CP008706.1	255035	255200	-			hypothetical protein	249.0283337	1.632191472	0.199952946	8.628771026	3.27E-16	1.55E-15	14.8095683
ABLW_RS16035	ABLW_3301	NZ_CP008706.1	3332005	3333378	+	WP_000062841.1		SDR family oxidoreductase	208.0228595	1.632005076	0.178337197	9.62087357	5.58E-20	3.28E-19	4.8715833
ABLW_RS05340	ABLW_1898	NZ_CP008706.1	182598	1859972	+	WP_000637362.1	casII	type I- F CRISPR- associated helicase Cas3	2369.632311	1.62035095	0.420518857	8.20935958	4.33E-19	2.42E-17	56.6191463
ABLW_RS08160	ABLW_1875	NZ_CP008706.1	1867840	1868231	+	WP_000132115.1		3- oxoacyl ACP reductase	919.570218	1.627824278	0.194391551	8.373945639	5.57E-17	2.80E-16	15.55284197
ABLW_RS1255	ABLW_2314	NZ_CP008706.1	2299784	2299863	+	WP_000905609.1		hypothetical protein	16.54701678	1.621832222	0.607620352	2.667821024	0.00763226	0.01808831	1.92773993
ABLW_RS0895	ABLW_1764	NZ_CP008706.1	17614	193507	-	WP_000203103.1		GDGDF domain- containing protein	967.9298172	1.6174946	0.202287225	7.97257197	1.55E-15	7.05E-15	14.1518168
ABLW_RS18545	ABLW_4113	NZ_CP008707.1	71310	73459	+	WP_000644930.1		hypothetical protein	47.6501111	1.6149679	0.32416785	4.975064045	6.52E-07	1.60E-06	5.79588087
ABLW_RS08695	ABLW_1786	NZ_CP008706.1	1782797	193030	-	WP_000160341.1		hypothetical protein	2409.900415	1.607695767	0.298342333	5.425100476	6.79E-08	1.55E-07	6.80968302
ABLW_RS04745	ABLW_1948	NZ_CP008706.1	1947325	1948785	+	WP_000063479.1	iaaH	indoleacetamide hydrolase	67.1630357	1.606281934	0.268497849	1.982475984	2.20E-09	6.53E-09	8.18506818
ABLW_RS00045	ABLW_0009	NZ_CP008706.1	1106	12153	+	WP_000724990.1		hypothetical protein	6807.483227	1.603993988	0.234123128	8.69616737	6.90E-12	2.47E-11	10.60730305
ABLW_RS05875	ABLW_003	NZ_CP008706.1	1239496	1242195	+	WP_000960044.1		Mifammy metalloprotease	1186.080745	1.6054193	0.247107411	6.819361706	3.73E-11	1.26E-10	9.899622455
ABLW_RS06690	ABLW_1784	NZ_CP008706.1	1783682	1783682	-	WP_01230584.1		DUF2150 domain- containing protein	602.0149778	1.60018867	0.238522765	6.708452661	1.97E-11	6.80E-11	10.1674919
ABLW_RS19155	ABLW_4028	NZ_CP008707.1	19145	19249	+	WP_000933769.1		toxic anion resistance protein	233.2066202	1.598469057	0.301768494	5.297004443	1.18E-07	3.06E-07	5.64278574
ABLW_RS02802	ABLW_0057	NZ_CP008706.1	12154	62143	-	WP_000349500.1		comparative transcription factor family protein	461.1204599	1.596273097	0.266312525	5.9383843	2.05E-09	6.90E-09	5.21467015
ABLW_RS19160	ABLW_3326	NZ_CP008706.1	3362788	3363198	+	WP_000898220.1		copper resistance protein CopC	71.11818368	1.59111708	0.296361410	1.36879119	7.93E-08	2.09E-07	6.57893371
ABLW_RS12990	ABLW_2675	NZ_CP008706.1	2676702	2688109	-	WP_001924719.1		hypothetical protein	3881.7100127	1.590678816	0.24484534	6.402065663	1.53E-19	4.47E-19	3.353643311
ABLW_RS05440	ABLW_1112	NZ_CP008706.1	1119148	1119133	-	WP_000357090.1		LipA/AnC family transcriptional regulator	247.5021967	1.589121672	0.367228564	4.327335161	1.5E-05	3.2E-05	4.493404968
ABLW_RS03230	ABLW_0656	NZ_CP008706.1	663238	663669	+	WP_00022555.1	mscL	large conductance mechanosensitive channel protein MscL	42.6144648	1.589068493	0.312727875	8.102269399	2.95E-18	1.6E-17	6.79317412
sRNA53	no	no	no	no	no	no	no	no	524.999025	1.589015214	0.40067915	9.196579905	7.32E-05	0.00014543	3.840002036
ABLW_RS02360	ABLW_0480	NZ_CP008706.1	492078	492641	+	WP_000884141.1		DUF4256 domain- containing protein	222.2239						

ABUW_RS9890	no	NZ_CP008706.1	281990	281437	-		hypothetical protein	78.59332906	1493740757	0.402132091	3.74555248	0.000203564	0.000382893	3.47622573
ABUW_RS9500	ABUW_2161	NZ_CP008706.1	214224	214274	-	WP_000183456.1	DUF931 domain-containing protein	594.584944	1493259396	0.2889516	115996241	4.53E-31	6.4E-30	29.26680273
ABUW_RS9670	ABUW_2195	NZ_CP008706.1	218119	218242	-	WP_000903541.1	alkane 1-monooxygenase	236.918285	1490489505	0.2598488	5.755947142	8.62E-09	2.46E-08	7.03964893
ABUW_RS9555	ABUW_1965	NZ_CP008706.1	967275	968199	-	WP_000800103.1	alpha/beta hydrolase	211.7760811	1488643421	0.238724638	6.23581913	4.49E-10	1.44E-09	8.55079287
ABUW_RS9205	ABUW_2467	NZ_CP008706.1	245975	2460530	-	WP_000617392.1	acyl-CoA dehydrogenase family protein	69.06541786	1488474065	0.30643301	1.24498076	2.96E-05	4.57E-05	3.3400938
ABUW_RS9990	ABUW_1887	NZ_CP008706.1	988336	989574	+	WP_000862283.1	NADH:flavin oxidoreductase/NADH oxidase family protein	98.036111	1489528572	0.275043929	5.402510625	6.57E-08	1.74E-07	6.739450752
ABUW_RS9765	ABUW_612	NZ_CP008706.1	606447	606647	-	WP_000462396.1		4.998927239	1482973242	1.089737916	1.36083152	0.173564238	0.214262368	0.664489768
ABUW_RS9100	ABUW_4016	NZ_CP008707.1	8119	8451	+	WP_000565581.1	hypothetical protein	857.9854142	1481952603	0.210810568	7.028834555	2.08E-12	7.73E-12	11.1182051
ABUW_RS1916	ABUW_3658	NZ_CP008706.1	3717569	3719365	+	WP_001144598.1	hypothetical protein	2025.442237	1480792396	0.204380199	7.245283067	4.32E-13	1.70E-12	11.76955108
ABUW_RS1675	ABUW_3450	NZ_CP008706.1	3436051	3437172	-	WP_000639214.1	endonuclease/exonuclease/phosphatase family protein	1153.705443	1478712176	0.143331035	10.31617548	5.92E-25	4.89E-24	23.31069114
ABUW_RS9335	ABUW_917	NZ_CP008706.1	919606	919705	-	WP_000938693.1	SMWKN4 family protein	260.8708719	1477803365	0.209740334	7.045871104	1.84E-12	6.89E-12	11.61787018
ABUW_RS9155	ABUW_0358	NZ_CP008706.1	380776	382101	+	WP_011908408.1	S8 family serine peptidase	272.4159303	1477365065	0.208518137	7.085047437	1.39E-12	5.26E-12	11.27901426
ABUW_RS9085	ABUW_971	NZ_CP008706.1	973297	973710	+	WP_000742419.1	hypothetical protein	79.17377796	1474003768	0.238101661	6.98868929	6.02E-10	1.86E-09	8.730487056
ABUW_RS1625	ABUW_2186	NZ_CP008706.1	2186889	2197101	-	WP_000531132.1	streptophore achromobactin biosynthesis protein AcuC	906.4027731	1468765132	0.290625401	5.053808532	4.33E-07	1.08E-06	5.966574258
ABUW_RS9875	ABUW_2004	NZ_CP008706.1	2000551	2000935	-	WP_000505492.1	DUF2523 domain-containing protein	18.51643624	1464199222	0.506520407	2.789228074	0.00382458	0.006210864	2.20684794
ABUW_RS9505	ABUW_1261	NZ_CP008706.1	059506	126121	+	WP_000560785.1	hypothetical protein	904.379185	1469636195	0.183779797	8.924566037	4.47E-19	2.58E-18	17.58838029
ABUW_RS1970	ABUW_4029	NZ_CP008707.1	17262	18542	+	WP_001933570.1	hypothetical protein	285.0588409	1460030779	0.202799195	5.55562904	2.77E-08	7.75E-08	11.97758234
ABUW_RS1695	ABUW_2241	NZ_CP008706.1	2230380	2230882	-	WP_000259997.1	integration host factor subunit beta	8662.41894	1453139303	0.00579654	11.0817611	0.09E-29	9.47E-28	27.02365002
ABUW_RS9200	ABUW_1884	NZ_CP008706.1	9179580	9180237	-	WP_000101759.1	iron-containing alcohol dehydrogenase	445.2221918	1451010641	0.107869679	9.191053377	3.88E-20	2.38E-19	18.82342304
ABUW_RS9810	ABUW_1677	NZ_CP008706.1	970232	971491	+	WP_000568879.1	serine hydrolase	857.9573919	1449116957	0.166819176	8.68675892	3.73E-18	2.03E-17	6.69210593
ABUW_RS1880	ABUW_2401	NZ_CP008706.1	237465	2388349	-	WP_000968303.1	biphosphoribosyl-dephospho-CoA synthase	107.7270866	1445192634	0.379746943	3.805505005	0.000141515	0.000271006	3.566220505
ABUW_RS1044	ABUW_2769	NZ_CP008706.1	2790961	2796966	+	WP_000811687.1	alpha/beta hydrolase	45.71772442	1443205793	0.30010462	4.807783991	1.535E-06	3.59E-06	5.444905551
ABUW_RS1475	ABUW_3390	NZ_CP008706.1	341304	343272	-	WP_001012702.1	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	7930.830663	1443008869	0.157887646	8.205015606	2.33E-16	1.18E-15	14.95407792
ABUW_RS9040	ABUW_1982	NZ_CP008706.1	986765	988934	+	WP_001013990.1	outer membrane protein transport protein	832.0989181	1442838894	0.213701052	6.75166832	1.46E-11	5.10E-11	10.29246262
ABUW_RS93016	ABUW_0733	NZ_CP008706.1	739688	739888	-	WP_001012025.1	AlpA family phage regulatory protein	914.8824111	1442603988	0.277402137	5.200406092	1.99E-07	5.08E-07	6.29416288
ABUW_RS1750	ABUW_2829	NZ_CP008706.1	283528	2836242	-	WP_000892316.1	hypothetical protein	467.594308	1439059401	0.300745202	2.78978752	1.78E-06	4.01E-06	5.968565627
sRNA5								no						
ABUW_RS1935	ABUW_3253	NZ_CP008706.1	3282473	3283921	-	WP_000778208.1	RNA polymerase factor sigma-54	103.6197108	1434734477	0.347319188	4.10818691	3.61E-05	7.33E-05	4.148860025
ABUW_RS1670	ABUW_4118	NZ_CP008707.1	73719	81011	+	WP_000162932.1	Y-family DNA polymerase	355.4776889	1430491432	0.214193376	6.16214751	1.01E-09	3.07E-09	8.59E16.925
ABUW_RS9840	ABUW_0946	NZ_CP008706.1	954063	954455	+	WP_000191986.1	DUF1232 domain-containing protein	11310742614	1425933568	0.350331973	4.070242285	4.70E-05	9.44E-05	4.625028006
ABUW_RS98825	ABUW_1814	NZ_CP008706.1	980588	918682	+	WP_000592702.1	ATP-dependent GTP protease ATP-binding subunit CtpA	1914.19663	1425393161	0.176200576	8.089052339	5.99E-16	2.79E-15	14.3543958
ABUW_RS9275	no	NZ_CP008706.1	287923	2873003	-		outer membrane assembly protein BarE	118143105	14228776717	0.335329313	4.027465746	5.64E-05	0.000104	3.049923869
ABUW_RS90145	ABUW_0257	NZ_CP008706.1	0203889	0294740	-	WP_000993522.1	PD-(D)EXK nuclease-like domain-containing protein	49.3803484	1421915647	0.304257482	4.733389255	2.96E-06	6.78E-06	5.98770306
ABUW_RS97415	ABUW_1519	NZ_CP008706.1	1504540	1505268	-	WP_000848611.1	aspartate/glutamate racemase family protein	922.6529467	1421395445	0.244210479	5.820322749	5.87E-09	1.70E-08	7.769551079
ABUW_RS19350	ABUW_4070	NZ_CP008707.1	415653	416417	+	WP_000270931.1	hypothetical protein	980.6468126	1418633325	0.313274101	4.510450194	6.44E-06	1.44E-05	4.850770887
ABUW_RS90705	ABUW_1438	NZ_CP008706.1	14130917	14130917	-	WP_000539192.1	acylferrase	49.82046937	1415488085	0.473255675	2.89732458	0.002819764	0.004659897	2.31923663
ABUW_RS90620	ABUW_0270	NZ_CP008706.1	0291859	0295912	+	WP_000203004.1	replication protein	49.9192187	1410851623	0.335681036	4.91714545	2.77E-05	5.68E-05	4.245651634
ABUW_RS98920	ABUW_1833	NZ_CP008706.1	1832863	1832863	+	WP_000172919.1	3-oxoacyl-CoA thiolase	94.450037377	140814375	0.344706632	4.08949775	4.41E-05	8.88E-05	6.051687034
ABUW_RS94825	ABUW_0984	NZ_CP008706.1	996126	997979	-	WP_000920020.1	rRNA	9500.691863	1407732437	0.197782831	7.171566423	1.10E-12	4.20E-12	11.37675071
ABUW_RS901765	ABUW_1590	NZ_CP008706.1	1590470	1593190	+	WP_001103432.1	outer membrane protein assembly factor	3874.655882	1407103343	0.14516582	8.937196822	3.22E-22	2.31E-21	20.05560773
ABUW_RS94195	ABUW_0710	NZ_CP008706.1	716525	717043	+	WP_000806443.1	hypothetical protein	621.0568335	1406025723	0.140555334	7.226716578	4.79E-11	1.04E-12	11.7019827
ABUW_RS10225	ABUW_2725	NZ_CP008706.1	271996	271977	-	WP_000178142.1	glutathione S-transferase N-terminal domain-containing protein	2101.894348	140472622	0.286604577	6.470189325	9.95E-11	3.23E-10	9.490791478
ABUW_RS16290	ABUW_3757	NZ_CP008706.1	3813340	3813777	-	WP_000483007.1	Dox1 family protein	80.8206783	1400966758	0.208819176	6.709123267	1.96E-11	6.78E-11	9.1677331
ABUW_RS905105	ABUW_1540	NZ_CP008706.1	0419006	0419434	+	WP_000851971.1	hypothetical protein	774.3826227	1400103933	0.251891009	4.957140713	6.31E-08	1.68E-07	6.774909718
ABUW_RS10580	ABUW_2177	NZ_CP008706.1	217690	2195937	-	WP_000158784.1	HAD family hydrolase	117126091	1396284664	0.149418475	3.54023431	9.16E-21	5.82E-20	19.23507702
ABUW_RS19355	ABUW_3366	NZ_CP008706.1	347042	3470773	-	WP_001019561.1	Bax inhibitor-1/VcrA family protein	10642.48459	1395621010	0.179561634	7.772378882	7.70E-15	3.35E-14	13.47495519
ABUW_RS92035	no	NZ_CP008706.1	281299	281848	-		hypothetical protein	324.7326784	1394862202	0.36144236	3.859155309	0.00010378	0.000220293	3.568602203
ABUW_RS16100	ABUW_0325	NZ_CP008706.1	347427	148458	-	WP_001184591.1	lipase secretion chaperone	175.0243159	1392381935	0.291762128	4.831198902	2.82E-06	6.48E-06	5.18424994
ABUW_RS98625	ABUW_1695	NZ_CP008706.1	1695429	1695412	+	WP_001238662.1	hypothetical protein	824.0595781	139217406	0.19643696	7.12310199	1.05E-12	4.03E-12	11.98491495
ABUW_RS19130	ABUW_3573	NZ_CP008706.1	3632075	3633247	+	WP_000212712.1	fadA	5429.800059	1391945397	0.257599141	5.04533275	6.53E-08	1.73E-07	6.76538897
ABUW_RS19186	ABUW_4019	NZ_CP008706.1	9682	9918	+	WP_001057663.1	hypothetical protein	776.2242829	1389317741	0.217539161	6.386776085	1.69E-10	5.48E-10	9.26194942
ABUW_RS90670	ABUW_0347	NZ_CP008706.1	0359651	060530	+	WP_000175593.1	PhoF family phenazine biosynthesis protein	434.2580702	1388504591	0.238347578	5.825545198	5.95E-09	1.65E-08	7.782519056
ABUW_RS16220	ABUW_4039	NZ_CP008707.1	23306	23662	+	WP_000701385.1	hypothetical protein	497.882776	1387011634	0.250763381	5.530716901	3.16E-08	8.72E-08	7.059433515
ABUW_RS16495	ABUW_2160	NZ_CP008706.1	2140911	2143017	+	WP_000734919.1	pilin	319.0895855	138690921	0.179933039	7.071919549	1.28E-14	5.64E-14	13.2639736
ABUW_RS930175	ABUW_0545	NZ_CP008706.1	651078	6511631	+	WP_000457783.1	glutathione anion transporter	92.151607	1384610077	0.333931932	4.15059685	3.36E-06	6.73E-06	9.147164936
ABUW_RS10840	ABUW_2230	NZ_CP008706.1	2219664	2220545	+	WP_002018281.1	MotA/MotB/FlaB protein channel family protein	85.5740238	1382510902	0.202450764	6.828889534	8.56E-12	3.03E-11	10.91855737
ABUW_RS10680	ABUW_2816	NZ_CP008706.1	2814965	2819737	-	WP_001040886.1	RH6 repeat protein	7419.751947	1381928428	0.196607125	7.028882756	2.08E-12	7.73E-12	11.1182051
ABUW_RS98885	ABUW_1828	NZ_CP008706.1	1824553	1825230	-	WP_000366082.1	DUF421 domain-containing protein	97.842121	1376503484	0.238427335	5.773261891	1.78E-09	2.22E-08	7.653647026
ABUW_RS90955	ABUW_1868	NZ_CP008706.1	1865485	1866702	+	WP_000820624.1	hypothetical protein	19.06203253	1376162342	0.150170423	2.74229543	0.000088895	0.009567924	2.01918283
sRNA15								no						
ABUW_RS10060	ABUW_2478	NZ_CP008706.1	2472											

ABUW_RS10500	ABUW_2780	NZ_CP008706.1	2774078	2775964	+	WP_170318969.1		AMP-binding protein	860.900914	1322083167	0.337667687	3.9533812	9.03E-05	0.0001076739	3.752667607
ABUW_RS1070	ABUW_2693	NZ_CP008706.1	2680667	2681656	-	WP_000427182.1		hypothetical protein	975.928066	132189373	0.28806739	4.588835032	4.46E-06	9.95E-06	4.002107691
ABUW_RS10290	ABUW_1908	NZ_CP008706.1	1903839	1910207	+	WP_000093480.1		cation-potential antiporter	9244.797181	1319024391	0.19504424	6.732856057	1.66E-11	5.79E-11	0.23273184
ABUW_RS1015	ABUW_1255	NZ_CP008706.1	1252728	1252985	-	WP_001000839.1		hypothetical protein	4119710716	1319148105	0.374877757	3.479731625	0.000501917	0.000900683	3.54109921
ABUW_RS10940	ABUW_1037	NZ_CP008706.1	1038194	1039570	+	WP_000842416.1		Do family serine endopeptidase	6454.739462	1318619336	0.232208337	5.66991864	1.43E-08	4.00E-08	7.39794009
ABUW_RS10790	ABUW_2219	NZ_CP008706.1	2224812	2254980	+	WP_000979740.1		hypothetical protein	87.84746433	1310301914	0.316007579	4.16193194	3.16E-05	6.46E-05	4.189787482
ABUW_RS103890	ABUW_1793	NZ_CP008706.1	1773502	1773801	+	WP_000336868.1		DUF4258 domain-containing protein	2287.631094	1310237283	0.188028701	6.968283434	3.21E-12	1.18E-11	0.9281079
ABUW_RS103630	ABUW_1737	NZ_CP008706.1	1740524	1741052	-	WP_000150705.1		hypothetical protein	75.3434767	1309923421	0.20108508	6.51051662	7.34E-11	2.44E-10	0.61051074
sRNA10	no	no	no	no	no	no	no	no	23.91516784	1306566479	0.54110041	2.414681075	0.0175337	0.023326024	1.632169282
ABUW_RS105595	ABUW_1143	NZ_CP008706.1	1168985	1169290	+	WP_000808069.1		YbdD/Yjk family protein	919.5373678	1305607077	0.308483676	4.232371649	2.31E-05	4.82E-05	4.139529692
ABUW_RS10160	ABUW_14025	NZ_CP008707.1	14320	16549	+	WP_001024502.1		hypothetical protein	648.6433325	1305357289	0.222800807	5.8588535	4.66E-09	1.36E-08	7.866491692
ABUW_RS1020	ABUW_2470	NZ_CP008706.1	2464283	2464006	+	WP_000220905.1		3-hydroxyacyl-CoA dehydrogenase	87.5478312	1304943605	0.270289402	4.827949574	1.38E-06	3.26E-06	5.4887824
ABUW_RS10430	ABUW_2559	NZ_CP008706.1	2548324	2549481	-	WP_000204305.1		winged helix-turn-helix domain-containing protein	697.848815	1303881102	0.150917361	6.830702523	5.64E-18	3.05E-17	6.5170016
ABUW_RS10210	ABUW_1440	NZ_CP008706.1	1452140	1454335	+	WP_001158905.1		TRAP transporter large permease subunit	1082.852946	1301830764	0.19937323	5.918231284	3.25E-09	9.57E-09	8.018908602
ABUW_RS141010	ABUW_2190	NZ_CP008706.1	2192793	2192752	+	WP_001045107.1		FlaX-like permease family protein	6355.184024	1300979223	0.1256635	9.815796825	9.82E-23	7.10E-22	2.114874165
ABUW_RS10440	ABUW_2602	NZ_CP008706.1	2594297	2595507	-	WP_000698630.1		chloride channel protein	359.4208533	1300299953	0.265707054	4.893584631	9.90E-07	2.38E-06	5.623423043
ABUW_RS10660	ABUW_1196	NZ_CP008706.1	117985	118528	+	WP_017708516.1		transglycosylase SLT domain-containing protein	232.098969	1298576819	0.219168512	6.192727273	9.00E-10	2.76E-09	6.55909091
ABUW_RS10690	ABUW_2818	NZ_CP008706.1	2823200	2823284	-	WP_002204621.1		TeR/AcrI family transcriptional regulator	61.1051607	1297516411	0.3189196	4.068705810	4.73E-05	9.50E-05	4.022216705
ABUW_RS105085	ABUW_1866	NZ_CP008706.1	1861803	1862817	+	WP_001077389.1	feaR	transcriptional regulator FeaR	98.07908245	1293542531	0.306232339	4.224053188	2.40E-05	4.98E-05	4.037200757
ABUW_RS10635	ABUW_2601	NZ_CP008706.1	2593279	2594187	-	WP_000465123.1		self repeat family protein	252.16368	1293335935	0.278988141	6.207173747	3.82E-06	8.62E-06	5.064402734
ABUW_RS102790	ABUW_1068	NZ_CP008706.1	106943	106885	-	WP_000729641.1		phage tail protein	104.0273842	1291083881	0.249704348	5.16920086	2.35E-07	5.98E-07	6.222288816
ABUW_RS1055	ABUW_2396	NZ_CP008706.1	2383951	2384883	-	WP_000146930.1	mdcH	malonate decarboxylase subunit epsilon	255.9385441	1287145064	0.255721654	5.035731224	4.76E-07	1.18E-06	5.928191903
ABUW_RS104045	ABUW_1082	NZ_CP008706.1	109373	91199	+	WP_000797007.1		DUF885 domain-containing protein	346.6061914	1286367283	0.250431228	5.150608937	2.80E-07	7.08E-07	6.146996217
ABUW_RS10760	ABUW_2215	NZ_CP008706.1	2220106	2220098	+	WP_085020889.1		glutathione S-transferase N-terminal domain-containing protein	366.1284102	128561610	0.168604256	8.98860127	2.43E-16	1.16E-15	6.93554201
ABUW_RS1010	ABUW_1054	NZ_CP008706.1	102448	102731	-	WP_000717852.1		hypothetical protein	23.4460944	128347012	0.433615416	2.196127103	0.003066149	0.000540371	2.297200824
ABUW_RS107380	no	NZ_CP008706.1	1988801	1989580	+	WP_000408738.1		DUF1025 domain-containing protein	97.1000487	1281062443	0.19773045	4.03361642	5.49E-05	0.00090714	3.959737051
ABUW_RS10995	ABUW_2676	NZ_CP008706.1	2686557	2686448	-	WP_001045792.1		hypothetical protein	87.8895879	1281177033	0.291933962	3.388585097	1.14E-05	2.45E-05	4.61808336
ABUW_RS10635	ABUW_2188	NZ_CP008706.1	2172192	2173615	-	WP_000883769.1		SlxR/AcrDPA family monooxygenase	1074.167092	1278516246	0.544716482	2.346882038	0.01932263	0.0270972	1557564103
ABUW_RS10930	ABUW_1055	NZ_CP008706.1	1051667	1052918	+	WP_001071622.1		MFS transporter	75.53041872	1276014464	0.50059626	3.450197101	0.000482684	0.00087156	3.0569232
ABUW_RS10250	ABUW_1349	NZ_CP008706.1	1305847	1306515	-	WP_000624451.1		glutathione S-transferase	929.0193193	1275294714	0.1610658	7.918740689	2.38E-15	1.07E-14	0.1701612
ABUW_RS108165	ABUW_1876	NZ_CP008706.1	1869306	1870160	+	WP_001097352.1		hypothetical protein	503.744639	1275807436	0.16561647	7.703474465	1.32E-14	5.65E-14	0.24795165
ABUW_RS108785	ABUW_1911	NZ_CP008706.1	1919322	1919930	-	WP_001023979.1		YjaJ/wal-mec operonase family protein	79.95090587	1274653338	0.289328134	4.405603114	1.06E-05	2.27E-05	4.64307413
ABUW_RS108925	ABUW_1834	NZ_CP008706.1	1821286	1831181	+	WP_000080893.1		3-carboxy-cis,cis-muconate cycloisomerase	87.40557731	1273307525	0.263549543	4.83178225	1.36E-06	3.21E-06	5.493404968
ABUW_RS10250	ABUW_2520	NZ_CP008706.1	2509867	2510469	-	WP_001133261.1		TeR/AcrI family transcriptional regulator	67.85542083	127184525	0.276071905	4.606176054	4.10E-08	9.22E-06	5.035269079
ABUW_RS103630	ABUW_1296	NZ_CP008706.1	1146234	1146434	+	WP_000034363.1		hypothetical protein	65.42528158	1271502147	0.416886915	4.618866915	3.95E-06	8.89E-06	5.051098239
ABUW_RS145470	ABUW_1031	NZ_CP008706.1	103388	938816	-	WP_000077687.1		SgcE/EcAc family oxidoreductase	109.0990779	1270955404	0.218081922	5.827876026	5.61E-09	1.62E-08	7.790448831
ABUW_RS10485	ABUW_2777	NZ_CP008706.1	2777149	2777149	+	WP_000411761.1	mhpT	3-(3-hydroxy-phenyl)serinate transporter MhpT	67.1681282	1267357185	0.30089448	4.21966549	2.53E-05	5.23E-05	6.48849811
ABUW_RS10800	ABUW_1381	NZ_CP008706.1	1394660	1395055	+	WP_001241011.1		metalloprotein metalloprotease	267.4629918	1267176372	0.288005103	4.399194441	1.09E-05	2.33E-05	4.632246407
ABUW_RS10945	ABUW_10274	NZ_CP008706.1	1028294	1029291	-	WP_001086587.1		hypothetical protein	167.1762873	1264790784	0.258589603	4.81102289	1.00E-06	2.41E-06	6.517826257
ABUW_RS10245	ABUW_1054	NZ_CP008706.1	106914	1067345	+	WP_000469967.1		GMAT family acyltransferase	123.5616885	1257223439	0.271405265	4.63418549	3.58E-06	8.10E-06	5.01914681
ABUW_RS10770	ABUW_2833	NZ_CP008706.1	2842993	2842993	-	WP_000285936.1		hypothetical protein	838.7995448	1255882149	0.235323969	5.33682205	9.46E-08	2.48E-07	6.05054839
ABUW_RS103635	ABUW_1708	NZ_CP008706.1	1707738	1707738	+	WP_000968542.1		molybdopterin-dependent oxidoreductase	442.918105	1252936190	0.20098154	6.234054933	4.54E-10	1.42E-09	8.84771855
ABUW_RS10250	ABUW_1341	NZ_CP008706.1	13187036	13188395	-	WP_001048745.1		hypothetical protein	621.666093	1252709244	0.169434399	7.857201771	3.93E-15	1.74E-14	0.173540575
ABUW_RS108930	ABUW_1835	NZ_CP008706.1	1831078	1831663	+	WP_000814773.1	pcd	3-oxoalipate enol-lactonase	96.910447	1252296639	0.29784274	4.304556537	2.62E-05	5.59E-05	4.268410235
ABUW_RS10495	ABUW_2779	NZ_CP008706.1	2772944	2773995	+	WP_001161903.1		aldehyde dehydrogenase	2293.35107	1247519369	0.280424754	4.44887777	8.64E-06	1.87E-05	4.72810933
sRNA90	no	no	no	no	no	no	no	no	8442.530602	1246366193	0.25310873	4.923659095	8.49E-07	2.06E-06	5.08122178
ABUW_RS1015	ABUW_14021	NZ_CP008707.1	14056	11165	+	WP_001097227.1		hypothetical protein	138.9124817	1245346586	0.388716775	3.377580086	0.000731458	0.001297686	2.886830181
ABUW_RS10610	ABUW_1052	NZ_CP008706.1	1051099	1052118	-	WP_000028947.1		hypothetical protein	512.7523056	1241166657	0.266217107	4.662234786	3.13E-06	7.13E-06	5.1469147
ABUW_RS108875	ABUW_1410	NZ_CP008706.1	1408389	1408769	+	WP_000810197.1		type II toxin-antitoxin system RelE/PaeI family toxin	6100.432159	1231030963	0.30170648	4.082153365	4.46E-05	8.98E-05	4.04672633
ABUW_RS101985	ABUW_1404	NZ_CP008706.1	1413180	1413180	+	WP_000332933.1		type II glutamine amidotransferase	60.617466	1238565425	0.259391405	4.77489001	1.80E-06	4.20E-06	5.37575071
ABUW_RS103650	ABUW_1741	NZ_CP008706.1	1742953	1743345	+	WP_001056658.1		hypothetical protein	63.8781693	1238056491	0.31849011	3.87510198	0.00010658	0.000207046	3.68939315
ABUW_RS103270	ABUW_1064	NZ_CP008706.1	1070429	1071633	-	WP_000734697.1		self repeat family protein	431.955547	1236024544	0.161059584	7.631685092	2.32E-14	9.78E-14	0.1006616
ABUW_RS10890	ABUW_1206	NZ_CP008706.1	1244971	1245512	-	WP_000872827.1		peptide MFS transporter	691.1449105	1234406682	0.228918458	5.39231874	6.96E-08	1.84E-07	7.15316277
ABUW_RS1010	ABUW_1469	NZ_CP008706.1	1466000	1462421	+	WP_000101937.1		SDR family oxidoreductase	31.71121622	1234254741	0.411896723	2.996510076	0.002730847	0.004522229	2.344647449
ABUW_RS10200	ABUW_14035	NZ_CP008707.1	140360	21194	+	WP_000780084.1		hypothetical protein	105.5361977	1234125808	0.299025726	4.146733992	3.71E-05	7.53E-05	4.123020504
ABUW_RS10385	ABUW_1491	NZ_CP008706.1	149668	150327	-	WP_000581089.1		hypothetical protein	594.2973548	1234057142	0.163386279	3.910843473	9.10E-05	0.000109315	3.714881022
ABUW_RS109165	no	NZ_CP008706.1	188217	1883471	+		abaQ	multidrug efflux MFS transporter AbaQ	30.58980082	1232568049	0.364077425	3.385455855	0.000710601	0.0012657	2.897169922
ABUW_RS10215	ABUW_14038	NZ_CP008706.1	140383	22895	-	WP_000102250.1		type II toxin-antitoxin system RelE/PaeI family toxin	6100.432159	1231030963	0.30170648	4.082153365	4.46E-05	8.98E-0	

ABLW_RS16875	ABLW_3269	NZ_CP008706.1	3289425	3301232	-	WP_000276867.1		DUF2339 domain-containing protein	2260.401498	1.171327783	0.139851034	8.3755388934	5.506E-17	2.77E-16	15.5572023
sRNA E4	no	no	no	no	no	no	no	no	427.5802554	1.93609195	0.398346227	9.936162237	0.003323005	0.005444222	2.264383378
ABLW_RS1919	ABLW_2660	NZ_CP008706.1	2655655	2656641	+	WP_01056512.1		right-handed parallel beta-helix repeat-containing protein	934.9875343	1.98842003	0.209942533	5.567347783	2.596E-08	7.12E-08	7.147520066
ABLW_RS20443	ABLW_5970	NZ_CP008706.1	591621	591877	+	WP_000691976.1			37.41935702	1.9782406	0.222274169	5.247347731	1.54E-07	3.97E-07	6.401094943
ABLW_RS20595	ABLW_5495	NZ_CP008706.1	541619	541852	+	WP_000437933.1		hypothetical protein	10.0233212	1.953585448	0.375048666	3.97326188	0.001888007	0.003190764	2.496105317
ABLW_RS2090	ABLW_2870	NZ_CP008706.1	266443	2664925	+	WP_00103266.1		DUF2280 domain-containing protein	53.0068924	1.93021652	0.403535041	2.882083425	0.003905051	0.006394846	2.84.98941
ABLW_RS18480	ABLW_3058	NZ_CP008706.1	3014083	3084958	-	WP_000992293.1		metal-dependent hydrolase	506.255932	1.92034638	0.261931701	4.448884816	8.63E-06	1.87E-05	4.728168393
ABLW_RS18280	ABLW_2842	NZ_CP008706.1	2636887	2641077	+	WP_000003555.1		HyD family type I secretion periplasmic adaptor subunit	292.1445758	1.91596261	0.174985519	6.637099278	3.20E-11	1.00E-10	9.962573502
ABLW_RS19540	ABLW_4102	NZ_CP008707.1	72279	73091	+	WP_001037429.1		conjugal transfer protein TraF	645.6728975	1.90884863	0.154090186	7.533801415	4.93E-14	2.04E-13	12.69036983
ABLW_RS10000	ABLW_2677	NZ_CP008706.1	2668857	2669212	+	WP_00100545.1		hypothetical protein	315.4473985	1.90639202	0.249644062	4.649176074	3.33E-06	7.58E-06	5.102330734
ABLW_RS18430	ABLW_0895	NZ_CP008706.1	8192682	893269	+	WP_00128280.1		hypothetical protein	161.91088	1.9009211	0.291830236	3.975229318	7.03E-05	0.000193275	3.856106833
ABLW_RS18030	ABLW_815	NZ_CP008706.1	810866	811028	+	WP_001986163.1		YnfA family protein	695.407039	1.90049564	0.220081653	5.270996233	1.36E-07	3.62E-07	6.453457337
ABLW_RS18585	ABLW_0728	NZ_CP008706.1	734397	735197	+	WP_000799186.1		PaaK family transcriptional regulator	81.0889952	1.959924863	0.256279208	4.526020162	6.01E-06	1.32E-05	4.879426089
ABLW_RS23265	ABLW_0481	NZ_CP008706.1	419278	4193941	+	WP_010176667.1		acyl-CoA dehydrogenase family protein	478.7224629	1.98226817	0.23762776	4.874121871	1.09E-06	2.62E-06	5.58898709
ABLW_RS1950	ABLW_2090	NZ_CP008706.1	2071977	2072720	+	WP_000848256.1		MFS transporter	76.28271016	1.956397865	0.277192892	4.192418536	3.01E-05	6.17E-05	4.209714836
ABLW_RS19175	ABLW_4030	NZ_CP008707.1	9647	98904	+	WP_000834290.1		hypothetical protein	22.29851608	1.95896467	0.597883742	1.933310095	0.05319764	0.073076471	1.06222434
ABLW_RS19210	ABLW_1922	NZ_CP008706.1	216619	2167774	+	WP_000421172.1		TGR18/14 family phosphatase	345.716745	1.95417378	0.339719665	3.397404084	0.00680194	0.001919838	2.91512487
ABLW_RS1940	ABLW_4037	NZ_CP008707.1	22237	22536	+	WP_001089429.1		helic-tum-helic transcriptional regulator	498.8094305	1.91862618	0.338956223	3.401274034	0.000570726	0.001201558	2.592047309
ABLW_RS19680	ABLW_590	NZ_CP008706.1	595244	593749	+	WP_045887726.1		hypothetical protein	985.4247155	1.910273738	0.252183344	4.585067896	4.59E-06	1.1E-05	4.954077021
ABLW_RS21485	ABLW_1663	NZ_CP008706.1	605820	605593	+	WP_010193932.1		hypothetical protein	37.20554944	1.94787371	0.463435634	2.477123554	0.010244601	0.01866901	1.707686872
ABLW_RS19900	no	NZ_CP008706.1	284329	2844051	+			glutathione S-transferase	11.3323059	1.91734245	0.240210709	4.776272827	1.79E-05	4.4E-06	5.37882371
ABLW_RS19335	ABLW_816	NZ_CP008706.1	81655	812710	+	WP_000993005.1		3-deoxy-7-phosphoglutamate synthase	990.652454	1.946577822	0.170273753	6.733732031	1.65E-11	5.76E-11	10.23907752
ABLW_RS180480	ABLW_817	NZ_CP008706.1	812757	813674	+	WP_01014721.1		alpha/beta hydrolase	273.2753721	1.946287965	0.198574889	5.172572623	7.81E-09	2.23E-08	6.751905107
ABLW_RS17405	ABLW_817	NZ_CP008706.1	813507	803739	+	WP_000692365.1		nuclear transcription factor 2 family protein	82.9493349	1.94362403	0.365730481	3.92718982	0.001078721	0.002999282	2.522619699
ABLW_RS15235	ABLW_2578	NZ_CP008706.1	257422	257199	+	WP_000653195.1		type V secretion system lumen protein Hcp	7035.970453	1.99982503	0.24354105	4.68062237	2.86E-06	6.55E-06	5.9377587
ABLW_RS18785	ABLW_894	NZ_CP008706.1	894155	897825	+	WP_000920881.1		hypothetical protein	387.581961	1.98969194	0.250278012	4.550815894	3.34E-06	1.18E-05	4.928117993
ABLW_RS1840	ABLW_3809	NZ_CP008706.1	387043	387053	+	WP_010163625.1		GmR family transcriptional regulator	430.4632464	1.98499372	0.242264199	4.699412359	2.81E-06	6.02E-06	5.220423509
ABLW_RS19360	ABLW_2543	NZ_CP008706.1	2535194	2536443	+	WP_000214021.1	abaf	isofomc in efflux MFS transporter AbaF	93.0008989	1.93522764	0.235273572	4.825431111	1.40E-06	3.30E-06	5.48148606
ABLW_RS184725	ABLW_0963	NZ_CP008706.1	973225	974205	+	WP_001022403.1		glycoyltransferase family 2 protein	90.8649627	1.93510189	0.26295661	4.3672049	1.89E-05	3.39E-05	4.47360723
ABLW_RS1845	ABLW_818	NZ_CP008706.1	818677	819427	+	WP_000005211.1		PsdR family transcriptional regulator	486.496771	1.91050188	0.206533402	5.495722118	3.95E-08	1.05E-07	6.97819701
ABLW_RS19190	ABLW_086	NZ_CP008706.1	109710	109910	+	WP_00512310.1		hypothetical protein	91.49219991	1.94941737	0.282248968	4.02166627	5.79E-05	0.00011627	3.382367307
ABLW_RS18480	ABLW_2900	NZ_CP008706.1	290893	2909381	+	WP_000691703.1		esterase	439.2773282	1.92963871	0.27167887	4.1794927	2.92E-05	5.98E-05	4.223288816
ABLW_RS19235	ABLW_3279	NZ_CP008706.1	331059	331055	+	WP_001016106.1		integration host factor subunit alpha	6958.754437	1.931415082	0.21961179	5.992361623	2.00E-07	5.1E-07	6.2919791
ABLW_RS10050	ABLW_2689	NZ_CP008706.1	267829	267843	+	WP_000350300.1		hypothetical protein	228.7599471	1.91329444	0.427332625	2.64721193	0.00815865	0.01051961	1.9024418
ABLW_RS17440	ABLW_3623	NZ_CP008706.1	361856	362135	+	WP_000722831.1		hypothetical protein	312.1956884	1.929937034	0.174284768	6.483280463	8.97E-11	2.97E-10	9.52724351
ABLW_RS19130	ABLW_1663	NZ_CP008706.1	1651074	1652207	+	WP_000783724.1		hypothetical protein	307.0754027	1.9257451	0.3245490578	3.458619425	0.000542969	0.00098437	3.008175739
ABLW_RS160550	ABLW_043	NZ_CP008706.1	1035706	1036035	+	WP_001012111.1	abeS	multidrug efflux MDR transporter AbeS	97.7116051	1.915554709	0.247426553	4.549045755	3.39E-06	1.18E-05	4.94013073
ABLW_RS191315	ABLW_819	NZ_CP008706.1	819449	819464	+	WP_010176604.1		hypothetical protein	97.8568493	1.94254827	0.374351751	3.003733431	0.002668889	0.004429058	2.335886362
ABLW_RS18295	ABLW_2226	NZ_CP008706.1	221918	221938	+	WP_001993958.1		ABC transporter substrate-binding protein	658.0852824	1.92211011	0.189774892	10.22165	1.98E-24	1.25E-23	22.90308999
ABLW_RS19220	ABLW_2511	NZ_CP008706.1	2505791	2506261	+	WP_000008105.1		hypothetical protein	432.7391408	1.92106502	0.844429047	1.327702578	0.84276382	0.228657081	0.64018453
ABLW_RS17450	ABLW_3243	NZ_CP008706.1	3272192	3273307	+	WP_000730427.1		hypothetical protein	503.004285	1.92668989	0.89079231	6.630435883	3.35E-11	1.5E-10	9.949321637
ABLW_RS19050	ABLW_1962	NZ_CP008706.1	217766	21819	+	WP_000090861.1		DUF1030 domain-containing protein	93.28269192	1.920474093	0.263119053	4.257556321	2.07E-05	4.33E-05	4.363512104
ABLW_RS19995	ABLW_3899	NZ_CP008706.1	3969637	3969536	+	WP_000109211.1		DnaC family protein	7716.966579	1.91829601	0.163395047	2.790230896	3.10E-13	1.24E-12	1.900657831
ABLW_RS11140	ABLW_2290	NZ_CP008706.1	2278041	2278271	+	WP_000101879.1		hypothetical protein	896.4927119	1.918251642	0.2306968	4.46057325	8.91E-06	1.77E-05	4.732026734
ABLW_RS191810	ABLW_5008	NZ_CP008706.1	501476	50189	+	WP_000592953.1	znuD2	TorB-dependent receptor ZnuD2	10663.74017	1.917759503	0.18944601	6.616286652	3.68E-11	1.24E-10	9.90857831
ABLW_RS11665	ABLW_2398	NZ_CP008706.1	238495	238632	+	WP_01017588.1	mdcE	biofilm-independent maltate deacetylase subunit gamma	319.6520009	1.917732392	0.275757089	4.05332416	5.05E-05	0.00010166	3.994946521
ABLW_RS190100	ABLW_869	NZ_CP008706.1	868737	8688224	+	WP_000005610.1		NAD-dependent phenylacetate/ethylpyruvate dehydrogenase	803.6095839	1.915724793	0.2198819	5.918044053	2.37E-07	6.01E-07	6.22105528
ABLW_RS10590	ABLW_5001	NZ_CP008706.1	1	951	+	WP_010100343.1	repM	replication initiation protein RepM	2709.803281	1.91050149	0.231318385	4.820454663	1.43E-06	3.38E-06	4.5718333
ABLW_RS19245	ABLW_2939	NZ_CP008706.1	295289	295417	+	WP_000371878.1		MFS transporter	282.8430433	1.912424014	0.251973434	4.423624385	9.71E-06	2.09E-05	4.67895374
ABLW_RS19390	ABLW_2656	NZ_CP008706.1	2652871	2653461	+	WP_000587964.1		hypothetical protein	752.3189605	1.92208856	0.260102085	4.276094251	1.90E-05	4.01E-05	4.396855627
sRNA	no	no	no	no	no	no	no	no	2022.389003	1.910893575	0.360202666	3.077892821	0.002004699	0.003502607	2.456601859
ABLW_RS19660	ABLW_886	NZ_CP008706.1	890238	891886	+	WP_038405894.1		replication initiation factor domain-containing protein	454.6604761	1.944489045	0.282640722	9.90774916	9.32E-05	0.000182028	3.73981801
ABLW_RS19440	ABLW_2561	NZ_CP008706.1	2551793	2551795	+	WP_000646734.1		nucleoside deaminase	525.7430051	1.918642071	0.281218847	3.91741087	8.95E-05	0.000175311	3.76810083
ABLW_RS19290	ABLW_899	NZ_CP008706.1	899600	900469	+	WP_000992595.1		metal-dependent hydrolase	925.1462623	1.909780121	0.264209829	8.62523388	3.16E-05	6.44E-05	4.9114193
ABLW_RS190235	ABLW_854	NZ_CP008706.1	850594	851950	+	WP_000421436.1		Cpr family outer membrane porin	88.16095702	1.909371709	0.317248383	3.46501911	0.000530194	0.000989775	3.918233309
ABLW_RS19680	ABLW_069	NZ_CP008706.1	684959	685919	+	WP_000902236.1		MBL-like metallo- hydrolase	409.3807034	1.90919131	0.162003192	7.224401446	5.03E-13	1.87E-12	1.70585337
ABLW_RS19630	ABLW_878	NZ_CP008706.1	882596	884128	+	WP_001087729.1		NAD(P)H-dependent oxidoreductase	524.2164710	1.909603372	0.188309707	5.820378237	5.87E-09	1.70E-08	7.769551679
ABLW_RS190500	ABLW_1663	NZ_CP008706.1	1654666	1655984	+	WP_000677758.1		Toll family protein	44.6186663	1.910415646	0.321253062	3.40590231	0.000619458	0.00189272	2.927225535
ABLW_RS18285	ABLW_0794	NZ_CP008706.1	771830	774268	+	WP_000274931.1		helic-tum-helic domain-containing protein	2209.489695	1.90399196	0.206218681				

ABUW_RS04665	ABUW_0951	NZ_CP008706.1	959594	961000	+	WP_000707105.1		amino acid permease	5173.800112	1.0314612	0.173228815	5.954328087	2.61E-09	7.75E-09	8.10E88297
ABUW_RS08860	ABUW_9521	NZ_CP008706.1	916919	917635	+	WP_00026302.1		SGNHGSDH lyase family protein	295.18901	1.030035815	0.165079465	6.236636271	4.39E-10	1.38E-09	8.86020914
ABUW_RS09510	ABUW_9555	NZ_CP008706.1	957263	958234	+	WP_012300601.1		acid phosphatase	57.64016102	1.02996612	0.289819609	3.553819614	0.00037968	0.000687669	3.66226093
sRNA26	no	no	no	no	no	no	no	no	2339.639348	1.029882959	0.316502415	3.253949766	0.00193124	0.001977362	2.703913816
ABUW_RS10615	ABUW_2184	NZ_CP008706.1	2186186	2186936	-	WP_001027746.1		(2Fe-2S)-binding protein	243.5196986	1.028424666	0.240650486	4.273520009	1.92E-05	4.06E-05	4.319473966
ABUW_RS16630	ABUW_3867	NZ_CP008706.1	3934716	3934630	-		inf	5S ribosomal rRNA	16003.2434	1.028372447	0.424646427	2.42174587	0.015447478	0.022923716	1.639719561
ABUW_RS09380	ABUW_1926	NZ_CP008706.1	1924491	1925834	+	WP_000053789.1		MFS transporter	132.9871524	1.027206753	0.284401452	3.61819646	0.000304056	0.000564085	3.248655449
ABUW_RS13915	ABUW_2863	NZ_CP008706.1	2872227	2872811	+	WP_001004367.1		5-formyltetrahydrofolate cyclo-ligase	250.3738432	1.02719474	0.242839763	4.229700525	2.34E-05	4.88E-05	4.31363731
ABUW_RS16500	ABUW_4104	NZ_CP008707.1	63525	64189	+	WP_000823102.1	taaV	type IV conjugative transfer system lipoprotein TaaV	245.69337	1.026290048	0.19140666	5.369291987	7.90E-08	2.09E-07	6.67985314
ABUW_RS03615	ABUW_0734	NZ_CP008706.1	739888	740112	-	WP_001288394.1		hypothetical protein	129.5891745	1.024692094	0.216529938	4.689023862	2.75E-06	6.31E-06	5.199970641
ABUW_RS05310	ABUW_1062	NZ_CP008706.1	1095526	1098288	+	WP_000480866.1		insulinase family protein	8493.173493	1.024333693	0.16607771	6.148174749	7.84E-10	2.42E-09	8.618164634
ABUW_RS02955	ABUW_0601	NZ_CP008706.1	600379	601842	+	WP_001218074.1		phospholipase D family protein	1406.252186	1.023084854	0.226027991	4.526363523	6.00E-06	1.32E-05	4.879426069
ABUW_RS02515	ABUW_0512	NZ_CP008706.1	523616	523730	+		inf	5S ribosomal rRNA	17140.83805	1.021455359	0.420496385	2.429155615	0.015133618	0.022499389	1.647829276
ABUW_RS16060	ABUW_3711	NZ_CP008706.1	3768947	3769061	-		inf	5S ribosomal rRNA	15970.15484	1.020758077	0.426009654	2.396091421	0.016570957	0.024446864	1.611776843
ABUW_RS00095	ABUW_0019	NZ_CP008706.1	23453	23567	+		inf	5S ribosomal rRNA	1712.73312	1.020079526	0.42160776	2.41498931	0.015541906	0.023046868	1.637388086
ABUW_RS02825	ABUW_0575	NZ_CP008706.1	572430	573260	-	WP_000600982.1		DUF3380 domain-containing protein	100.43348	1.018624375	0.206651519	4.929188897	8.26E-07	2.00E-06	5.698970004
ABUW_RS18660	ABUW_2397	NZ_CP008706.1	2384896	2385504	-	WP_000245146.1		malonate decarboxylase holo-ACP synthase	177.8855566	1.017339866	0.289885391	3.509455453	0.000449025	0.000819349	3.086531072
ABUW_RS04620	ABUW_0942	NZ_CP008706.1	948551	949117	+	WP_000868729.1		TerR/AcrR family transcriptional regulator	167.9163537	1.016182955	0.206080511	4.930999776	8.18E-07	1.99E-06	5.70146924
ABUW_RS02350	ABUW_0478	NZ_CP008706.1	491384	491498	+		inf	5S ribosomal rRNA	17161.31524	1.015091048	0.420880329	2.41828201	0.016872759	0.023485621	1.629197952
ABUW_RS06670	ABUW_1367	NZ_CP008706.1	1382851	1383234	+	WP_000735997.1		hypothetical protein	656.8044979	1.014752504	0.19448926	5.21641776	1.87E-07	4.78E-07	6.320572103
ABUW_RS08725	ABUW_1792	NZ_CP008706.1	1786986	1787285	-	WP_085918945.1		cyl operon YbgE family protein	324.3220714	1.0142961	0.42163813	2.405605344	0.016145696	0.02387193	1.622112468
ABUW_RS08965	ABUW_1842	NZ_CP008706.1	1837597	1838916	+	WP_001134256.1		carbohydrate protein	249.4563322	1.01272586	0.16239801	5.263425467	1.41E-07	3.66E-07	6.346518915
ABUW_RS16800	ABUW_3254	NZ_CP008706.1	3284173	3284287	-		inf	5S ribosomal rRNA	15947.94678	1.011436206	0.428469521	2.360579122	0.018246268	0.026732672	1.57295763
ABUW_RS12420	ABUW_2557	NZ_CP008706.1	2546814	2547473	+	WP_001007559.1		epoxyoxygenase reductase QueH	2542.090483	1.0125441	0.19454535	3.165160748	0.001549973	0.002648363	2.077022488
ABUW_RS08850	ABUW_1819	NZ_CP008706.1	1814373	1816397	+	WP_000006188.1		NADPH-dependent 2,4-dienoyl-CoA reductase	731.8025046	1.009906452	0.318884368	3.160558148	0.001545199	0.002641327	2.578177829
ABUW_RS01015	ABUW_0205	NZ_CP008706.1	230706	231680	-	WP_000912176.1		LysR family transcriptional regulator	558.8023826	1.007628558	0.164433402	6.127862438	8.91E-10	2.73E-09	6.363837553
ABUW_RS20310	ABUW_3241	NZ_CP008706.1	3269064	3270431	+	WP_052692485.1	flE	putative pilus assembly protein FlE	638.8774502	1.007012299	0.138386557	2.726807206	3.42E-13	1.35E-12	1.869666261
ABUW_RS19155	ABUW_4026	NZ_CP008707.1	15564	15797	+	WP_000241707.1		hypothetical protein	123.8908658	1.006824973	0.317994288	3.16617135	0.001544588	0.002641327	2.578177829
ABUW_RS16740	ABUW_3278	NZ_CP008706.1	3270425	3272089	-	WP_003118481		outer membrane protein transport protein	1058.666229	1.006381594	0.119120415	8.448439269	2.95E-17	1.15E-16	15.82102363
ABUW_RS14460	ABUW_2948	NZ_CP008706.1	2995619	2996326	+	WP_001115353.1		DUF1275 domain-containing protein	47.50594831	1.005021709	0.333951222	3.009486546	0.002616897	0.003434969	2.361587785
ABUW_RS19145	ABUW_4024	NZ_CP008707.1	15282	15184	+	WP_000009660.1		ParB/RepB/SpoJ family partition protein	4128.770335	1.000485308	0.205877446	4.880887819	1.06E-06	2.53E-06	5.968879479
ABUW_RS04215	ABUW_0899	NZ_CP008706.1	839466	839999	+	WP_000626045.1		hypothetical protein	2200.79021	1.004123754	0.160625366	6.21339857	4.07E-10	1.28E-09	8.89279003
ABUW_RS16565	ABUW_4117	NZ_CP008707.1	78560	79552	-	WP_001132594.1		hypothetical protein	975.016785	1.00342316	0.214223615	4.683998816	2.81E-06	6.46E-06	5.169767482
ABUW_RS1665	ABUW_2184	NZ_CP008706.1	2179868	2181073	+	WP_001053251.1		acyl-CoA dehydrogenase family protein	377.0871456	1.000433385	0.155047549	6.452429521	1.10E-10	3.61E-10	4.944249278

Table S2. RNA-seq data: Absolute and relative expression (LEP/MEP > 2-fold down)

ABUW_RS16455	ABUW_3386	NZ_CP008706.1	3425871	3426890	+	WP_000578593.1	nagZ	beta-N-acetylhexosaminidase	1549.255862	-1.001561526	0.134977303	-7.420221821	1.17E-13	4.76E-13	12.32239305
ABUW_RS06510	ABUW_1334	NZ_CP008706.1	1345301	1346149	+	WP_000633128.1	adeH	multidrug efflux RND transporter outer membrane subunit AdeH	134.6861596	-1.002910962	0.214397006	-4.677821679	2.90E-06	6.84E-06	5.177831921
ABUW_RS04185	ABUW_0853	NZ_CP008706.1	833559	834932	+	WP_000305015.1	cobA	uracil phosphoribosyl transferase	1637.289101	-1.003999468	0.16191433	-6.197855339	5.72E-10	1.78E-09	8.749579998
ABUW_RS16300	ABUW_3355	NZ_CP008706.1	3392712	3393728	-	WP_001854431.1	ilvC	ketol-acid reductoisomerase	33596.40446	-1.004677057	0.1349432	-7.445183683	9.88E-14	3.97E-13	12.4020949
ABUW_RS20540	ABUW_3593	NZ_CP008706.1	3550865	3551245	+	WP_001008811.1		hypothetical protein	30.1554133	-1.006474245	0.465033648	-2.163404132	0.030441016	0.043307504	1.363436846
ABUW_RS01470	ABUW_0209	NZ_CP008706.1	322614	324035	+	WP_000840834.1		FAD-dependent oxidoreductase	3029.088102	-1.007301244	0.242593051	-4.152228286	3.29E-05	6.71E-05	4.17327748
ABUW_RS16990	ABUW_3292	NZ_CP008706.1	3325855	3326391	-	WP_000124015.1		ribosome-associated protein	2548.159747	-1.007374048	0.144719985	-6.960849571	3.38E-12	1.25E-11	10.90308999
ABUW_RS16735	ABUW_3442	NZ_CP008706.1	3487097	3487474	+	WP_001029768.1		winged helix-helix transcriptional regulator	296.2047532	-1.007651549	0.138646202	-7.267799075	3.65E-13	1.44E-12	11.84163751
ABUW_RS05160	ABUW_1049	NZ_CP008706.1	1057584	1058531	+	WP_151283637.1	raeD	EamA family transporter RaeD	591.3136576	-1.008225813	0.167340635	-6.024990963	1.69E-09	5.07E-09	8.294992041
ABUW_RS00795	ABUW_0180	NZ_CP008706.1	178603	179400	+	WP_000505317.1		MBL fold metallo-hydrolase	282.1384124	-1.008556528	0.199478341	-5.055970089	4.28E-07	1.07E-06	5.970616222
ABUW_RS01860	ABUW_0379	NZ_CP008706.1	404084	405988	+	WP_000696734.1	dsx	1-deoxy-D-xylulose-5-phosphate synthase	3868.501371	-1.008966652	0.15444217	-6.532887234	6.45E-11	2.15E-10	6.96756154
ABUW_RS16645	ABUW_3223	NZ_CP008706.1	3252347	3253567	-	WP_000268100.1	argJ	functional glutamate N-acetyltransferase/amino-acid acetyltransferase	5186.723679	-1.012975646	0.19059862	-6.508136155	1.77E-17	9.22E-17	16.03526908
ABUW_RS01860	ABUW_0277	NZ_CP008706.1	295060	295195	+			IRNA-Ala	415.4331193	-1.014283058	0.232344285	-4.365431497	1.27E-05	2.71E-05	4.567030709
ABUW_RS11420	ABUW_2348	NZ_CP008706.1	2330063	2330404	+	WP_001047284.1	ysaH	L-valine transporter subunit YsaH	125.5199258	-1.01490498	0.22321951	-6.54666789	5.45E-06	1.21E-05	4.91721463
ABUW_RS05405	ABUW_1105	NZ_CP008706.1	1127791	1123885	+	WP_001057073.1		acyl-CoA deacylase	19930.02931	-1.015873495	0.217108105	-3.747155916	0.000178879	0.000338518	3.470418234
ABUW_RS05465	ABUW_1117	NZ_CP008706.1	1157873	1159270	+	WP_000107954.1	pslA	phosphate ABC transporter permease PslA	358.9252746	-1.016703841	0.238043686	-4.271080890	1.95E-05	4.10E-05	4.387216143
ABUW_RS16880	ABUW_3270	NZ_CP008706.1	3301387	3304158	+	WP_001134663.1	polA	DNA polymerase I	4650.070155	-1.017944522	0.09276445	-10.97343354	5.13E-28	5.03E-27	26.29843201
ABUW_RS00535	ABUW_0108	NZ_CP008706.1	120081	120914	+	WP_000787753.1		SDR family NAD(P)-dependent oxidoreductase	763.9679881	-1.017975393	0.143624136	-7.087773845	1.36E-12	5.17E-12	11.28650946
ABUW_RS11295	ABUW_2323	NZ_CP008706.1	2307578	2307654	+			IRNA-Ile	34.15747999	-1.018007313	0.545576843	-1.865928377	0.060205187	0.084020134	10.97510044
ABUW_RS16790	ABUW_3859	NZ_CP008706.1	3926609	3927175	-	WP_001090743.1		5'-nucleotidase	441943964	-1.018500986	0.18508953	-6.741825958	2.29E-16	1.27E-17	16.89619628
ABUW_RS01885	ABUW_0038	NZ_CP008706.1	46497	46847	+	WP_000555783.1		hypothetical protein	46.04445358	-1.019981005	0.320689039	-3.180582035	0.00169744	0.002524126	2.59788897
ABUW_RS16460	ABUW_3791	NZ_CP008706.1	3853269	385414	+	WP_000051192.1		DUF1624 domain-containing protein	142.4977023	-1.021473523	0.190192924	-5.370723053	7.84E-08	2.07E-07	6.684029655
ABUW_RS16785	ABUW_3858	NZ_CP008706.1	3925954	3926574	+	WP_001196827.1		TerR/AcrR family transcriptional regulator	386.9665303	-1.021490246	0.154239059	-6.622772788	3.53E-11	1.07E-10	9.924453099
ABUW_RS16910	ABUW_3477	NZ_CP008706.1	3524309	3524671	-	WP_000095970.1		hypothetical protein	516.1506293	-1.022467294	0.215556846	-4.787791988	1.59E-06	3.95E-06	5.403402604
ABUW_RS08220	ABUW_688	NZ_CP008706.1	1863570	1864694	+	WP_000127451.1		YdcF family protein	683.253688	-1.023042583	0.14659187	-9.17783448	1.49E-22	1.05E-21	20.9788107
ABUW_RS16865	ABUW_2235	NZ_CP008706.1	2224254	2225396	+	WP_000293387.1		c1 division protein ZapE	5597.54974	-1.026693497	0.147817467	-6.945684828	3.77E-12	13.8E-11	10.8602091
ABUW_RS06095	ABUW_1247	NZ_CP008706.1	1288430	1289203	+	WP_001050536.1		ABC transporter permease	1112.74554	-1.026895912	0.192493932	-5.334507497	9.58E-08	2.15E-07	6.600326279
ABUW_RS02195	ABUW_0447	NZ_CP008706.1	460260	460336	+			IRNA-Arg	3943.338504	-1.027678899	0.351485947	-2.923812197	0.003457733	0.005637882	2.248881818
ABUW_RS00815	ABUW_0184	NZ_CP008706.1	182957	183613	+	WP_001028615.1	pdhH	pyridoxalase-5-phosphate oxidase	2905.4524	-1.027787502	0.155133354	-6.625187149	3.47E-11	1.75E-10	9.933941306
ABUW_RS02435	ABUW_0496	NZ_CP008706.1	507167	507979	+	WP_000284347.1	nmA	RNA (adenine(5'-N6)-lign) (adenine(5'-N6)-N6)-dimethyltransferase Rse	4622.731277	-1.028306544	0.161595182	-6.353376288	2.15E-10	1.78E-10	9.68773006
ABUW_RS05880	ABUW_0214	NZ_CP008706.1	1242291	1242875	+	WP_000925669.1		aminoacyloxyisomerase/anthranilate synthase component I	1340.84241	-1.02896742	0.198226929	-9.057499001	1.96E-12	9.89E-12	9.89841029
ABUW_RS14975	ABUW_3085	NZ_CP008706.1	3110226	3112763	-	WP_000397522.1	pgfF	peptidoglycan editing factor PgfF	719.221855	-1.029132248	0.105342543	-7.603908001	2.87E-14	1.21E-13	9.9172483
ABUW_RS01801	ABUW_0225	NZ_CP008706.1	246467	246991	+	WP_000607919.1		hypothetical protein	29.1846697	-1.029527073	0.383654089	-2.683502650	0.000728542	0.010129033	1.945806308
ABUW_RS17210	ABUW_3375	NZ_CP008706.1	3597388	3597895	+	WP_000177020.1		Na ⁺ /H ⁺ antiporter subunit E	835.9779905	-1.030882034	0.271343486	-3.799177378	0.065145017	0.000277871	3.556166776
ABUW_RS14640	ABUW_3017	NZ_CP008706.1	3040490	3041519	+	WP_001091065.1		tyrosine-tye recombinase/Integrase	350.7218809	-1.030947384	0.93090277	-5.31730326	1.06E-07	2.76E-07	6.550909918
ABUW_RS11115	ABUW_2347	NZ_CP008706.1	2329339	2330061	+	WP_000741226.1		AAC family ABC transporter permease	178.881469	-1.03126484	0.880909907	-5.482358235	1.20E-08	1.07E-07	6.946921557
ABUW_RS02920	ABUW_893	NZ_CP008706.1	1894330	1894878	+	WP_000324266.1	Rrt2	family transcriptional regulator	1342.923786	-1.031332691	0.152281791	-6.712527971	1.27E-11	4.43E-11	3.53506927
ABUW_RS16400	ABUW_3375	NZ_CP008706.1	3414531	3415229	-	WP_000058788.1		tetracycline-coupled repeat protein	1843.184202	-1.031344498	0.106315174	-7.566618747	3.83E-14	1.60E-13	12.95880062
ABUW_RS16720	ABUW_3439	NZ_CP008706.1	3428982	3438740	+	WP_000258761.1		hypothetical protein	282.334251	-1.0324765	0.10098613	-5.727943655	1.02E-08	2.88E-08	7.546075072

ABLUW_RS1860	ABLUW_3668	NZ_CP008706.1	3726049	+	WP_000372102.1		metallorepressor Anr/SnfB family transcription factor	3417627471	-1.032354616	-0.201229855	-5.100255912	2.896-07	7.31E-07	6.196082619
ABLUW_RS1875	ABLUW_2865	NZ_CP008706.1	2249466	225055	-	WP_000646460.1	nucleotidyltransferase family protein	1294.664029	-1.035161471	0.164905881	-6.277286574	3.45E-10	1.096E-09	8.862973502
ABLUW_RS1990	ABLUW_0197	NZ_CP008706.1	6284040	920501	-	WP_000027499.1	sulfate ABC transporter ATP-binding protein	610.7820234	-1.035366655	0.196478099	-7.586225848	3.29E-14	1.38E-13	5.86012001
ABLUW_RS1945	ABLUW_3608	NZ_CP008706.1	3667367	366810	-	WP_000730342.1	gspN type II secretion system protein N	9203.606859	-1.035983959	0.133676979	-7.749905514	9.20E-15	3.98E-14	5.40011893
ABLUW_RS1470	ABLUW_2980	NZ_CP008706.1	2996925	2997365	-	WP_000359621.1	YnfM family protein	34.31636574	-1.036300428	0.398903996	-2.603743778	0.009221868	0.01426266	1.84997262
ABLUW_RS1975	ABLUW_3630	NZ_CP008706.1	3688743	3690089	-	WP_000908240.1	UDP-N-acetylmannosyl-L-alanine--D-glutamate ligase	803.843463	-1.036324191	0.186278733	-5.279899787	1.29E-07	3.35E-07	6.47495915
ABLUW_RS4880	ABLUW_0995	NZ_CP008706.1	9007534	9007586	-	WP_001007564.1	protein TorR	338.660339	-1.037664	0.209846427	-4.9447458971	7.62E-07	1.86E-06	5.730487056
ABLUW_RS502	ABLUW_0445	NZ_CP008706.1	4604043	460403	+		rRNA-Ser	812.3373528	-1.038466865	0.252824805	-4.107456407	4.00E-05	8.00E-05	4.092051478
ABLUW_RS10750	ABLUW_2415	NZ_CP008706.1	2400886	2401827	+	WP_001985666.1	serine acetyltransferase	33.30845396	-1.039402416	0.41925597	-2.48705104	0.010280681	0.019349837	17.13222689
ABLUW_RS20340	ABLUW_0697	NZ_CP008706.1	699303	700083	-	WP_001098767.1	YdcF family protein	415.0640924	-1.044780347	0.29624765	-3.526710695	0.000420753	0.000769503	3.117199683
ABLUW_RS0315	ABLUW_0694	NZ_CP008706.1	698755	698830	+		rRNA-Vai	184.8079502	-1.047178239	0.270265896	-3.874622192	0.00010679	0.000207353	3.683289677
ABLUW_RS9140	ABLUW_3483	NZ_CP008706.1	3531912	3532567	+	WP_000207244.1	SOR family oxidoreductase	89.97795197	-1.047746399	0.230827432	-4.539089623	5.65E-06	1.25E-05	4.903089987
ABLUW_RS12906	ABLUW_2906	NZ_CP008706.1	2919138	2914306	-	WP_001161045.1	SPOR domain-containing protein	111.3482049	-1.048178952	0.238206765	-4.400290439	1.08E-05	2.32E-05	4.634510015
ABLUW_RS201490	ABLUW_8334	NZ_CP008706.1	8320409	8320591	-	WP_001003277.1	zhc1-ribon and DUF3426 domain-containing protein	135.590553	-1.049739942	0.128106671	-8.94264466	2.52E-16	1.21E-15	14.91721463
ABLUW_RS4680	ABLUW_0954	NZ_CP008706.1	962644	963489	+	WP_000923484.1	dnaG-dependent DNA primase	2511277209	-1.051072835	0.19260197	-5.456583416	4.85E-08	1.30E-07	6.880056648
ABLUW_RS0820	ABLUW_0185	NZ_CP008706.1	93614	93574	+	WP_000196361.1	recJ single-stranded-DNA-specific exonuclease RecJ	2689.826037	-1.054192306	0.19862107	-7.5373679	4.80E-14	2.00E-13	12.69897
ABLUW_RS5025	ABLUW_0444	NZ_CP008706.1	951977	952156	+	WP_000109632.1	hypothetical protein	982.274449	-1.055493105	0.223194966	-4.735002241	2.24E-06	5.20E-06	5.283996656
ABLUW_RS10505	ABLUW_0232	NZ_CP008706.1	295039	295275	+	WP_001161654.1	potassium transporter Knp	4.83.108665	-1.057854534	0.162414373	-6.96546104	3.95E-12	1.43E-11	10.84466306
ABLUW_RS100180	ABLUW_0852	NZ_CP008706.1	832220	833491	+	WP_000566842.1	serR serine--rRNA ligase	4697.708007	-1.057886821	0.210188961	-5.260790144	1.43E-07	3.71E-07	6.43602609
ABLUW_RS14050	ABLUW_2893	NZ_CP008706.1	2901203	290715	-	WP_000462918.1	hypothetical protein	623.813973	-1.05956723	0.178653178	-4.948343433	3.01E-09	8.88E-09	8.051687034
ABLUW_RS18815	ABLUW_3864	NZ_CP008706.1	3933023	3933055	+	WP_000186002.1	peptidylglycyl isomerase	3675.631733	-1.062307109	0.114924649	-9.243509878	2.39E-20	1.48E-19	18.82738379
ABLUW_RS1870	ABLUW_3328	NZ_CP008706.1	3364317	3365366	-	WP_000393100.1	DUF312 domain-containing protein	90.8518953	-1.062896808	0.236622609	-4.491949482	7.06E-06	1.54E-05	4.812475979
ABLUW_RS14045	ABLUW_0846	NZ_CP008706.1	826186	828226	-	WP_000547891.1	site-specific recombinase	2124.79079	-1.066860412	0.133050015	-8.03202174	9.59E-16	4.38E-15	3.1652589
ABLUW_RS12930	ABLUW_2867	NZ_CP008706.1	2876230	2877396	+	WP_000423004.1	disoxygenase	35.0237624	-1.06861754	0.29669962	-3.60163228	0.000316945	0.000584991	3.23285081
ABLUW_RS100970	ABLUW_0222	NZ_CP008706.1	926289	926317	-	WP_001078581.1	NS rRNA (cytosolic) N(40S, N23)-methyltransferase	479.826475	-1.069134367	0.17743401	-6.025532355	1.69E-09	5.08E-09	8.29544943
ABLUW_RS18685	no	NZ_CP008706.1	674650	675740	-	WP_085940648.1	B4 family transposase GAbA1	663.7118997	-1.070094262	0.248260642	-4.31666108	1.63E-05	3.45E-05	4.462180005
ABLUW_RS1790	ABLUW_2636	NZ_CP008706.1	2635492	2635815	+	WP_000144889.1	heredonin family protein	8039.22118	-1.070609418	0.194846922	-5.49418074	3.92E-08	1.06E-07	6.97490451
ABLUW_RS19035	ABLUW_0597	NZ_CP008706.1	556024	556239	-	WP_001025149.1	hypothetical protein	7717689067	-1.071660389	0.19504745	-6.634853907	3.25E-11	1.01E-10	9.95807315
ABLUW_RS12635	ABLUW_2147	NZ_CP008706.1	2102616	2103212	-	WP_000490551.1	recR recombinon protein RecR	1702.548689	-1.072430693	0.19875894	-7.728726655	1.00E-14	4.67E-14	13.3306631
ABLUW_RS14940	ABLUW_2393	NZ_CP008706.1	3434980	3435600	-	WP_000034283.1	eda hydroyl-2-oxoglutarate aldolase D-2-hydroxy-3-deoxy-phosphogluconate	3023.139621	-1.075899027	0.239436559	-4.463454273	7.00E-06	1.53E-05	4.819308659
ABLUW_RS17025	ABLUW_3500	NZ_CP008706.1	3547333	3548219	-	WP_000102346.1	mutI glutamate racemase	883.340622	-1.077146266	0.160741933	-6.701999064	2.07E-11	7.14E-11	10.14630179
ABLUW_RS1720	ABLUW_3559	NZ_CP008706.1	3616267	3616707	+	WP_000102728.1	Holliday junction resolvase RuvX	2028.792214	-1.077228714	0.201508331	-5.358104147	8.41E-08	2.21E-07	6.656607724
ABLUW_RS1035	ABLUW_2273	NZ_CP008706.1	2258391	2258984	+	WP_000810861.1	septom formation protein Maf	768.481404	-1.077899345	0.19347288	-6.047180527	6.47E-15	3.90E-15	14.08139339
ABLUW_RS20285	ABLUW_0106	NZ_CP008706.1	186427	186557	-	WP_000650776.1	phoB phosphate regulon transcriptional regulator PhoB	605.3423269	-1.078847911	0.1254029	-5.008519337	5.49E-07	1.35E-06	5.89866232
ABLUW_RS18745	ABLUW_0567	NZ_CP008706.1	566793	566793	-	WP_000963311.1	phage tail sheath protein	82.3937995	-1.079985176	0.31149247	-4.374404469	0.00059724	0.00105082	2.9750741
ABLUW_RS1210	ABLUW_2488	NZ_CP008706.1	2484413	2485228	+	WP_001184921.1	tsfR family transcriptional regulator TsfR	224.0987496	-1.081167784	0.191957249	-5.632336328	1.78E-08	4.94E-08	7.306217031
ABLUW_RS1606	ABLUW_03197	NZ_CP008706.1	339222	340376	-	WP_000768943.1	VWA domain-containing protein	3920.51718	-1.081215614	0.154708832	-6.988710924	2.77E-12	1.02E-11	99.999983
ABLUW_RS100705	ABLUW_187	NZ_CP008706.1	183481	184104	+	WP_000528791.1	PAS domain-containing protein	101.817431	-1.08166104	0.286745292	-3.77185313	0.00018204	0.00030868	3.19491506
ABLUW_RS13355	ABLUW_2751	NZ_CP008706.1	2741860	2742432	-	WP_000495834.1	rmbB ribonuclease HII	1225.097271	-1.082937666	0.20205492	-5.359620531	3.34E-08	2.19E-07	6.699558885
ABLUW_RS184285	ABLUW_0873	NZ_CP008706.1	855054	856250	+	WP_000197871.1	cdhB tartrate dehydrogenase complex dihydriolipoylysine-residue succinyltransferase	32270.21645	-1.082898916	0.20402731	-4.504437599	6.65E-06	1.46E-05	4.83564714
ABLUW_RS1470	ABLUW_3389	NZ_CP008706.1	3429704	3430989	+	WP_001154438.1	glutamate-5-semialdehyde dehydrogenase	4300.60118	-1.084041187	0.134025194	-8.088338598	6.05E-16	2.82E-15	14.54750089
ABLUW_RS19050	ABLUW_0786	NZ_CP008706.1	768288	768828	+	WP_000043392.1	hypothetical protein	384.761428	-1.085492711	0.257652236	-4.21016024	5.52E-05	5.21E-05	4.28312277
ABLUW_RS19140	ABLUW_0287	NZ_CP008706.1	305929	306261	+	WP_000186961.1	hypothetical protein	874.7885375	-1.08719703	0.12611928	-8.621839319	6.59E-16	3.57E-15	6.44077675
ABLUW_RS04915	ABLUW_0302	NZ_CP008706.1	914220	918053	+	WP_000471670.1	putL phosphoribosylformylglycanide synthase	20234.41058	-1.088427028	0.171873996	-6.332704441	2.41E-10	7.73E-10	9.11820506
ABLUW_RS0416	ABLUW_0116	NZ_CP008706.1	932616	932611	+	WP_000106804.1	hypothetical protein	7919651703	-1.090044601	0.257759198	-4.230494945	2.33E-05	4.48E-05	4.314282621
ABLUW_RS0930	ABLUW_014	NZ_CP008706.1	932818	932893	-		rRNA-Aan	78.801741006	-1.092260325	0.45466115	-2.403795303	0.01622856	0.023981649	16.2010958
ABLUW_RS18955	ABLUW_3893	NZ_CP008706.1	3960729	3961889	+	WP_000823196.1	glutathionylpermease synthase family protein	394.666072	-1.093096502	0.233570283	-4.641004341	3.46E-06	7.84E-06	5.95683917
ABLUW_RS18185	ABLUW_2719	NZ_CP008706.1	2701265	2702371	+	WP_000512831.1	beta-keatoacyl-ACP synthase II	2294.787525	-1.095472829	0.114100617	-7.766027223	6.10E-15	3.51E-14	15.45456928
ABLUW_RS140455	ABLUW_0908	NZ_CP008706.1	902493	903161	+	WP_001078001.1	methyltransferase	1172.794836	-1.097198197	0.190579628	-6.832735846	8.33E-12	2.95E-11	10.53017798
ABLUW_RS16665	ABLUW_3428	NZ_CP008706.1	3474860	3474492	-	WP_000056681.1	TerR/ActR family transcriptional regulator	9257.636849	-1.097659971	0.123252942	-8.905700673	3.30E-19	3.04E-18	17.5170242
ABLUW_RS16215	ABLUW_3154	NZ_CP008706.1	3166947	3168356	-	WP_000460625.1	flh signal recognition particle protein	6817.362227	-1.097898693	0.16019132	-6.857567828	7.00E-12	2.50E-11	10.6025999
ABLUW_RS16095	ABLUW_3718	NZ_CP008706.1	3776743	3778489	-	WP_000182542.1	hypothetical protein	89.0048823	-1.098455339	0.285000937	-3.853441128	0.000116469	0.000224954	3.64790628
ABLUW_RS1930	ABLUW_2472	NZ_CP008706.1	2465336	2466198	+	WP_000081481.1	krfR family transcriptional regulator	327.4067358	-1.099344267	0.19619183	-5.605128628	2.08E-08	5.76E-08	7.23957179
ABLUW_RS16575	ABLUW_3410	NZ_CP008706.1	3417512	3418587	+	WP_001186409.1	hypothetical protein	473.8246607	-1.101891359	0.160380736	-6.870228737	6.41E-12	2.31E-11	10.63038802
ABLUW_RS190180	ABLUW_0033	NZ_CP008706.1	316847	40270	+	WP_001195320.1	TerR/ActR family transcriptional regulator	86.5338779	-1.103468605	0.176018136	-6.269037067	6.63E-10	1.15E-09	8.9393021
ABLUW_RS17910	ABLUW_2421	NZ_CP008706.1	2408441	2409301	-	WP_000476792.1	transporter substrate-binding domain-containing protein	278.3937033	-1.104426391	0.210081677	-5.257100616	1.46E-07	3.78E-07	6.4225062
no	no	no	no	no	no	no	no	297.166871	-1.106416245	0.200423627	-5.359920235	8.33E-08	2.19E-07	6.699595885
ABLUW_RS06665	ABLUW_0166	NZ_CP008706.1	930477	932723	+	WP_000062052.1	1-oxo-2-oxoglutarate-3-phosphoshikimate 1-carboxyvinyltransferase	1556.554492	-1.108448798	0.168186329	-7.016692019	2.37E-12	8.78E-12	11.05655048
ABLUW_RS17645	ABLUW_3624	NZ_CP008706.1	3642394	3644271	+	WP_001072861.1	bifC dehydrogenase/phenylpyruvate synthase ThcC	1866.559403	-1.108456529	0.				

ABUW_R5340	ABUW_359	NZ_CP008706.1	1385821	3186240	+	WP_00200700.1	hypothetical protein	774.904291	-1.91543122	0.168001291	-6.915884013	4.72E-11	1.7E-11	0.76703889
ABUW_RS06410	ABUW_194	NZ_CP008706.1	125596	1256197	+	WP_00072210.1	DUF4468 domain-containing protein	3641237914	-1.915764383	0.231016236	-5.028886284	4.93E-07	1.22E-06	5.91940469
ABUW_RS0680	no	NZ_CP008706.1	561809	562899	+	WP_08504068.1	IS4 family transposase ISaba1	5119797972	-1.922999416	0.253453274	-4.588618693	4.46E-06	9.98E-06	5.00740662
ABUW_RS0760	ABUW_568	NZ_CP008706.1	1656202	1657077	+	WP_00107509.1	pmc peptide chain release factor(Nb) glutamine methyltransferase	554.8797616	-1.913394289	0.159943745	-1.7237775028	3.50E-13	1.86E12091	
ABUW_RS0205	ABUW_3740	NZ_CP008706.1	3796249	3797088	-	WP_00490209.1	zinc ABC transporter substrate-binding protein	769.847394	-1.91349046	0.15327191	-1.7593735610	3.1E-14	1.30E-13	92.8880655
ABUW_RS030	ABUW_3481	NZ_CP008706.1	3535064	3535739	+		tRNA-Lys	506.105311	-1.91367743	0.442007416	-2.632716102	0.008470659	0.01045981	1.884523258
ABUW_RS1465	ABUW_2367	NZ_CP008706.1	2338870	2340300	+	WP_000078700.1	pyridoxal phosphate-dependent aminotransferase	1436.88727	-1.915919378	0.244306296	-4.772363204	1.28E-07	4.25E-06	5.3719107
ABUW_RS0305	ABUW_0266	NZ_CP008706.1	283550	284965	+	WP_00516306.1	TolC family protein	359.0277373	-1.916012424	0.243265797	-4.793610284	1.64E-06	3.85E-06	5.4453927
ABUW_RS0210	ABUW_3741	NZ_CP008706.1	3797216	3797710	+	WP_00009318.1	transcriptional repressor	660.4077478	-1.916433973	0.159610015	-1.7306208017	2.75E-13	1.90E-12	11.95607731
ABUW_RS1780	ABUW_3651	NZ_CP008706.1	3712156	3712548	-	WP_001083669.1	DNA adenine methylase	2614.953082	-1.9166917676	0.162036706	-1.7201953797	5.95E-13	2.3E-12	11.63638802
ABUW_RS1440	ABUW_2148	NZ_CP008706.1	2132322	2132551	-	WP_001024697.1	YbaH/EbC family nucleoid-associated protein	2580.819171	-1.916842997	0.1930469	-6.9184514	4.78E-12	1.73E-11	10.7619539
ABUW_RS1665	ABUW_3628	NZ_CP008706.1	3686539	3687471	+	WP_000216752.1	gluQRS tRNA glutamyl-Q(34) synthetase GluQRS	3349.753706	-1.919818696	0.2160976841	-1.5447339851	2.94E-08	8.07E-08	7.09310645
ABUW_RS1670	ABUW_3248	NZ_CP008706.1	3278235	3279524	+	WP_001053727.1	hslD histidinol dehydrogenase	4674.78727	-1.919918249	0.12242376	-9.570455768	1.06E-21	7.16E-21	20.14569396
ABUW_RS0860	ABUW_1782	NZ_CP008706.1	178057	1781565	+	WP_000129940.1	aspartate aminotransferase family protein	118.130404	-1.970033839	0.16009390	-1.7044449265	1.86E-12	6.95E-12	11.988052
ABUW_RS1670	ABUW_3419	NZ_CP008706.1	3494075	3493361	-	WP_000787677.1	gfp glutamate/aspartate proton symporter GFP	5622.555218	-1.97166643	0.230671248	-5.078946105	3.80E-07	9.50E-07	6.022276395
ABUW_RS0016	ABUW_0024	NZ_CP008706.1	158348	160231	+	WP_000169747.1	parE DNA topoisomerase IV subunit II	2496.763635	-1.9751919	0.163020310	-1.7208683192	8.58E-13	2.20E-12	11.65737732
ABUW_RS0010	ABUW_0002	NZ_CP008706.1	1690	2738	+	WP_001037350.1	DNA polymerase II subunit beta	61387.10526	-1.97420056	0.137844823	-8.526905375	1.50E-17	7.9E-17	9.162352
ABUW_RS1250	ABUW_2535	NZ_CP008706.1	2494964	2505634	+	WP_001055133.1	hella-tun-hell transcriptional regulator	653.575809	-1.975816655	0.163453969	-7.16327770	6.3E-13	2.45E-12	11.6160332
ABUW_RS16705	ABUW_3436	NZ_CP008706.1	3479863	3480162	-	WP_002038961.1	RNA-binding protein	440.1722554	-1.976832075	0.173494334	-6.78310326	1.18E-11	4.13E-11	0.3840495
ABUW_RS0575	ABUW_016	NZ_CP008706.1	158555	159160	+	WP_000088344.1	type VIa secretion system pilin protein VgGp	3080.660732	-1.976914609	0.23124411	-5.089476242	3.59E-07	9.02E-07	6.04475942
ABUW_RS1735	ABUW_3036	NZ_CP008706.1	306230	3063497	+	WP_000092403.1	hypothetical protein	3869.052455	-1.984858809	0.160424481	-1.7385768497	1.52E-13	6.14E-13	9.2118393
ABUW_RS1810	ABUW_3179	NZ_CP008706.1	3777003	3779117	-	WP_001020674.1	TonB-dependent copper receptor	2121.61489	-1.985353709	0.281781932	-4.206634901	2.59E-05	5.35E-05	4.271464218
ABUW_RS05020	ABUW_0105	NZ_CP008706.1	116879	118237	+	WP_000273188.1	phosphatase protein sensor histidine kinase PhoR	1072.405025	-1.99270026	0.1752492	-6.806293278	1.00E-11	3.54E-11	0.40509674
ABUW_RS1805	ABUW_3288	NZ_CP008706.1	3292661	3932498	+	WP_001028146.1	iesS isoleucine-:Cys ligase	21461.64893	-1.99479415	0.15130345	-1.7899796075	2.79E-15	1.25E-14	90.3008999
ABUW_RS1640	ABUW_3222	NZ_CP008706.1	3251106	3252200	-	WP_001078262.1	nadA quinolinate synthase NadA	924.969616	-1.995769371	0.1347715	-1.8586806107	3.29E-19	1.91E-18	9.7186663
ABUW_RS08875	ABUW_1824	NZ_CP008706.1	1819883	1820371	-	WP_001024535.1	hypothetical protein	6328.296387	-1.97411925	0.162867087	-1.735207559	1.95E-13	7.85E-13	9.10510034
ABUW_RS0440	ABUW_0925	NZ_CP008706.1	153194	1540557	-	WP_000798643.1	lytic transglutaminase domain-containing protein	295.5962987	-1.992119856	0.172605097	-6.959121671	3.42E-12	1.26E-11	9.89962945
ABUW_RS1820	ABUW_3054	NZ_CP008706.1	3080842	3081789	+	WP_001027614.1	tnxB thiorodan-:disulfide reductase	5187.262095	-1.99261936	0.173237444	-6.859042272	6.93E-12	2.48E-11	16.80545832
ABUW_RS1220	ABUW_2254	NZ_CP008706.1	229585	2297963	+	WP_000090437.1	aspartate aminotransferase	5497.210832	-1.992030095	0.330850152	-6.33155661	0.000279976	0.00020175	3.28253732
ABUW_RS0255	ABUW_0104	NZ_CP008706.1	299682	270639	+	WP_000051071.1	HAMP domain-containing protein	3163.332235	-1.992061071	0.175189962	-6.864653625	6.67E-12	2.39E-11	10.4216021
ABUW_RS03035	ABUW_0617	NZ_CP008706.1	161842	1619171	+	WP_000377321.1	tyrB typtophan synthase subunit beta	4653.874164	-1.994533418	0.20734511	-5.809319737	6.27E-09	1.81E-08	7.742321425
ABUW_RS07035	ABUW_1444	NZ_CP008706.1	143594	1436168	+	WP_000068686.1	quinone-dependent dihydrodione dehydrogenase	3385.06076	-1.995146718	0.170356897	-1.707424336	1.50E-12	5.65E-12	11.24179515
ABUW_RS1810	ABUW_3357	NZ_CP008706.1	3384252	3389176	+	WP_000422094.1	acetolactate synthase 3 large subunit	1214.23542	-1.996082073	0.175602895	-6.866644937	6.57E-12	2.36E-11	10.627088
ABUW_RS0185	ABUW_0242	NZ_CP008706.1	239592	260321	+	WP_001005588.1	hypothetical protein	355.1900212	-1.996322991	0.16456835	-1.7798545535	6.26E-15	2.74E-14	10.56224941
ABUW_RS1830	ABUW_3848	NZ_CP008706.1	3955433	3956828	+	WP_000015510.1	mlp 1-acetyltransaminase L-alanyl-gamma-D-glutamyl-meso-diaminopimelate	844.723123	-1.996576401	0.199284448	-6.054543705	1.14E-09	2.46E-09	8.370904011
sRNA 62		no	no	no	no	no	no	1675.922477	-1.99805589	0.281895276	-4.218685599	1.82E-05	3.85E-05	4.1453927
ABUW_RS1030	ABUW_2746	NZ_CP008706.1	2734576	273742	-	WP_000165680.1	ATP phosphoribosyltransferase regulatory subunit	7177.988004	-1.9912101886	0.241294306	-5.020064107	5.17E-07	1.28E-06	5.89279003
ABUW_RS1830	ABUW_3367	NZ_CP008706.1	3407299	3408495	-	WP_000094936.1	on oligoribonuclease	2244.009604	-1.992356073	0.1310191	-9.232081023	2.65E-20	1.64E-19	9.7815619
ABUW_RS1035	ABUW_2889	NZ_CP008706.1	2896828	2897817	+	WP_001047619.1	LysR family transcriptional regulator	2414.815854	-1.994678774	0.190939393	-1.112314764	9.68E-29	1.00E-27	27
ABUW_RS1610	ABUW_3112	NZ_CP008706.1	313432	3140084	+	WP_000504141.1	elongation factor P/hydroxylase	2918.255909	-1.99780989	0.146326717	-1.829766116	1.06E-16	5.2E-16	9.28318276
ABUW_RS1715	ABUW_3558	NZ_CP008706.1	3516713	3516827	+	WP_001079301.1	YggJ/AgfI family protein	3023.74262	-1.997473625	0.194740073	-1.6262057957	3.80E-10	1.20E-09	8.920819754
ABUW_RS1595	ABUW_3614	NZ_CP008706.1	3617235	3617352	+	WP_031944168.1	henC hydrosymethylene sulfone	923.302183	-1.9981931	0.1618401	-6.731810243	1.80E-11	6.23E-11	9.20519515
ABUW_RS1615	ABUW_3196	NZ_CP008706.1	3224919	3225401	-	WP_000249482.1	tsvN rodent	1472.464774	-1.998278407	0.130394783	-1.9339971607	8.36E-05	0.000194374	3.784166976
ABUW_RS1675	ABUW_4051	NZ_CP008706.1	401031	401085	-	WP_032488579.1	aminoglycoside N-acetyltransferase AAC(6)-b3	8002.57231	-1.998493276	0.26387096	-4.642018216	3.45E-06	7.82E-06	5.106793247
ABUW_RS1625	ABUW_4055	NZ_CP008706.1	401295	401371	+	WP_000480966.1	APH(4)-family aminoglycoside C-phosphotransferase	480.2357999	-1.999090273	0.144197557	-2.778594897	0.005495457	0.00863272	2.0636527
ABUW_RS1675	ABUW_3761	NZ_CP008706.1	3761287	3797148	-	WP_000027559.1	FKBP-type peptidyl-prolyl-co-trans isomerase	779.064807	-1.99916024	0.222409177	-5.516470604	3.46E-08	9.43E-08	7.02548307
ABUW_RS0130	ABUW_0331	NZ_CP008706.1	332928	334140	-	WP_000077811.1	secA phosphoglycerate dehydrogenase	5382.22402	-1.999733621	0.16246482	-1.785103481	3.99E-15	1.77E-14	9.175202673
ABUW_RS00700	ABUW_0141	NZ_CP008706.1	155034	155058	-	WP_000123651.1	xth exodeoxyribonuclease II	614.719968	-1.999122812	0.17320492	-1.700501078	2.47E-12	9.15E-12	10.3090538
ABUW_RS1845	ABUW_3748	NZ_CP008706.1	37480577	38080803	+	WP_000467262.1	SPOR domain-containing protein	2085.38125	-1.999299562	0.1479532	-4.308702069	9.68E-17	4.77E-16	16.3214882
ABUW_RS1815	ABUW_3742	NZ_CP008706.1	3797686	3798474	+	WP_001102011.1	znuC zinc ABC transporter ATP-binding protein ZnuC	624.710048	-1.99942049	0.162824297	-1.8044584961	8.63E-16	3.97E-15	14.4010949
ABUW_RS0460	ABUW_0950	NZ_CP008706.1	1657719	1659105	-	WP_000048860.1	nadA DNA repair protein RadA	774.8793501	-1.999759012	0.160723083	-8.189002165	3.38E-16	1.59E-15	16.79802808
ABUW_RS1695	ABUW_2261	NZ_CP008706.1	2246373	2247008	-	WP_000264044.1	MsbA/TolE/ExbB protein channel family protein	104.525071	-1.999844827	0.172486494	-1.7000931472	1.00E-12	3.85E-12	11.41453927
sRNA48		no	no	no	no	no	no	90.425978	-1.99996307	0.380266482	-1.236054484	0.0011842	0.00209373	2.8781171
ABUW_RS1805	ABUW_4057	NZ_CP008706.1	405714	405735	-	WP_001021670.1	ANT(3)-family aminoglycoside nucleotidyltransferase AadA2	653.4054952	-1.9991234309	0.425958699	-2.889986076	0.00385289	0.00262401	2.20420281
ABUW_RS1695	ABUW_0224	NZ_CP008706.1	246048	246362	+	WP_000543307.1	hella-tun-hell transcriptional regulator	103.87726	-1.999123393	0.314816529	-3.914468223	9.06E-05	0.00017291	3.7191301
ABUW_RS05070	ABUW_0115	NZ_CP008706.1	179784	1798389	+	WP_001040411.1	disulfide bond formation protein B	864.3654077	-1.999256035	0.171981027	-1.68780221	7.88E-13	2.97E-12	10.52724355
ABUW_RS1105	ABUW_2289	NZ_CP008706.1	2278707	2277792	+	WP_000204082.1	tnmA tRNA (uridine54)-C5-methyltransferase TmA	191.12599	-1.999184715	0.163080294	-1.181349326	4.84E-16	2.27E-15	16.64397414
ABUW_RS1675	ABUW_3249	NZ_CP008706.1	3279630	3280313	-	WP_001007241.1	ATP phosphoribosyltransferase	3459.919972	-1.999298993	0.187407863	-8.334019359	7.8E-17	3.89E-16	5.41010054
ABUW_RS0315	ABUW_0813	NZ_CP008706.1	1088346	1089729	-	WP_000078676.1	DUF3144 domain-containing protein	414.2000642	-1.999359782	0.158103161				

ABUW_RS1605	ABUW_2365	NZ_CP008706.1	2352483	2354053	-	WP_000868609.1	ahpF	aldehyde hydroxylation reductase subunit F	198.1769534	-1.293106846	0.203749821	-6.346542257	2.406	0	7.08E-10	9.94966742
ABUW_RS0495	ABUW_0875	NZ_CP008706.1	857894	858060	+	WP_000485793.1	sucC	ADP-forming succinate-CoA ligase subunit beta	53007.9766	-1.29311914	0.245886428	-5.258977292	1.456	0	3.74E-07	6.42783398
ABUW_RS0640	ABUW_0337	NZ_CP008706.1	358322	359551	+	WP_000790181.1		MFS transporter	448.1333756	-1.29432041	0.208884653	-3.075210073	0.00203543	0.00352833	2.45242749	
ABUW_RS0453	ABUW_0337	NZ_CP008706.1	128081	1290446	+	WP_000162520.1		DUF3465 domain-containing protein	331399369	-1.295880074	0.205294193	-6.312396087	2.756	0	8.78E-10	9.05605484
ABUW_RS0735	ABUW_0444	NZ_CP008706.1	1530044	1531094	-	WP_000448193.1	air	alanine racemase	576.361621	-1.296709859	0.146365211	-8.859413035	8.046	9	4.56E-10	17.34193516
ABUW_RS0470	ABUW_0952	NZ_CP008706.1	961141	961085	+	WP_000255106.1		hypothetical protein	785.4073993	-1.299864381	0.226237548	-5.745495078	9.91E-09	2.61E-08	7.583359493	
ABUW_RS0780	ABUW_0197	NZ_CP008706.1	9510241	9510363	-	WP_000098476.1		glutamine amidotransferase	494.3682003	-1.300774758	0.21169075	-6.90021684	7.275	0	2.23E-09	6.647817452
ABUW_RS0475	ABUW_2889	NZ_CP008706.1	2907107	2908366	-	WP_000193744.1	lysS	lysine-tRNA ligase	5649.794757	-1.303465525	0.176238931	-7.396183766	1.406	0	5.69E-13	12.44888773
ABUW_RS0715	no	NZ_CP008706.1	851927	852056	+			hypothetical protein	129.199285	-1.304981051	0.165088908	-7.904718553	2.695	0	1.20E-14	13.05081975
ABUW_RS0840	ABUW_3869	NZ_CP008706.1	13932848	13938323	-			rRNA-Ala	3588.094969	-1.305677565	0.270276392	-4.830897577	1.365	06	3.22E-06	5.49214458
ABUW_RS1925	ABUW_3115	NZ_CP008706.1	1315588	1316404	+	WP_000093856.1	scpB	SMC-Scp complex subunit ScpB	180.246169	-1.306128682	0.140144429	-9.319875852	1.165	20	7.34E-10	9.14303394
ABUW_RS08625	ABUW_0771	NZ_CP008706.1	1768924	1769871	-	WP_000162618.1	prfB	5-phosphofructokinase	739.5559454	-1.306247452	0.179857596	-7.262631026	3.806	0	1.50E-12	11.62300874
ABUW_RS0185	ABUW_0342	NZ_CP008706.1	346467	346517	+	WP_000118036.1		endonuclease	10.1829436	-1.306322558	0.192754315	-6.777137834	1.235	11	4.30E-11	10.36653154
ABUW_RS0585	ABUW_0011	NZ_CP008706.1	1235279	1236338	-	WP_000882145.1	tpdD	anthranilate phosphoribosyltransferase	1957.808095	-1.306362917	0.16402197	-7.961638018	1.708	0	7.69E-15	14.16073366
ABUW_RS0610	ABUW_3457	NZ_CP008706.1	1504451	1504612	+	WP_001284373.1	inIA	translation initiation factor P-1	5107.830075	-1.307580895	0.225766422	-5.791742561	6.976	09	2.00E-08	7.698970004
ABUW_RS0135	ABUW_3422	NZ_CP008706.1	1346898	1346993	+	WP_000551918.1		DUF4165 domain-containing protein	2120.405216	-1.309588225	0.118088864	-1.018993842	1.405	28	1.42E-17	26.84771767
ABUW_RS1650	ABUW_3019	NZ_CP008706.1	1044331	1044384	-	WP_000857095.1		DNA2 family efflux NTS transporter permease subunit	462.2073541	-1.310011699	0.230504883	-4.670154557	3.91E-06	6.88E-06	5.92311962	
ABUW_RS1165	ABUW_2283	NZ_CP008706.1	2285651	2286925	+	WP_000161643.1	gcvH	glycine cleavage system protein GcvH	864.4170354	-1.310921956	0.164748263	-7.956514596	1.775	05	8.80E-15	4.09991001
ABUW_RS1080	ABUW_0525	NZ_CP008706.1	533465	534079	-	WP_000645707.1		sepiation protein lepZ	1089.801304	-1.310184975	0.10443002	-9.753744484	1.785	22	1.25E-11	20.30308999
ABUW_RS0350	ABUW_2752	NZ_CP008706.1	2742488	2742887	-	WP_000735756.1		hypothetical protein	2995.543435	-1.312514122	0.204395686	-6.42132568	1.355	10	4.4E-10	9.355661411
ABUW_RS0325	ABUW_0635	NZ_CP008706.1	615754	616344	-	WP_000109208.1		patatin family protein	1060.087583	-1.315288898	0.149690532	-9.061286409	1.295	0	7.65E-19	18.19338554
ABUW_RS0555	ABUW_0214	NZ_CP008706.1	2318703	2319623	+	WP_0004243165.1		LysR family transcriptional regulator	124.5325339	-1.316208614	0.218020573	-6.02708541	1.675	09	5.01E-09	8.300162374
ABUW_RS1780	ABUW_3571	NZ_CP008706.1	1362500	1362915	-	WP_0001916652.1		hypothetical protein	2150.826286	-1.319493989	0.264220419	-4.976882546	6.48E-07	1.09E-06	5.786022876	
ABUW_RS0105	ABUW_0326	NZ_CP008706.1	344862	344917	+	WP_000208695.1	tuB	rRNA pseudouridine(S) synthase TuB	865.4788989	-1.3181369452	0.204408228	-4.639904427	1.205	0	9.40E-1093	
ABUW_RS1240	ABUW_3747	NZ_CP008706.1	1380233	1380233	+	WP_001900284.1		arginine-tRNA ligase	5864.716431	-1.3197335039	0.1074191	-12.26558825	1.395	34	0.20E-33	32.6944863
ABUW_RS0925	ABUW_3480	NZ_CP008706.1	3530565	3530641	+			rRNA-Lys	1074.255812	-1.318076954	0.45243469	-2.912927726	0.003576334	0.005821839	2.234398609	
ABUW_RS0780	ABUW_1453	NZ_CP008706.1	1444515	1445525	+	WP_000632623.1	tsaD	nosine(37'-N6)-thymine/arabanylate transferase complex transferase subunit	870.178368	-1.32106746	0.182588477	-6.848997239	7.395	12	2.63E-11	10.58004425
ABUW_RS1925	ABUW_3088	NZ_CP008706.1	2293182	2293394	-	WP_000303093.1		hypothetical protein	101693497	-1.322218885	0.282173542	-4.985658303	2.795	06	6.41E-06	5.93149197
ABUW_RS0755	ABUW_0162	NZ_CP008706.1	187724	188626	+	WP_000240700.1		UDP-3'-O-acryl-N-acetylglucosamine deacetylase	2634.371151	-1.322178738	0.12141057	-10.8695514	1.295	27	1.23E-26	25.91002449
ABUW_RS0435	ABUW_0811	NZ_CP008706.1	862194	863147	+	WP_0001072941.1	tpS	tyrosylphosphatase	4321.733557	-1.323751949	0.198914623	-6.654881023	2.845	11	9.68E-11	10.9142644
ABUW_RS1750	ABUW_3545	NZ_CP008706.1	3604180	3604236	-			rRNA-Met	1164.45452	-1.32701805	0.18342563	-4.233020018	2.305	05	4.79E-05	4.320572103
ABUW_RS1740	ABUW_3543	NZ_CP008706.1	3703634	3705181	-	WP_0001028749.1		2,3-bisphosphoglycerate-independent phosphoglycerate mutase	7635.63303	-1.329245519	0.162500891	-7.283500999	3.255	13	1.29E-12	11.88941629
ABUW_RS0380	ABUW_2076	NZ_CP008706.1	2057651	2058421	-	WP_000179748.1		SDR family oxidoreductase	273.1669339	-1.329662355	0.09571852	-1.194192083	0.055941073	0.076532357	1.18E-1491	
ABUW_RS0300	ABUW_0308	NZ_CP008706.1	124878	124927	+	WP_0012319701.1		chondrate lyase	430.2364287	-1.330430475	0.174307209	-7.632676106	2.305	14	9.71E-14	10.0178077
ABUW_RS1645	ABUW_3404	NZ_CP008706.1	3451261	3451944	+	WP_0001984475.1		Fe2+-dependent dioxygenase	759.4841698	-1.330485107	0.130605752	-8.95041767	6.81E-23	4.96E-22	21.30419332	
ABUW_RS0425	ABUW_0086	NZ_CP008706.1	194238	195305	+	WP_000862934.1		DNA cytosine methyltransferase	1565.751811	-1.330514239	0.16504664	-8.061433964	7.54E-16	3.48E-15	14.45717457	
ABUW_RS0915	ABUW_3897	NZ_CP008706.1	3568632	3569359	+	WP_000214897.1	hpt	hypoanthine phosphoribosyltransferase	2927.396254	-1.331724471	0.172338878	-7.727359539	1.605	14	4.72E-14	13.320505
ABUW_RS0585	ABUW_0445	NZ_CP008706.1	1286947	1287597	-	WP_001161740.1		hypothetical protein	863.6229666	-1.332062489	0.160195764	-8.317085626	9.02E-17	4.48E-16	16.35065615	
ABUW_RS0835	ABUW_0619	NZ_CP008706.1	187814	188116	+	WP_000350418.1		helic-tum-helic transcriptional regulator	680.683356	-1.332403835	0.190401222	-6.997874378	2.605	12	1.01772877	
ABUW_RS1340	ABUW_3363	NZ_CP008706.1	3442621	3444615	+	WP_000165905.1		Made family efflux pump subunit	826.4497942	-1.333317687	0.210132208	-6.345107195	2.225	0	7.14E-10	9.146301798
ABUW_RS1255	ABUW_2731	NZ_CP008706.1	2719389	2719624	-	WP_000874290.1		aspartate carboxyltransferase	3039.282274	-1.333739905	0.190300502	-6.089570581	1.019	3.44E-09	4.65341654	
ABUW_RS0760	ABUW_0609	NZ_CP008706.1	1604100	1604268	+	WP_000303651.1	htq	rRNA chaperone Hfq	1465.423571	-1.334420083	0.227451905	-5.866596485	4.44E-09	1.29E-08	7.89941922	
ABUW_RS1725	ABUW_3538	NZ_CP008706.1	3597982	3598187	+	WP_0001614076.1		monovalent cation/H+ antiporter subunit F	211.7022229	-1.334564377	0.310209294	-4.277045459	1.895	05	4.00E-05	4.397940039
ABUW_RS1075	ABUW_2202	NZ_CP008706.1	2187926	2189143	+	WP_000828390.1		IscS sulfurlylase cysteine desulfurase	9405.00116	-1.3361782354	0.189931544	-7.038127101	1.955	12	7.26E-12	11.01908338
ABUW_RS0170	ABUW_0319	NZ_CP008706.1	1343566	1343931	+	WP_000718336.1		prephn-type N-terminal cleavage/methylation domain-containing protein	505.5426716	-1.337126875	0.167919937	-8.487118859	5.525	17	1.30E-16	15.8860565
ABUW_RS1790	ABUW_3613	NZ_CP008706.1	3671463	3672230	-	WP_000897420.1		unorthophosphorylase	582.3963972	-1.339697822	0.189492354	-7.069930772	1.555	12	5.83E-12	11.21433145
ABUW_RS0265	ABUW_0054	NZ_CP008706.1	508977	509435	+	WP_000102828.1		YggH family nucleic acid chaperon	505.2437464	-1.340568553	0.206370002	-6.493946712	8.25E-11	2.74E-10	9.592264247	
ABUW_RS0245	ABUW_0498	NZ_CP008706.1	509862	5099305	-	WP_000165436.1		DUF2174 domain-containing protein	977.7700001	-1.341400057	0.171647355	-7.819415056	5.31E-15	2.33E-14	13.6234468	
ABUW_RS1610	ABUW_3256	NZ_CP008706.1	3287705	3288785	-			rRNA-Ala	3602.73212	-1.342882027	0.271057311	-4.954055433	7.25E-07	1.77E-06	5.750262734	
ABUW_RS1640	ABUW_2808	NZ_CP008706.1	2807165	2807165	+	WP_001764322.1		amino acid permease	1298.801533	-1.343660629	0.175078879	-7.674601944	1.06E-14	7.06E-14	15.61953	
ABUW_RS0170	ABUW_0644	NZ_CP008706.1	650590	650995	+	WP_000953247.1		DUF314 domain-containing protein	442.1350918	-1.343683846	0.219675338	-6.186688447	9.55E-10	2.92E-09	8.534517169	
ABUW_RS0235	ABUW_3342	NZ_CP008706.1	3376560	3376468	+	WP_004432485.1	duaA	rRNA dihydrouridine(202a) synthase DuaA	1015.587621	-1.346454715	0.231540332	-5.852059309	6.06E-109	1.75E-08	17.755691951	
ABUW_RS0280	no	NZ_CP008706.1	2881956	2882194	-			hypothetical protein	55.44343002	-1.347014262	0.248794199	-5.41419199	6.16E-08	1.64E-07	6.78519562	
ABUW_RS1730	ABUW_3501	NZ_CP008706.1	3546268	3548179	-	WP_000248028.1		DUF1085 domain-containing protein	907.778379	-1.347997169	0.198995632	-7.934268103	2.105	05	9.54E-15	14.02045183
ABUW_RS1670	ABUW_3719	NZ_CP008706.1	3732479	3733554	-			rRNA-Ala	3600.446472	-1.350230921	0.273990711	-4.928910105	8.31E-07	2.40E-06	5.696039343	
ABUW_RS1930	ABUW_3116	NZ_CP008706.1	1308446	1307169	+	WP_000192491.1	ruB	23S rRNA pseudouridine(205) synthase RuB	3305.744847	-1.35213989	0.100889452	-11.78891156	6.82E-29	4.06E-28	27.30916037	
ABUW_RS07716	ABUW_0719	NZ_CP008706.1	1567343	1567780	+	WP_000993407.1		2-amino-4-hydroxy-6-hydroxymethylthiohydropyridine diphosphokinase	779.5521183	-1.353336716	0.102576824	-10.20817723	1			

ABUW_RS1165	ABUW_2295	NZ_CP008706.1	228194	2283129	-	WP_000219068.1	9t	transketolase	9541.20729	-1.42201909	0.06437127	-10.3505691	4.96E-25	3.45E-24	23.4627609
ABUW_RS3349	ABUW_2748	NZ_CP008706.1	273739	2739649	+	WP_000194957.1	alsS	alanine-rRNA ligase	9488.96599	-1.14167699	0.08503511	-7.52445995	1.05E-12	4.01E-12	11.39685563
ABUW_RS4200	ABUW_2925	NZ_CP008706.1	293528	2937359	-	WP_001876411.1		inorganic phosphate transporter	8412.527363	-1.14199438	0.07062576	-6.28833493	1.95E-16	5.25E-17	16.2510374
ABUW_RS4255	ABUW_2936	NZ_CP008706.1	295070	2951923	-	WP_000085675.1		glutamine	2786.73827	-1.14958067	0.03204744	-6.687307455	3.71E-16	9.26E-17	16.69446683
ABUW_RS4465	ABUW_2979	NZ_CP008706.1	2996647	2996922	+	WP_000061107.1		hypothetical protein	31.9468771	-1.149025079	0.46382783	-3.059379907	0.002219764	0.003790497	2.430684676
ABUW_RS5910	ABUW_1976	NZ_CP008706.1	980186	981510	+	WP_000045119.1	adeC	multidrug efflux RND transporter outer membrane channel subunit AdeC	1049.9853	-1.142160342	0.07160291	-8.078123664	6.58E-16	3.06E-15	14.5127857
ABUW_RS01055	ABUW_0258	NZ_CP008706.1	272077	274425	+	WP_000191061.1		rRNA-binding transcriptional accessory protein	14293.87794	-1.1421714653	0.243268283	-5.84616213	5.03E-09	1.46E-08	7.835647184
ABUW_RS01575	ABUW_0280	NZ_CP008706.1	297574	298515	+	WP_001985558.1		sulfate ABC transporter substrate-binding protein	290.290245	-1.142229309	0.204349271	-6.959796326	3.41E-12	1.25E-11	16.90308999
ABUW_RS1605	ABUW_2263	NZ_CP008706.1	2247942	2248724	-	WP_000057212.1		glutamine	2370.24718	-1.142226809	0.69786364	-8.95060515	5.53E-19	3.17E-18	9.48940474
ABUW_RS1635	ABUW_2269	NZ_CP008706.1	225556	2256193	-	WP_001074011.1		fructose-bisphosphate aldolase class I	16851.2851	-1.142308039	0.17378701	-8.98743741	2.64E-19	1.26E-15	14.89962945
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.224330055	1.96E-15	9.45E-16	16.02456819
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001090065.1		hypothetical protein	845.1754442	-1.142410885	0.05856958	-8.15349923	2.95E-41	6.46E-40	39.8976748
ABUW_RS1678	ABUW_3250	NZ_CP008706.1	3280313	3281569	-	WP_000357156.1	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	930.1652407	-1.142377919	0.17317848	-8.2243			

ABUW_RS05090	ABUW_4046	NZ_CP008706.1	Q164817	Q147461	+	WP_000590566.1		RNA-(ms)[2]c[6]A)- hydroxylase	1863.334563	-1.747193704	0.02987872	-13.522771461	1.95E-41	2.6E-40	39.58335949
ABUW_RS07580	ABUW_1033	NZ_CP008706.1	Q157893	Q183945	+	WP_00105043.1	cyoA	ubiquinol oxidase subunit II	79095.44868	-1.750359369	0.235245586	-7.440565997	1.00E-13	4.10E-13	Q.2387284
ABUW_RS05050	ABUW_1745	NZ_CP008706.1	Q142356	Q140344	+	WP_000064475.1	lpaA	acyl-ACP--UDP-N-acetylglycosamine C-acyltransferase	Q155.63392	-1.0750388505	0.02533195	-11.67544662	1.75E-30	2.02E-29	28.69446863
ABUW_RS1476	ABUW_3032	NZ_CP008706.1	Q305997	Q306135	+	WP_000047036.1		PE/PtRpf family type Ia plus A1Pass	995.7358021	-1.751830899	0.973736699	-9.967230579	2.0E-23	1.60E-22	21.79588002
ABUW_RS0620	ABUW_3218	NZ_CP008706.1	Q326504	Q326670	-			RNA- Pro	982.580712	-1.754471212	0.394974831	-4.44.986498	8.9E-06	1.93E-05	4.71442091
ABUW_RS07800	ABUW_1897	NZ_CP008706.1	Q184385	Q184783	+	WP_001022838.1		membrane protein	618.4302649	-1.754718161	0.222197065	-7.825832857	2.27E-15	1.02E-14	13.99109983
ABUW_RS10325	ABUW_2745	NZ_CP008706.1	Q273492	Q273451	+	WP_000519782.1		adenylosuccinate synthase	30542.30006	-1.755068063	0.93547833	-10.73102178	7.26E-27	6.62E-26	25.1794201
ABUW_RS03085	ABUW_0623	NZ_CP008706.1	Q162485	Q162561	+	WP_00107186.1		acetyl CoA carboxylase carboxyltransferase subunit beta	25245.9105	-1.757057392	0.214646575	-8.8581612	2.70E-16	1.29E-15	14.88941029
ABUW_RS08880	ABUW_1825	NZ_CP008706.1	Q182055	Q182232	+	WP_000148658.1		CTP synthase	1878120598	-1.75799852	0.9066891	-10.9417467	7.28E-28	7.03E-27	26.1504467
ABUW_RS04955	ABUW_1331	NZ_CP008706.1	Q145956	Q142282	-	WP_001147934.1		DUF3820 family protein	243.8693799	-1.7580305	0.070784926	-10.29382707	7.5E-25	6.19E-24	23.21467016
ABUW_RS06700	ABUW_1373	NZ_CP008706.1	Q188648	Q188645	-	WP_00167820.1	thiS	sulfur carrier protein ThiS	575.6828887	-1.758647619	0.93497217	-10.75643762	5.53E-27	5.06E-26	25.25884848
ABUW_RS04095	ABUW_0836	NZ_CP008706.1	Q18464	Q1843	-	WP_00012871.1		valine- γ RNA ligase	17885.59965	-1.759880111	0.93089082	-9.114293356	7.92E-20	4.76E-19	13.22293305
ABUW_RS1975	ABUW_3692	NZ_CP008706.1	Q375801	Q375245	+	WP_000027792.1		trimeric intracellular cation channel family protein	8010978912	-1.761850399	0.234201773	-7.522788483	5.36E-14	2.22E-13	Q.65364703
ABUW_RS06090	ABUW_1051	NZ_CP008706.1	Q186783	Q186520	+	WP_00102090.1	tsaA	Flp pil assembly complex A1Pass component TsaA	494.7244398	-1.764379278	0.80864694	-9.793146709	1.20E-22	8.6E-22	21.05448995
ABUW_RS1085	ABUW_2279	NZ_CP008706.1	Q226419	Q226475	+	WP_000240310.1		DUF2058 domain-containing protein	546.2726127	-1.765315407	0.252208194	-6.999439388	2.57E-12	9.50E-12	11.02227639
ABUW_RS1430	ABUW_3785	NZ_CP008706.1	Q3446482	Q3447892	-	WP_000178999.1		amino acid permease	1684.638181	-1.7773739106	0.22287056	-7.958608568	1.74E-15	7.88E-15	14.9347378
ABUW_RS20020	ABUW_4046	NZ_CP008707.1	Q16577	Q17569	+	WP_001818192.1		ThiB ATP-binding protein	585.781511	-1.77656182	0.250682309	-7.086716294	1.37E-12	5.2E-12	11.28316228
ABUW_RS04545	ABUW_0926	NZ_CP008706.1	Q154561	Q154665	+	WP_000217149.1	BcA	RNA 2'-thiocytidine[32] synthetase TbcA	3018.347193	-1.777556324	0.869537727	-10.4847343	1.02E-25	8.87E-25	24.0619939
ABUW_RS18500	ABUW_3811	NZ_CP008706.1	Q1873252	Q1874338	+	WP_00193019.1	dtiI	D-lactate dehydrogenase	Q186.212284	-1.782183889	0.250883253	-8.85751975	7.0E-12	2.50E-11	10.60209999
ABUW_RS0390	ABUW_1869	NZ_CP008706.1	Q139590	Q139568	-	WP_010257872.1	nuoJ	NADH-quinone oxidoreductase subunit J	11018451	-1.782185645	0.261454963	-6.816419437	9.33E-12	3.30E-11	10.48184806
ABUW_RS03530	ABUW_0717	NZ_CP008706.1	Q172320	Q172311	+	WP_001021007.1	mreD	rod shape-determining protein MreD	Q15.99917	-1.784673941	0.253964895	-7.027240593	2.1E-12	7.8E-12	11.0734897
ABUW_RS10135	ABUW_1327	NZ_CP008706.1	Q130443	Q1311892	+	WP_000092730.1		YebC/PmpR family DNA-binding transcriptional regulator	8240.275071	-1.785525058	0.21387279	-3.848537747	6.19E-17	3.45E-16	15.4621809
ABUW_RS10970	ABUW_2876	NZ_CP008706.1	Q185501	Q188709	+	WP_000809134.1	mrdA	penicillin-binding protein 2	977.5536938	-1.787699197	0.073394429	-10.9146218	2.40E-24	1.89E-23	22.7235382
ABUW_RS1840	ABUW_3727	NZ_CP008706.1	Q375838	Q378652	+	WP_000372831.1		IMS transporter	378.413434	-1.788033029	0.90080404	-11.0750972	6.6E-29	6.95E-28	27.158012
ABUW_RS04035	ABUW_0824	NZ_CP008706.1	Q179457	Q180083	-	WP_000434847.1		1-acyl-sn-glycerol-3-phosphate acyltransferase	495.028035	-1.788196123	0.09628023	-8.847521884	3.64E-19	2.10E-18	17.67778071
ABUW_RS08035	ABUW_1546	NZ_CP008706.1	Q160874	Q164344	+	WP_000527015.1		TonB-dependent siderophore receptor	2039.817431	-1.787729189	0.376548099	-4.746417607	2.07E-06	4.82E-06	5.13695262
ABUW_RS04095	ABUW_0100	NZ_CP008706.1	Q110721	Q110164	+	WP_00102027.1		D-lysine- RNA(1)hydroxylase	540.6645882	-1.788446031	0.09602683	-8.210097107	1.42E-37	2.44E-36	35.6101617
ABUW_RS05505	ABUW_1025	NZ_CP008706.1	Q114780	Q114838	-	WP_000741964.1		NADH hydroxylase	8007.287291	-1.789880588	0.91912804	-3.955785422	8.30E-21	5.29E-20	19.27654433
ABUW_RS1815	ABUW_3478	NZ_CP008706.1	Q324597	Q325299	+	WP_000827305.1		Rae/Rag family thiolase	Q1833.0218	-1.789964734	0.2163631	-8.317457364	9.45E-17	4.66E-16	15.33161008
ABUW_RS07540	ABUW_1545	NZ_CP008706.1	Q131747	Q132592	-	WP_000175891.1	dnbB	replicative DNA helicase	9327.621725	-1.790653833	0.09322997	-10.7392584	5.9E-43	1.43E-41	40.84466166
ABUW_RS17230	ABUW_3541	NZ_CP008706.1	Q359942	Q360741	+	WP_000103036.1	mIB	translation initiation factor F-2	10708.377	-1.791866307	0.88550249	-9.024749710	1.80E-19	1.06E-18	17.97469413
ABUW_RS17225	ABUW_3540	NZ_CP008706.1	Q359841	Q359842	+	WP_000897046.1		ribosome-binding factor A	14401.44544	-1.793818937	0.997155	-8.980075921	2.7E-19	1.58E-18	17.97014291
ABUW_RS14415	ABUW_2969	NZ_CP008706.1	Q298249	Q2984271	+	WP_000042343.1		BCTC family transporter	7253.254778	-1.799103575	0.336628229	-5.34451891	9.07E-08	2.38E-07	6.623423403
ABUW_RS21010	no	NZ_CP008706.1	Q170840	Q170880	+	WP_000480937.1		hypothetical protein	807.597211	-1.799161697	0.232410039	-7.739999055	9.94E-15	4.28E-14	10.36855623
ABUW_RS05170	ABUW_1053	NZ_CP008706.1	Q101940	Q103160	+	WP_00102491.1	cgfA	Otg family OTase CgfA	88.0154131	-1.799377332	0.89970091	-9.472005431	2.75E-21	1.81E-20	9.74232143
ABUW_RS17120	ABUW_3519	NZ_CP008706.1	Q358857	Q358866	-	WP_001029357.1	pspO	30S ribosomal protein S15	38383.46633	-1.799438417	0.91964582	-9.373804272	7.00E-21	4.49E-20	9.34773366
ABUW_RS08040	ABUW_0170	NZ_CP008706.1	Q188145	Q189203	+	WP_000180049.1		alkene reductase	910.5455979	-1.802550038	0.07755718	-10.9163942	3.26E-24	2.55E-23	22.59345982
ABUW_RS18995	ABUW_3494	NZ_CP008706.1	Q342358	Q343563	-	WP_001084664.1		TICR03862 family flavoprotein	345.0468804	-1.80449744	0.93408529	-11.04289596	2.37E-28	2.36E-27	26.627098
ABUW_RS19795	ABUW_2424	NZ_CP008706.1	Q2410721	Q241080	+	WP_00104472.1		amino acid ABC transporter permease	6113.979628	-1.808116607	0.355307408	-5.083240004	3.7E-07	9.30E-07	6.03197051
ABUW_RS18610	ABUW_3417	NZ_CP008706.1	Q346570	Q346568	+	WP_000590865.1		proliprotein diacylglycerol ether transferase	1692.8671	-1.806664079	0.25919999	-6.96694724	8.80E-10	1.80E-09	18.84772495
ABUW_RS17535	ABUW_3602	NZ_CP008706.1	Q361933	Q361168	+			RNA- Thr	4673.477769	-1.807491291	0.269952482	-6.694484291	2.9E-11	7.44E-11	10.6247706
ABUW_RS10860	ABUW_2851	NZ_CP008706.1	Q296307	Q2964238	-	WP_000896578.1		bifunctional 3,4-dihydroxy-2-ketone-4-phosphate synthase/GTP cyclohydratase	480.2621055	-1.809734569	0.219624705	-8.24012944	1.72E-16	8.3E-16	15.06039898
ABUW_RS07470	ABUW_0995	NZ_CP008706.1	Q10623	Q107373	-	WP_001018189.1		bi-functional 3,4-dihydroxy-2-ketone-4-phosphate synthase/GTP cyclohydratase	8709.710993	-1.8118196	0.218972729	-8.599165499	8.03E-18	4.29E-17	16.36754271
ABUW_RS01465	ABUW_0294	NZ_CP008706.1	Q13080	Q130525	+	WP_001017040.1		type IV plus secretin PIQ family protein	3165.449165	-1.810813872	0.91610397	-11.21883195	3.26E-29	3.49E-28	27.45717457
ABUW_RS08605	ABUW_1167	NZ_CP008706.1	Q176584	Q1765379	-	WP_001029188.1		hypothetical protein	82.2292752	-1.82180571	0.233917249	-7.788244702	6.79E-15	2.96E-14	10.52870789
ABUW_RS06645	ABUW_1362	NZ_CP008706.1	Q137420	Q137678	+	WP_001085431.1		dicarboxylate/amino acid cation symporter	4123.145006	-1.824408855	0.218687723	-8.295939428	1.08E-16	5.28E-16	16.27736608
ABUW_RS1415	ABUW_2913	NZ_CP008706.1	Q292249	Q292763	+	WP_001141952.1		carbonic anhydrase	Q153.85559	-1.824183087	0.07325244	-10.70973662	9.16E-27	8.33E-26	25.073935
ABUW_RS07090	ABUW_0159	NZ_CP008706.1	Q176219	Q176375	-	WP_000194085.1		TonB-dependent siderophore receptor	5408.21811	-1.82552155	0.377184364	-4.839840588	1.30E-06	3.08E-06	5.51449483
ABUW_RS18795	ABUW_3454	NZ_CP008706.1	Q350174	Q3502345	+	WP_00017072.1		asparaginase	856.330021	-1.827330983	0.21849409	-8.426625469	3.56E-17	1.81E-16	17.64232143
ABUW_RS16335	ABUW_3221	NZ_CP008706.1	Q325917	Q325993	-			RNA- Pro	954.140052	-1.83142426	0.33218567	-5.94368789	3.50E-08	9.54E-08	7.02045825
ABUW_RS10405	ABUW_2892	NZ_CP008706.1	Q289820	Q290167	+	WP_000595799.1		CIM45 family transporter	3737.767202	-1.837610958	0.93496394	-9.496827407	2.16E-21	1.43E-20	19.84466396
ABUW_RS20210	no	NZ_CP008706.1	Q211445	Q214658	+	WP_000219721.1		hypothetical protein	718.987162	-1.842996067	0.68821797	-2.877926042	0.007407986	0.01649759	1.9395757
ABUW_RS18415	ABUW_3174	NZ_CP008706.1	Q320172	Q320722	+	WP_000973142.1	nuoE	NADH-quinone oxidoreductase subunit NuoE	15467.0391	-1.848312593	0.28789303	-6.428868273	1.30E-10	4.26E-10	19.37090401
ABUW_RS17310	ABUW_2876	NZ_CP008706.1	Q283136	Q283250	+	WP_001084663.1	pyrC	thymidylase	3906.959362	-1.848962767	0.156196991	-13.57837239	5.38E-42	1.25E-40	39.39030999
ABUW_RS20995	no	NZ_CP008706.1	Q299026	Q299154	+	WP_001819055.1		hypothetical protein	8.340742432	-1.849720966	0.741713017	-2.483792284	0.02638648	0.019007508	17.02174818
ABUW_RS17318	ABUW_3816	NZ_CP008706.1	Q382315	Q383197	+	WP_001803861.1	mtI	ribonuclease T	2362.840551	-1.8491971097	0.146862107	-12.622388197	1.59E-36	2.53E-35	34.59887148
ABUW_RS02250	ABUW_0458	NZ_CP008706.1	Q170499	Q171074	+	WP_000543071.1		xanthine phosphoribosyltransferase	2287.203375	-1.850036246	0.204006212	-9.068528967	12.1E-19	7.17E-19	18.14488084
ABUW_RS04440															

ABLU_RS4835	ABLU_0894	NZ_CP008706.1	89229	892368	-	WP_00016645.1	carA	glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit	8564.727879	-1.938406259	0.26622586	-7.281059245	3.3E-13	1.3E-12	11.882727
ABLU_RS500	ABLU_0448	NZ_CP008706.1	1269200	929015	-	WP_00018669.1		ABC transporter ATP-binding protein	902.974036	-1.939838269	0.242731235	-7.991702995	1.33E-15	6.05E-15	14.2884443
ABLU_RS0890	ABLU_0827	NZ_CP008706.1	162387	824456	+	WP_0000784432.1	eno	phosphopyruvate hydratase	24287.51993	-1.939804007	0.166225369	-1.24785519	2.09E-35	3.8E-34	33.50031292
ABLU_RS1955	ABLU_2873	NZ_CP008706.1	2862101	2882784	-	WP_01020244.1	ark	adenylate kinase	91028.67971	-1.940332878	0.163757355	-11.688295	2.8E-32	2.83E-31	30.54452156
ABLU_RS0595	ABLU_0333	NZ_CP008706.1	134007	945260	+	WP_000457893.1		serine hydroxymethyltransferase	9056.10559	-1.941601874	0.184588495	-10.51863824	7.09E-26	6.09E-25	24.21638271
ABLU_RS1045	ABLU_3099	NZ_CP008706.1	312433	312410	+	WP_000055594.1	pfl	aminocacyl- RNA hydrolase	5605.845596	-1.944893633	0.179801901	-11.05669478	2.03E-28	2.03E-27	26.69250396
ABLU_RS1045	ABLU_2709	NZ_CP008706.1	269193	2692722	-	WP_000423280.1		LyxR family transcriptional regulator	327.7681079	-1.946878398	0.259533443	-7.50454821	6.3E-14	2.61E-13	12.58335949
ABLU_RS18165	ABLU_2917	NZ_CP008706.1	2927564	2682022	-	WP_001027211.1	nfsA	Fe-S biogenesis protein NfsA	4343.830476	-1.947370745	0.166852099	-8.892558141	4.48E-23	3.30E-22	21.48148606
ABLU_RS1625	ABLU_1305	NZ_CP008706.1	316391	3160335	+	WP_01084189.1		RNA-dihydropyrimidine synthase	586.956988	-1.949471273	0.264107045	-7.380529569	1.58E-13	6.36E-13	12.9654288
ABLU_RS1885	ABLU_3273	NZ_CP008706.1	330567	3307020	-	WP_012300732.1	sis	RNA lysidine(24) synthetase Tis	697.1043529	-1.949722674	0.145644226	-13.3868678	7.22E-41	1.53E-39	38.81630857
ABLU_RS1645	ABLU_2271	NZ_CP008706.1	225662	2257869	-	WP_01011693.1		phosphoglycerate kinase	4507.690302	-1.951916641	0.157777385	-11.10106765	1.24E-28	1.27E-27	26.89619628
ABLU_RS0340	ABLU_0691	NZ_CP008706.1	698433	698508	+			RNA-Vai	1356.04106	-1.959676553	0.306094824	-6.402187826	1.53E-10	4.97E-10	9.303643611
ABLU_RS04430	ABLU_0903	NZ_CP008706.1	898936	899021	-			RNA-Leu	26.65423437	-1.960077213	0.600419736	-3.264544259	0.001096403	0.001007344	7.42710972
ABLU_RS0250	ABLU_0509	NZ_CP008706.1	519991	520067	+			RNA-Ile	805.813469	-1.960358452	0.345016621	-5.681924676	1.33E-08	3.74E-08	7.42710972
ABLU_RS1630	ABLU_3421	NZ_CP008706.1	3468384	3468893	+	WP_000312548.1		dihydrofolate reductase	1024.604444	-1.961050537	0.214000049	-9.164974712	4.96E-20	3.02E-19	58.5999306
ABLU_RS0480	ABLU_0907	NZ_CP008706.1	908980	16203	+	WP_01026789.1	serB	phosphoserine phosphatase SerB	3787.788393	-1.961944376	0.188226895	-14.9343896	1.0E-45	2.76E-44	43.55019032
ABLU_RS1750	ABLU_3595	NZ_CP008706.1	365865	3658678	-	WP_000832994.1	nuvG	transcription termination/intertermination protein NuvG	9055.55763	-1.962419009	0.220706962	-8.89148657	6.03E-19	3.45E-19	17.4621909
ABLU_RS1620	ABLU_3885	NZ_CP008706.1	3954183	3954665	-	WP_00094603.1	puvE	5-(carboxymethyl)pyridoxal ribonucleotide mutase	2890.894609	-1.965762289	0.172397591	-11.40240281	4.06E-30	4.81E-29	28.33629907
ABLU_RS0330	ABLU_0681	NZ_CP008706.1	68480	68688	+	WP_0000505931.1		methyl-accepting chemotaxis protein	870.1720525	-1.965913369	0.230662353	-8.51821891	1.7E-17	8.85E-17	10.0487690
ABLU_RS0080	ABLU_0016	NZ_CP008706.1	8888	8904	+			RNA-Ile	16562.46857	-1.966929197	0.342737194	-12.738885859	9.5E-09	2.71E-08	7.56730730
ABLU_RS0470	ABLU_0739	NZ_CP008706.1	1736031	1737227	-	WP_000184643.1		1-deoxy-D-xylose-5-phosphate reductoisomerase	5527.045310	-1.971216401	0.165710595	-11.90089627	1.97E-32	1.53E-31	30.81830834
ABLU_RS0235	ABLU_0475	NZ_CP008706.1	487753	487835	+			RNA-Ile	5548.671819	-1.973636402	0.343597353	-5.751983786	8.82E-09	2.52E-08	7.598599459
ABLU_RS1975	no	NZ_CP008706.1	3321274	3321825	-	WP_012297364.1	intC	translation initiation factor F-3	9125.632424	-1.974739028	0.188760317	-10.47003864	1.91E-25	1.01E-24	23.99967863
ABLU_RS07875	ABLU_810	NZ_CP008706.1	1606674	1606732	+	WP_000221672.1	UDP-2,3-deacetylcoenzyme diphosphate	774.8509653	-1.976450347	0.177569174	-11.10059377	8.90E-29	9.26E-28	27.0358461	
ABLU_RS1885	ABLU_3063	NZ_CP008706.1	300052	300986	-	WP_000246374.1	rpsL	30S ribosomal protein S12	38230.13657	-1.984054472	0.22185933	-8.97192083	2.93E-19	1.7E-18	17.7670339
ABLU_RS19015	ABLU_3093	NZ_CP008706.1	312651	3121665	+			RNA-Gln	527.5723739	-1.990089966	0.334529238	-5.94826854	2.70E-09	7.98E-09	8.09797790
ABLU_RS07795	ABLU_0696	NZ_CP008706.1	562937	569416	-	WP_002014361.1		MFS transporter	496.3089794	-1.990408466	0.212421607	-9.370188619	7.25E-21	4.64E-20	19.3348022
ABLU_RS19375	ABLU_3755	NZ_CP008706.1	3744837	3746195	-	WP_000729980.1		NCS2 family permease	1374.1321845	-1.99183372	0.189798597	-10.45208873	9.39E-26	8.03E-25	24.09528445
ABLU_RS0465	ABLU_1384	NZ_CP008706.1	328191	327015	-	WP_00046501.1		hydropathic protein	527.3788477	-2.000019171	0.219605543	-9.094800507	9.47E-20	5.67E-19	20.9441454
ABLU_RS1970	ABLU_3529	NZ_CP008706.1	358914	3589733	+	WP_00061221.1		2-oxoglutarate-dependent hydroxylase	2723.244778	-2.003425446	0.209542484	-9.562949686	1.97E-21	7.80E-21	26.2662795
ABLU_RS16420	ABLU_3175	NZ_CP008706.1	3201736	3203523	-	WP_000652160.1	nuoG	NADH-quinone oxidoreductase subunit QD	25903.6877	-2.007417771	0.281869268	-7.121804335	1.07E-12	4.07E-12	11.39504059
ABLU_RS17295	ABLU_3554	NZ_CP008706.1	3610240	361689	-	WP_01118150.1	rmbB	23S rRNA (cytosine(225)-2'-O-methyltransferase RmbB	966.970679	-2.01083186	0.161922241	-12.41698888	2.1E-35	3.8E-34	33.49757288
ABLU_RS17485	ABLU_633	NZ_CP008706.1	519763	520032	-	WP_01006304.1	fs	GlnA-binding transcriptional regulator Fts	556.1875505	-2.012470147	0.214543681	-10.38055616	5.59E-21	4.24E-20	19.37283414
ABLU_RS1405	ABLU_3172	NZ_CP008706.1	319789	3199873	-	WP_00010097.1	nuoG	NADH-quinone oxidoreductase subunit NuoG	6159.78942	-2.014102131	0.293207864	-6.87368054	6.28E-12	2.26E-11	10.6489596
ABLU_RS17690	ABLU_3633	NZ_CP008706.1	3636272	3639235	-	WP_01019121.1		femous iron transport protein A	2492.346434	-2.017899921	0.249620089	-8.084244849	6.26E-15	2.9E-15	14.53610701
ABLU_RS04450	ABLU_0907	NZ_CP008706.1	91004	902252	+	WP_01228510.1	tdp	thylakoid tetraphosphate dihydrogenase/methylenetetrahydrofolate cyclase	7404.85964	-2.02342488	0.209586647	-6.654381713	4.7E-22	3.16E-21	40.0248932
ABLU_RS0585	ABLU_1611	NZ_CP008706.1	169163	169722	+	WP_000035083.1	elo	elongation factor F	337.6106363	-2.023884676	0.207031704	-9.714292724	1.45E-22	1.03E-21	20.88716278
ABLU_RS03340	ABLU_0679	NZ_CP008706.1	681804	684166	+	WP_001010106.1		response regulator	1923.299273	-2.025089214	0.196680607	-10.29610049	7.34E-25	5.97E-24	23.22402567
ABLU_RS07725	ABLU_0682	NZ_CP008706.1	569758	571797	+	WP_012300567.1	kdpB	potassium-transporting ATPase subunit KdpB	246.7248029	-2.029639403	0.200724334	-10.11671196	4.9E-24	3.82E-23	22.41793664
ABLU_RS16470	ABLU_3185	NZ_CP008706.1	321523	324536	+	WP_000025826.1		ribonucleotide-diphosphate reductase subunit beta	2689.112616	-2.032557384	0.196046698	-11.26277192	1.05E-29	2.17E-28	27.66340247
ABLU_RS18965	ABLU_3895	NZ_CP008706.1	3936232	3946197	+	WP_000052288.1	guaD	guanine deaminase	1380.433526	-2.034197104	0.195053488	-10.85217733	1.55E-24	2.30E-23	23.8086754
ABLU_RS16765	ABLU_3042	NZ_CP008706.1	3067499	3069211	-	WP_000661612.1	dsf	dUTP deaminase	803.3596598	-2.04017876	0.175568581	-11.62035219	3.25E-31	3.93E-30	29.4060745
ABLU_RS07890	ABLU_814	NZ_CP008706.1	807409	807919	-	WP_000099661.1		peptidyl-prolyl cis-trans isomerase	8065.265	-2.042979616	0.220428197	-9.268324296	1.89E-20	1.26E-19	18.9231979
ABLU_RS18940	ABLU_3890	NZ_CP008706.1	3958282	3958878	+	WP_000051338.1		undecaprenyl-diphosphate	367.8492863	-2.069213372	0.210614861	-9.802291081	1.08E-22	7.88E-22	21.6347378
ABLU_RS18940	ABLU_3777	NZ_CP008706.1	3758762	3768783	-	WP_010186685.1	bmG	branched-chain amino acid transport system E carrier protein	4073.025376	-2.069894784	0.235607165	-8.785364333	1.56E-18	8.72E-18	17.0544833
ABLU_RS1740	ABLU_3037	NZ_CP008706.1	3003600	3064105	-	WP_000732976.1		bacteriohemerythrin	7815.817915	-2.076829889	0.322523276	-6.439140161	1.20E-10	3.94E-10	9.404403778
ABLU_RS04445	ABLU_0734	NZ_CP008706.1	1731685	1733028	+	WP_000856681.1	rnoD	30S ribosomal protein S12 methyltransferase RnoD	3784.765729	-2.081973563	0.17490856	-11.9032104	1.76E-32	1.50E-31	30.82390874
ABLU_RS03940	ABLU_0679	NZ_CP008706.1	681804	684166	+	WP_001010106.1		heavymetal-associated domain-containing protein	1418.196303	-2.085666719	0.370174756	-5.634275931	1.16E-08	4.89E-08	7.330619141
ABLU_RS18680	ABLU_2278	NZ_CP008706.1	2283456	2284175	+	WP_010116532.1		DUF1275 domain-containing protein	8383.876519	-2.085829468	0.187694485	-11.1025453	1.22E-28	1.25E-27	26.90308999
ABLU_RS18780	ABLU_3451	NZ_CP008706.1	3497362	3494840	+	WP_000862762.1	asd	aspartate-semialdehyde hydroxymethyltransferase	5789.966179	-2.09200193	0.250312835	-8.357450568	6.40E-17	3.2E-16	15.49349497
ABLU_RS02516	ABLU_0532	NZ_CP008706.1	541022	541051	-	WP_000051669.1	yajC	proteintyrosine phosphatase subunit YajC	3581.923945	-2.09501188	0.183144204	-10.84487057	2.06E-27	1.93E-26	25.7444269
ABLU_RS03330	ABLU_0677	NZ_CP008706.1	682476	683114	+	WP_000858514.1		hydropathic protein	105.5958524	-2.095531932	0.24287287	-6.648955374	5.20E-18	2.8E-17	15.9259368
ABLU_RS04645	ABLU_0738	NZ_CP008706.1	1735206	1736303	+	WP_000893489.1		phosphatidate cytidyltransferase	5468.340154	-2.010772225	0.187035827	-11.23192417	2.84E-29	3.05E-28	27.51670016
ABLU_RS04490	ABLU_0737	NZ_CP008706.1	1734454	1735206	+	WP_000102222.1	upsG	6-trans, poly-cis-epsilon-aminocaproate transferase	3193.332732	-2.101919187	0.177580747	-11.83336646	6.62E-32	3.37E-31	40.1723701
ABLU_RS0295	ABLU_0262	NZ_CP008706.1	279723	281084	+	WP_000090021.1	etfA	energy-dependent translocation thiolate protein EtfA	27429.015219	-2.103444713	0.197933226	-11.69989427	1.28E-31	1.57E-30	29.80410035
ABLU_RS18850	ABLU_3660	NZ_CP008706.1	3680280	3681740	-	WP_010126196.1	tsf	elongation factor Tsf	72138.72487	-2.103636239	0.211602214	-9.84819696	5.57E-23	2.26E-22	21.71686877
ABLU_RS02940	ABLU_0598	NZ_CP008706.1	595739	597157	-	WP_0000986451.1	aspB	aspartate--RNA ligase	26296.28745	-2.110613367	0.193420147	-10.88890531	1.30E-27	1.23E-26	25.91009489
ABLU_RS04335	ABLU_0924	NZ_CP008706.1	912031	912336	-	WP_000948355.1	hpxK	protease HpxK	9940.750187	-2.111971299	0.310709562	-6.765306241	1.33E-11	4.66	

ABUW_RS1615	ABUW_3722	NZ_CP008706.1	3780308	3781462	+	WP_00075285.1		LysM peptidoglycan-binding domain-containing protein	1542.025642	-2.250907683	0.172980755	-13.0124746	1.045E-38	1.96E-37	36.70774393																
ABUW_RS1650	ABUW_3720	NZ_CP008706.1	3739994	314.054	-	WP_00015142.1	bioA	adenosylmethionine-8- amino- 7- oxononanoate transaminase	3760.010881	-2.25171713	0.1634.6082	33.77904245	3.4E-43	8.42E-42	10.01468791																
ABUW_RS17515	ABUW_3598	NZ_CP008706.1	3695338	3605028	-	WP_00102961.0	tuf	elongation factor Tu	18728.8966	-2.260673023	0.22018415	10.26873042	9.95E-25	8.00E-24	23.05969101																
ABUW_RS17445	ABUW_3584	NZ_CP008706.1	3642842	3544266	-	WP_00094804.1		TRAP transporter large permease subunit	30.6105.945	-2.264788197	0.222652653	9.9035709	4.02E-23	2.96E-22	21.52870829																
ABUW_RS1280	ABUW_2319	NZ_CP008706.1	2304109	2304498	-	WP_00161759.1		PACe efflux transporter	486.7408237	-2.265.923084	0.534959152	4.237793025	2.24E-05	4.7E-05	4.326979993																
ABUW_RS15020	ABUW_3094	NZ_CP008706.1	3121693	3121977	+			IRN4- Gln	266.3045712	-2.268022581	0.306065763	-7.4.0245941	1.26E-13	5.52E-13	12.29073034																
ABUW_RS17830	ABUW_3661	NZ_CP008706.1	3727648	3722837	-	WP_0005.97809.1		BL3-like element BspU1 family transposase	707.609.856	-2.26918792	0.233776396	-9.706368275	2.83E-22	1.96E-21	20.70774393																
ABUW_RS1075	ABUW_2277	NZ_CP008706.1	2262287	2263489	+	WP_000889009.1	satI	serine/threonine protein SerI	4686.74791	-2.274696114	0.1923832	-11.82736994	2.94E-32	3.77E-31	42.24265865																
ABUW_RS1635	ABUW_3402	NZ_CP008706.1	3447176	3448510	-	WP_001188432.1		Trigger factor	29049.37583	-2.276473777	0.16500306	-1.75509867	4.75E-43	1.9E-41	40.93554201																
ABUW_RS01290	ABUW_0263	NZ_CP008706.1	281653	282156	+	WP_000272434.1		hypothetical protein	4441725076	-2.279287621	0.255587614	-8.97832847	4.76E-19	2.74E-18	17.56224944																
ABUW_RS04890	ABUW_0997	NZ_CP008706.1	1008708	1009115	-	WP_001273591.1	ybgC	tol-pal-system-associated acyl-CoA thioesterase	1707.351791	-2.282526803	0.218532848	-10.44477672	1.55E-25	13.E-24	23.8827287																
ABUW_RS1515	ABUW_3317	NZ_CP008706.1	3107434	3108078	-	WP_00016597.1	bioD	ATP-dependent dehydrobin synthetase BioD	998.9619666	-2.283087944	0.146886072	-15.54325689	1.77E-54	6.78E-53	52.9877031																
ABUW_RS05980	ABUW_1224	NZ_CP008706.1	1264544	1265926	-	WP_000994842.1		adenosylhomocysteine	924.919.852	-2.286.96367	0.19018628	-12.02523097	2.62E-33	3.59E-32	31.44490555																
ABUW_RS0705	ABUW_0346	NZ_CP008706.1	3673758	368635	+	WP_000360761.1		hypothetical protein	4246.64182	-2.288185001	0.23566822	-8.51938989	1.49E-76	1.46E-74	73.8356474																
ABUW_RS03210	ABUW_0652	NZ_CP008706.1	1657052	1658512	-	WP_000004874.1		amino acid permease	4980.014265	-2.288745872	0.223808586	-10.22635417	15.9E-24	1.20E-23	22.92088875																
ABUW_RS1545	ABUW_3119	NZ_CP008706.1	3108825	3109982	-	WP_000054321.1		8- amino- 7- oxononanoate synthase	1540.319106	-2.289223565	0.163726619	-13.9816878	2.0E-44	5.22E-43	22.8232395																
ABUW_RS03335	ABUW_0678	NZ_CP008706.1	1683387	1683780	+	WP_000389061.1	piIG	teaching motility response regulator PiG	5691783327	-2.284464657	0.255426777	-8.963220672	3.15E-19	1.83E-18	7.73754891																
ABUW_RS0405	ABUW_1631	NZ_CP008706.1	1620051	1630628	-	WP_001026286.1		MFS transporter	204.7277776	-2.30596167	0.225284314	-10.23576398	1.37E-24	1.09E-23	22.9620735																
ABUW_RS03345	ABUW_0680	NZ_CP008706.1	1684227	1684763	+	WP_000729762.1		putine-binding chemotaxis protein CheW	2158.743622	-2.306748325	0.281637933	-8.81566835	3.18E-18	6.64E-18	17.1783192																
ABUW_RS02000	ABUW_0041	NZ_CP008706.1	48599	49789	-	WP_001097146.1		MFS transporter	339.7205052	-2.30730959	0.239884689	-9.61841033	6.69E-22	4.53E-21	20.74339018																
ABUW_RS1620	ABUW_2307	NZ_CP008706.1	2292146	2293135	+	WP_000175300.1	bioB	biotin synthase BioB	10798.82802	-2.320516378	0.18373196	-16.76271849	4.57E-63	2.88E-61	60.54060751																
ABUW_RS16920	ABUW_3278	NZ_CP008706.1	3319238	3321838	+	WP_000898769.1		hypothetical protein	20722.671928	-2.332018107	0.340692906	-16.844927276	7.65E-12	1.72E-11	10.565431																
ABUW_RS16885	ABUW_3838	NZ_CP008706.1	3906199	3907044	+	WP_000026026.1		carboxylating nucleotide-nucleotide diphosphorylase	597.7837611	-2.332235719	0.236279318	-19.87087297	5.58E-23	4.95E-22	21.83727814																
ABUW_RS16005	ABUW_3968	NZ_CP008706.1	3969443	3971003	-	WP_001188000.1	ydC	membrane protein insertase YdC	33583.20947	-2.335261933	0.216995029	-15.95899096	1.87E-27	1.75E-26	25.75969615																
ABUW_RS17020	ABUW_2823	NZ_CP008706.1	2828665	2830023	+	WP_001986427.1	argG	argininosuccinate synthase	8253.635988	-2.367888453	0.237875505	-9.95431.94	2.4E-23	1.8E-22	21.1423243																
ABUW_RS07070	ABUW_1451	NZ_CP008706.1	1443681	1444127	-	WP_00020940.1		GaIII/Pyv' domain-containing protein	20557.98746	-2.36919968	0.183477968	-12.9127203	3.82E-38	6.96E-37	36.9739976																
ABUW_RS04970	ABUW_013	NZ_CP008706.1	1824711	1825441	-	WP_00057724.1	queE	7- carboxy- 7- deazaguanine synthase QueE	5361255099	-2.37074008	0.205759005	-11.5219024	1.02E-30	1.20E-29	28.92088875																
ABUW_RS16090	ABUW_3198	NZ_CP008706.1	310635	3131069	-	WP_000191001.1	fabG	3- oxoacyl-ACP reductase FabG	4823.46471	-2.380691746	0.200191.6	-11.89741414	1.22E-32	1.59E-31	30.79860288																
ABUW_RS14875	ABUW_3065	NZ_CP008706.1	3092709	3093638	+	WP_000832710.1		beta- ketoseryl- ACP synthase II	44223.62646	-2.383748554	0.190526822	-12.67359994	5.88E-36	5.57E-37	35.758107																
ABUW_RS16500	ABUW_3819	NZ_CP008706.1	3875819	3876565	-	WP_001022772.1	tsrR	transcriptional regulator LsrR	9208.841217	-2.384551151	0.326406697	-17.088292362	1.35E-12	5.9E-12	11.2873503																
ABUW_RS03216	ABUW_0653	NZ_CP008706.1	1656534	1656547	-	WP_000371532.1		methyltransferase	2401.291798	-2.386490768	0.232104320	-9.46519465	2.93E-21	1.93E-20	10.71442499																
ABUW_RS00335	ABUW_0007	NZ_CP008706.1	17878	19609	-	WP_00061982.1		ATP-binding cassette domain-containing protein	6338.690281	-2.386781064	0.181229511	-13.06997638	13.9E-39	2.65E-38	37.57678413																
ABUW_RS03220	ABUW_0654	NZ_CP008706.1	1659610	1660668	-	WP_000078056.1		uracil xanthine permease	1750.287403	-2.392971287	0.312538931	-17.65554278	19.9E-14	8.10E-14	10.0915408																
ABUW_RS16025	ABUW_3095	NZ_CP008706.1	3121789	3121863	+			IRN4- Gln	198.176355	-2.393001951	0.183812572	-17.076693026	1.48E-12	5.57E-12	11.2541448																
ABUW_RS14440	ABUW_2974	NZ_CP008706.1	2998022	2991692	+	WP_001092229.1		hypothetical protein	8514026276	-2.39748765	0.274383338	-8.737273586	2.38E-19	13.E-17	16.8822787																
ABUW_RS03225	ABUW_0655	NZ_CP008706.1	161147	1622982	+	WP_00108092.1	typA	translational GTPase TypA	37234.40902	-2.400186637	0.233492124	-10.30521467	6.67E-25	5.47E-24	23.2420297																
<table> <tr> <td>sRNA20</td><td></td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td><td>no</td></tr> </table>																sRNA20		no	no	no	no	no	no	no	no	no	no	no	no	no	no
sRNA20		no	no	no	no	no	no	no	no	no	no	no	no	no	no																
ABUW_RS04245	ABUW_0865	NZ_CP008706.1	1844476	1845408	-	WP_000994655.1		rhodanese-related sulfotransferase	4834.555696	-2.410058648	0.220443167	-10.96000966	5.95E-28	5.80E-27	28.23657201																
ABUW_RS16235	ABUW_3176	NZ_CP008706.1	3203608	3204285	-	WP_000878003.1		NADH-quinone oxidoreductase subunit B	8071788965	-2.417983293	0.289267698	-16.58898249	6.33E-17	3.17E-16	5.48984074																
ABUW_RS01675	ABUW_0320	NZ_CP008706.1	334138	3344389	+	WP_000260334.1	pspP	SOS ribosomal protein S16	25973.41621	-2.428772544	0.2634885	-9.217755409	3.03E-20	1.87E-19	18.7281639																
ABUW_RS17000	ABUW_3841	NZ_CP008706.1	3810171	3919827	-	WP_001027322.1	iph	ribonuclease PH	4069185881	-2.429522599	0.195116817	-15.66263848	2.72E-55	1.95E-53	52.958560731																
ABUW_RS01655	ABUW_0316	NZ_CP008706.1	3338302	339210	+	WP_000149374.1		hypothetical protein	436.9271162	-2.435768915	0.240976578	-10.679073	5.10E-24	3.96E-23	22.40230451																
ABUW_RS16035	ABUW_3097	NZ_CP008706.1	3122066	3123016	+	WP_001133287.1		ribose- phosphate pyrophosphatase	3143110587	-2.438883766	0.230317919	-10.58920678	3.34E-26	2.95E-25	24.53017798																
ABUW_RS19485	ABUW_2361	NZ_CP008706.1	2347819	2348458	+	WP_001584788.1		rRNA methyltransferase	1384.045969	-2.4401179975	0.181282179	-11.07167273	4.77E-39	9.02E-38	37.0400516																
ABUW_RS04155	ABUW_0849	NZ_CP008706.1	1829992	1830249	+	WP_000201932.1	pmA	SOS ribosomal protein L27	30326.02303	-2.446109146	0.210006835	-11.7429947	7.67E-32	9.5E-31	30.0218148																
ABUW_RS1585	ABUW_2381	NZ_CP008706.1	2386857		-	WP_000114471.1		ATP-binding cassette domain-containing protein	719.963052	-2.474849683	0.4522316851	-5.472884668	4.43E-08	1.9E-07	6.92443309																
ABUW_RS18600	ABUW_3062	NZ_CP008706.1	3099882	3099352	-	WP_001181805.1	pslG	SOS ribosomal protein S7	687111.9824	-2.489550379	0.290729793	-11.84783493	2.2E-32	2.85E-31	30.5451545																
ABUW_RS02420	ABUW_0493	NZ_CP008706.1	505580	505546	-	WP_000224768.1	rpsL	SOS ribosomal protein S19	40333.8864	-2.489292912	0.217188897	-11.46249952	2.04E-30	2.34E-29	28.6307814																
ABUW_RS16040	ABUW_3098	NZ_CP008706.1	3123116	3123412	+	WP_001073422.1	ipfY	SOS ribosomal protein L25	8014.32645	-2.490270684	0.264203363	-19.44650481	3.50E-21	2.29E-20	19.64016452																
ABUW_RS17775	ABUW_3226	NZ_CP008706.1	3220330	3220296	+	WP_000001662.1	psrT	SOS ribosomal protein S20	5845.673991	-2.498523116	0.220061228	-11.35374789	7.1E-30	7.95E-29	28.0963287																
ABUW_RS17900	ABUW_2423	NZ_CP008706.1	2410066	2410731	-	WP_000418072.1		amino acid ABC transporter permease	108.884913	-2.501165831	0.1496983395	-5.325216639	1.0E-07	2.64E-07	6.75899073																
ABUW_RS18280	ABUW_3755	NZ_CP008706.1	3810187	3811675	-	WP_000210705.1	guaA	guanine- dependent GMP synthase	92269.38414	-2.506994681	0.228188815	-10.98745543	4.39E-28	4.32E-27	26.36451025																
ABUW_RS15165	ABUW_3732	NZ_CP008706.1	3789300	3790744	-	WP_000194811.1	alpD	FGF1 ATP synthase subunit beta	596844.2032	-2.508421545	0.2433219591	-10.30874025	6.43E-25	5.29E-24	27.31654433																
ABUW_RS01600	ABUW_0316	NZ_CP008706.1	3373784	3383395	+	WP_000079179.1		PIW family protein	353.5944366	-2.50983815	0.268510324	-13.742785657	8.99E-21	5.7E-20	29.2433359																
ABUW_RS10900	ABUW_2342	NZ_CP008706.1	2325711	2326802	+	WP_000816572.1	ychF	mtox- regulated ATPase YchF	3196.90602	-2.519337844	0.267918905	-9.369783549	2.77E-21	4.65E-20	19.33245705																
ABUW_RS16540	ABUW_2189	NZ_CP008706.1	2160091	2160978	+	WP_000118176.1		sulfate exporter TsdY/SatE family protein	9187.46087	-2.519141456	0.379147625	-16.646658736	3.06E-11	1.02E-10	9.99199928																
ABUW_RS01890	ABUW_0323	NZ_CP008706.1	345951	346319	+	WP_000014062.1	pslB	SOS ribosomal protein L19	33588.52231	-2.519354304	0.227345352	-11.08161784	1.54E-28	1.52E-27	28.8096																

ABUW_RS16790	ABUW_3453	NZ_CP008706.1	3500053	3501915	+	WP_000967566.1		hypothetical protein	1224.585304	-2.876190298	0.219120201	-13.49522814	1.67E-41	3.76E-40	39.42481268
ABUW_RS06040	ABUW_0336	NZ_CP008706.1	1279220	1280095	+	WP_0001025378.1		elongation factor Ts	41943.25274	-2.89343525	0.217604052	-13.2967894	2.42E-40	5.02E-39	38.29929628
ABUW_RS02425	ABUW_0448	NZ_CP008706.1	505559	505987	-	WP_000854895.1	rpIM	50S ribosomal protein L13	44506.47449	-2.931623182	0.21725242	-13.40362775	1.71E-41	3.82E-40	39.41793664
ABUW_RS04040	ABUW_0253	NZ_CP008706.1	266667	266742	+			RNA-Phe	53.84837325	-2.941513135	0.177396052	-5.094446537	3.50E-07	8.80E-07	6.055517328
ABUW_RS15270	ABUW_3145	NZ_CP008706.1	3170913	3171785	-	WP_001159880.1		5'-methylthioadenosine(S)-adenosylhomocysteine nucleosidase	878.1775849	-2.944494766	0.200005463	-14.71765649	4.97E-49	1.59E-47	46.79802088
ABUW_RS01545	ABUW_0314	NZ_CP008706.1	336833	337393	+	WP_002164578.1	pIV	type IV plus modification protein PIV	167.2603096	-2.955413197	0.323885739	-9.42463629	7.16E-20	4.33E-19	18.3035121
ABUW_RS02050	ABUW_0417	NZ_CP008706.1	437657	437974	+	WP_001062685.1	rpIX	50S ribosomal protein L24	44858.95409	-2.957839987	0.229723927	-12.87562869	6.17E-38	1.10E-36	35.95860731
ABUW_RS00710	ABUW_0143	NZ_CP008706.1	165698	165877	-	WP_001998816.1		TonB-dependent siderophore receptor	669.1208509	-2.963345071	0.383651002	-7.724064468	1.15E-14	4.83E-14	13.91605287
ABUW_RS01440	ABUW_0293	NZ_CP008706.1	312270	312797	+	WP_000959059.1		plus assembling protein PIP	402.4531548	-2.964273354	0.304580044	-12.88252934	7.31E-38	1.29E-36	35.88941029
ABUW_RS14710	ABUW_3031	NZ_CP008706.1	3058852	3059889	+	WP_000355491.1		type IV plus twiching motility protein PIT	604.5924693	-2.993196616	0.258262764	-11.56973354	4.65E-31	5.54E-30	29.25649024
ABUW_RS17835	ABUW_3663	NZ_CP008706.1	3722859	3723731	-	WP_000021528.1		signal peptidase I	237.5434144	-3.001339654	0.33743166	-8.894659304	5.86E-19	3.35E-19	17.47495195
ABUW_RS17270	ABUW_3549	NZ_CP008706.1	3605867	3607579	+	WP_001274987.1	pIB	type IV-A plus assembly ATPase PIB	1238.801225	-3.019002366	0.21451626	-14.23920179	5.23E-46	1.46E-44	43.83564714
ABUW_RS12335	ABUW_2727	NZ_CP008706.1	2714369	2715085	+	WP_000020060.1	tmB	tRNA(guanosine(46)-N7)-methyltransferase TmB	806.9630589	-3.024887983	0.262695456	-11.51480892	1.11E-30	1.30E-29	28.88605665
ABUW_RS16350	ABUW_3365	NZ_CP008706.1	3406102	3406905	-	WP_002027450.1		enoyl-ACP reductase	24203.58424	-3.030807101	0.210782323	-14.31095411	1.87E-46	5.42E-45	44.26600071
ABUW_RS00635	ABUW_0126	NZ_CP008706.1	143273	143998	-	WP_0010176274.1		ion channel protein Lx	2811.272538	-3.089032264	0.235892657	-12.00507598	3.51E-39	6.77E-38	37.16941193
ABUW_RS02045	ABUW_0418	NZ_CP008706.1	437279	437647	+	WP_001982634.1	rpIN	50S ribosomal protein T54	106725.8474	-3.089837024	0.245585923	-12.58190708	2.67E-36	4.20E-35	34.37675071
ABUW_RS02095	ABUW_0426	NZ_CP008706.1	441333	442652	+	WP_002000592.1	secY	preprotein translocase subunit SecY	174538.7486	-3.103716754	0.249728556	-12.42835741	1.83E-35	2.79E-34	33.5543958
ABUW_RS02055	ABUW_0418	NZ_CP008706.1	437990	438526	+	WP_000101917.1	rpIE	50S ribosomal protein L5	24190.0444	-3.11676418	0.263816068	-11.8024147	3.30E-32	4.21E-31	30.3757179
ABUW_RS02060	ABUW_0419	NZ_CP008706.1	438536	438841	+	WP_001074624.1	rpIN	50S ribosomal protein L14	45389.76961	-3.173365817	0.245715644	-12.91478949	3.71E-38	6.80E-37	36.16749199
ABUW_RS16180	ABUW_3735	NZ_CP008706.1	3793313	3793849	+	WP_000818995.1		FOF1ATP synthase subunit delta	50071.63658	-3.178545162	0.28276515	-11.30042855	13.1E-29	1.44E-28	27.84375751
ABUW_RS08280	ABUW_8996	NZ_CP008706.1	1693467	1694837	-	WP_000939648.1	accC	acetyl-CoA carboxylase biotin carboxylase subunit	23673.18733	-3.201064007	0.220529177	-14.51581352	9.62E-48	2.91E-46	45.53610701
ABUW_RS16185	ABUW_3736	NZ_CP008706.1	3793862	3794332	-	WP_001024691.1		FOF1ATP synthase subunit B	36085.43341	-3.211649283	0.293379587	-10.9470782	6.86E-28	6.65E-27	26.17717835
ABUW_RS16165	ABUW_3814	NZ_CP008706.1	3876585	3878252	-	WP_01857993.1	ldp	L-lactate permease	5075.973923	-3.226430373	0.349304368	-9.236730676	2.54E-20	1.57E-19	18.80410035
ABUW_RS02090	ABUW_0425	NZ_CP008706.1	440847	441287	+	WP_0001075340.1	rpIO	50S ribosomal protein L15	81988.17951	-3.23800658	0.264810253	-12.22764809	2.21E-34	3.71E-33	32.49894074
ABUW_RS16165	ABUW_3285	NZ_CP008706.1	3318233	3318427	-	WP_001096359.1	rpml	50S ribosomal protein L35	12405.93484	-3.256466586	0.241456903	-10.486714878	1.87E-41	4.16E-40	39.38299966
ABUW_RS02085	ABUW_0424	NZ_CP008706.1	440667	440843	+	WP_000849088.1	rpmlD	50S ribosomal protein L30	58027.68502	-3.271710881	0.265255851	-12.33439666	5.91E-35	8.73E-34	33.08968765
ABUW_RS16160	ABUW_3284	NZ_CP008706.1	3317882	3318221	-	WP_000124588.1	rpIT	50S ribosomal protein L20	33645.3677	-3.286732498	0.256917246	-12.70296172	1.60E-37	3.04E-36	35.51712642
ABUW_RS17275	ABUW_3550	NZ_CP008706.1	3607609	3608835	+	WP_000279216.1		type I secretion system F family protein	1140.985159	-3.28842493	0.217216337	-15.45922228	6.54E-54	2.44E-52	115.0261017
ABUW_RS02100	ABUW_0427	NZ_CP008706.1	442673	442789	+	WP_000867907.1	rpmlJ	50S ribosomal protein L36	9327.939558	-3.292927428	0.229195963	-14.52572458	8.33E-48	2.54E-46	45.59519663
ABUW_RS02005	ABUW_0408	NZ_CP008706.1	433778	434098	+	WP_001058538.1	rpIW	50S ribosomal protein L23	57055.1086	-3.335098406	0.295619273	-11.2819117	1.61E-29	1.77E-28	27.76202673
ABUW_RS02115	ABUW_0430	NZ_CP008706.1	443672	444298	+	WP_000155204.1	rpID	30S ribosomal protein S4	143627.8764	-3.33936771	0.272447487	-12.25692241	1.54E-34	2.23E-33	32.65199514
ABUW_RS02080	ABUW_0423	NZ_CP008706.1	440163	440660	+	WP_001141025.1	rpIE	50S ribosomal protein S5	127117.1713	-3.345282273	0.278884158	-11.99523951	3.76E-33	5.11E-32	31.62916791
ABUW_RS02075	ABUW_0422	NZ_CP008706.1	439810	440180	+	WP_001031194.1	rpIR	50S ribosomal protein L18	42395.19474	-3.366656469	0.282421258	-11.9206903	9.23E-33	1.23E-31	30.91009489
ABUW_RS02070	ABUW_0421	NZ_CP008706.1	439262	439795	+	WP_000091932.1	rpIF	50S ribosomal protein L6	77599.17305	-3.380191176	0.26042436	-12.97595064	1.60E-38	2.95E-37	36.53017798
ABUW_RS02100	ABUW_0431	NZ_CP008706.1	444316	445323	+	WP_000198631.1	rpOA	DNA-directed RNA polymerase subunit alpha	3172918397	-3.388204302	0.284737922	-11.8993785	1.16E-32	1.55E-31	30.8096683
ABUW_RS14435	ABUW_2973	NZ_CP008706.1	2989890	2990530	+	WP_000714073.1	mgo	malate dehydrogenase (quinone)	13528.92757	-3.44827299	0.279762167	-12.32573108	6.58E-35	9.68E-34	33.0142464
ABUW_RS02065	ABUW_0420	NZ_CP008706.1	438853	439248	+	WP_000062616.1	rpIH	30S ribosomal protein S8	14162.66771	-3.44935248	0.25390199	-10.58537494	4.89E-42	1.15E-40	39.93930216
ABUW_RS08270	ABUW_8998	NZ_CP008706.1	1695291	1695746	-	WP_000099412.1	aroQ	type I3-dehydroquininate dehydratase	2697.680364	-3.487247655	0.12365886	-28.20099853	5.68E-175	1.16E-171	170.9393022
ABUW_RS02125	ABUW_0432	NZ_CP008706.1	445342	445719	+	WP_001021380.1	rpIQ	50S ribosomal protein L17	87978.97395	-3.503322	0.255100527	-13.73148892	6.58E-43	1.59E-41	40.79860288
ABUW_RS02020	ABUW_0411	NZ_CP008706.1	435235	435564	+	WP_001982638.1	pIV	50S ribosomal protein L22	52252.33271	-3.583844737	0.318165433	-11.2640021	1.97E-29	2.76E-28	27.66958623
ABUW_RS01995	ABUW_0406	NZ_CP008706.1	432529	433167	+	WP_001982642.1	rpIC	50S ribosomal protein L3	151789.6693	-3.61250027	0.313766724	-11.5133139	1.61E-30	1.32E-29	28.87942607
ABUW_RS05005	ABUW_1020	NZ_CP008706.1	1031308	1031916	-	WP_000149921.1		alpha/beta hydrolase	280.8572397	-3.62166653	0.539849836	-6.709025903	1.96E-11	6.78E-11	10.16877031
ABUW_RS08265	ABUW_8997	NZ_CP008706.1	1694854	1695273	-	WP_000354611.1	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein	7165.670085	-3.659388789	0.215253883	-17.00033608	8.16E-65	5.58E-63	62.2533658
ABUW_RS02030	ABUW_0413	NZ_CP008706.1	436322	436735	+	WP_000941215.1	rpIP	50S ribosomal protein L16	174795.373	-3.667174094	0.315325235	-11.61828966	3.55E-31	4.27E-30	29.36957212
ABUW_RS02105	ABUW_0428	NZ_CP008706.1	442897	443253	+	WP_000090815.1	rpIM	30S ribosomal protein S13	81939.95891	-3.675617917	0.279835694	-13.13491452	2.08E-39	4.08E-38	37.38933984
ABUW_RS05010	ABUW_1021	NZ_CP008706.1	1031947	1032954	+	WP_001021600.1		sulfate ABC transporter substrate-binding protein	524.9851564	-3.68976358	0.585058815	-6.306654108	2.85E-10	9.09E-10	9.041436117
ABUW_RS02000	ABUW_0407	NZ_CP008706.1	433179	433781	+	WP_001050255.1	rpID	50S ribosomal protein L4	190424.3185	-3.724835051	0.332482391	-11.20310473	3.94E-29	4.72E-28	27.3757179
ABUW_RS14420	ABUW_2970	NZ_CP008706.1	2984356	2985159	+	WP_000196965.1	betI	transcriptional regulator BetI	4254.12659	-3.744827766	0.375648588	-9.96896362	2.08E-23	1.57E-22	21.80410035
ABUW_RS02035	ABUW_0414	NZ_CP008706.1	436735	436932	+	WP_000849928.1	rpmlC	50S ribosomal protein L29	45189.28456	-3.757469668	0.315161082	-11.92237838	9.05E-33	1.21E-31	30.91721463
ABUW_RS08165	ABUW_1769	NZ_CP008706.1	1766667	1767173	+	WP_000734811.1		PEGA domain-containing protein	206.5046435	-3.763480564	0.297498469	-12.65041993	1.11E-36	1.29E-35	34.74714697
ABUW_RS02025	ABUW_0412	NZ_CP008706.1	435566	436318	+	WP_000529922.1	rpSC	50S ribosomal protein S3	129866.0493	-3.767510213	0.321688887	-11.72331973	9.68E-32	1.70E-30	29.8208197
ABUW_RS02110	ABUW_0429	NZ_CP008706.1	443273	443659	+	WP_001044016.1	rpSK	30S ribosomal protein S11	59266.30441	-3.7705923	0.278466384	-13.54056546	9.01E-42	2.06E-40	39.68618278
ABUW_RS14450	ABUW_2976	NZ_CP008706.1	2992193	2993527	+	WP_001027133.1		amino acid permease	704.2848933	-3.786790633	0.238699162	-15.86427991	1.03E-58	5.01E-55	54.30016936
ABUW_RS02010	ABUW_0409	NZ_CP008706.1	434110	434934	+	WP_001021945.1	rpIB	50S ribosomal protein L2	171297.5468	-3.825551035	0.31610947	-12.10198176	1.03E-33	1.43E-32	31.84669396
ABUW_RS14430	ABUW_2972	NZ_CP008706.1	2986720	2988378	+	WP_001021934.1	betA	choline dehydrogenase	5009.563738	-3.832033599	0.449898106	-8.51636377	1.65E-17	8.68E-17	16.0148027
ABUW_RS02015	ABUW_0410	NZ_CP008706.1	434948	435223	+	WP_001131819.1	rpS5	30S ribosomal protein S19	97612.51417	-3.914342002	0.337833478	-11.58655383	4.82E-31	5.73E-30	29.21945438
ABUW_RS08010	ABUW_1641	NZ_CP008706.1	1637480	1637818	+	WP_001024308.1		hypothetical protein	2614524357						

ABUW_R507960	ABUW_1631	NZ_CP008706.1	162862	162902	+	WP_000750672.1		spore coat protein U domain-containing protein	7973.259285	9.240392697	0.41784272	22.11452362	2.29E-108	4.86E-06	105.3105036
ABUW_R50025	ABUW_2064	NZ_CP008706.1	204977	204823	-	WP_000414010.1		hypothetical protein	395.3538908	9.98245717	0.69120609	13.3090011	2.05E-40	3.29E-39	38.4822745
ABUW_R509050	ABUW_1859	NZ_CP008706.1	185629	185628	+	WP_000387550.1		hypothetical protein	559.554375	9.93852478	0.522787359	17.58621901	3.14E-69	1.30E-67	66.8842675
ABUW_R50005	ABUW_2060	NZ_CP008706.1	204577	204192	-	WP_00127338.1		hypothetical protein	327.167935	9.99029711	0.475603188	8.90293702	1.08E-79	6.79E-77	77.8685431
ABUW_R51915	ABUW_1923	NZ_CP008706.1	1943284	194474	+	WP_000404190.1		teishase-4-phosphate synthase	9244.358405	9.930527545	0.41846455	2157934197	2.81E-103	4.53E-91	100.3442861
ABUW_R509060	ABUW_1961	NZ_CP008706.1	195796	195473	+	WP_00184464.1		aromatic ring-hydroxylating dioxygenase subunit alpha	1047.428429	8.78619778	0.434833461	20.245427	7.82E-91	6.65E-89	88.1972343
ABUW_R51330	ABUW_1971	NZ_CP008706.1	1983396	1985072	-	WP_00180661.1		mechanosensitive ion channel	4149.22789	8.727432938	0.301077035	28.95852011	2.19E-94	2.21E-91	80.6559985
ABUW_R509065	ABUW_1862	NZ_CP008706.1	1836484	1858969	+	WP_001850937.1		aromatic ring-hydroxylating dioxygenase subunit beta	714.8232945	8.670386918	0.424702719	20.4181053	1.23E-92	1.07E-90	89.96923783
ABUW_R513300	ABUW_2530	NZ_CP008706.1	2521848	2525221	-	WP_001160642.1		enoyl-CoA hydratase/isomerase family protein	734.6383576	8.65160187	0.51687859	16.80298721	2.32E-63	8.06E-62	61.05956634
ABUW_R50765	ABUW_1468	NZ_CP008706.1	1457939	1458733	+	WP_000368984.1		PGC-1 family deacetylase	1565.513356	8.635421607	0.439068092	19.66761067	4.09E-86	2.99E-84	83.52309859
ABUW_R509045	ABUW_1858	NZ_CP008706.1	1855092	1856240	+	WP_085922623.1		acyl-CoA dehydrogenase family protein	206.1651671	8.620816189	0.603272025	11.29009009	2.52E-46	5.08E-45	44.29394498
ABUW_R507500	ABUW_1636	NZ_CP008706.1	152327	152557	-	WP_000889008.1		hypothetical protein	54.86.89278	8.587029502	0.408294599	21.03143351	3.38E-98	4.47E-96	95.35016903
ABUW_R51850	ABUW_2435	NZ_CP008706.1	2423144	2424022	+	WP_000432325.1		glucose-1-dehydrogenase	1873.767352	8.416243084	0.456801043	18.41186506	1.07E-75	5.98E-74	73.22316554
ABUW_R51860	ABUW_2437	NZ_CP008706.1	2426277	2427686	-	WP_001145690.1		iron-containing redox enzyme family protein	67.30.685542	8.363319714	0.414391656	20.18216489	1.40E-90	1.10E-88	87.94622656
ABUW_R51320	ABUW_2534	NZ_CP008706.1	2525000	2525390	-	WP_000389648.1	paal	12-phenylacetyl-CoA epoxidase subunit B	2333.557698	8.314062256	0.600287878	18.8501298	1.27E-43	2.33E-42	41.63348911
ABUW_R507800	ABUW_1469	NZ_CP008706.1	1458708	1459307	+	WP_000581927.1		class I SAM-dependent methyltransferase	1036.37545	8.311661595	0.430426443	19.3129501	4.40E-83	3.06E-81	80.5147289
ABUW_R507850	ABUW_1617	NZ_CP008706.1	1616977	1617951	+	WP_000947654.1		hypothetical protein	1143.003934	8.279542377	0.414807416	18.73634484	2.50E-78	1.50E-76	75.82252387
ABUW_R512310	ABUW_2532	NZ_CP008706.1	2523716	2524216	-	WP_001177936.1	paaj	phenylacetate-CoA oxygenase subunit PaaJ	257.10170063	8.264475415	0.533373454	15.49491928	3.75E-54	9.76E-53	52.0166255
ABUW_R509040	ABUW_1967	NZ_CP008706.1	1933946	1935055	+	WP_001821999.1		amidase	41.98.331482	8.216266219	0.580565166	16.7439628	1.25E-58	3.74E-57	56.42745558
ABUW_R509055	ABUW_1860	NZ_CP008706.1	1856639	1857196	+	WP_001010502.1		nuclear transport factor 2 family protein	479.0790308	8.954489922	0.424309562	19.30067437	5.30E-83	3.63E-81	80.44107369
ABUW_R51216	ABUW_2533	NZ_CP008706.1	2524232	2524987	-	WP_001161799.1	paac	phenylacetate-CoA oxygenase subunit PaaC	2868.519042	8.180186377	0.579356995	14.11643014	2.88E-45	5.58E-44	43.25300117
ABUW_R51325	ABUW_2503	NZ_CP008706.1	2525323	2526261	-	WP_000411028.1	paAa	phenylacetate-CoA epoxidase subunit A	8269.755897	8.569296909	0.587158466	18.82064198	8.14E-44	1.5E-42	41.82081676
ABUW_R51295	ABUW_2520	NZ_CP008706.1	2521057	2521948	-	WP_000382629.1		2-(1,2-epoxy-1,2-dihydrophenylacetyl)-CoA isomerase	1400.627279	8.182950354	0.411879722	19.7162817	1.76E-86	1.3E-84	83.881897
ABUW_R51305	ABUW_2531	NZ_CP008706.1	2522030	2523369	-	WP_000177461.1	paak	phenylacetate-CoA oxygenase/reductase subunit PaaK	1815.753594	8.097091734	0.558389902	11.5008257	1.20E-47	2.54E-46	45.59549009
ABUW_R502620	ABUW_0053	NZ_CP008706.1	58624	58782	-	WP_0004040267.1		DUF1028 domain-containing protein	5808.425003	8.0478787	0.352760002	22.81999526	3.33E-15	9.58E-13	10.2184666
ABUW_R508050	ABUW_1651	NZ_CP008706.1	1645792	1646262	+	WP_001021384.1		hypothetical protein	984.5032291	8.005230507	0.508106766	16.75501854	6.34E-56	1.74E-54	53.75973749
ABUW_R51250	ABUW_2730	NZ_CP008706.1	2716700	271875	-	WP_000260486.1		OmxA family protein	75.19.248165	7.986637105	0.203440468	39.16954494	0	0	nrNAI
ABUW_R512975	ABUW_2673	NZ_CP008706.1	2666326	2666784	-	WP_001158471.1		phenylacetate-CoA oxygenase/reductase subunit PaaK	4619.200979	7.925729072	0.384826072	20.59551558	3.00E-94	3.03E-92	91.51907969
ABUW_R513010	ABUW_2678	NZ_CP008706.1	2670707	2671000	+	WP_000644336.1		DUF4142 domain-containing protein	4259.376016	7.873897555	0.601801989	13.08401912	4.06E-39	6.16E-38	37.2107005
ABUW_R505435	ABUW_1111	NZ_CP008706.1	1129345	1130975	+	WP_001183471.1		aldehyde dehydrogenase family protein	129.13.9369	7.776372519	0.267523376	20.06797218	9.12E-86	1.23E-82	99.1118224
ABUW_R509070	ABUW_1963	NZ_CP008706.1	1935980	1935977	+	WP_000815905.1		SDR family oxidoreductase	955.5863172	7.749946628	0.42105846	18.3204411	1.51E-75	8.23E-74	73.08459073
ABUW_R507965	ABUW_1632	NZ_CP008706.1	1629185	1629699	+	WP_000713911.1		molecular chaperone	344.5361065	7.744833621	0.433053774	17.88424461	1.56E-71	7.08E-70	69.14979193
ABUW_R512725	ABUW_2621	NZ_CP008706.1	2618549	2619007	-	WP_001027331.1		hypothetical protein	494.1498428	7.661097107	0.37016822	20.89637016	3.73E-95	3.94E-93	92.40224067
ABUW_R507185	ABUW_1470	NZ_CP008706.1	1459304	1459948	+	WP_000590470.1		glycosyltransferase	1575.612586	7.447335459	0.404197072	19.38981296	1.59E-75	8.52E-74	73.06977631
ABUW_R512665	ABUW_2607	NZ_CP008706.1	2600772	2602025	-	WP_001887220.1		divalent metal cation transporter	3164.692455	7.322185059	0.40144985	21.516174	1.07E-72	7.1198814657	
ABUW_R511860	ABUW_2458	NZ_CP008706.1	2446955	2450437	+	WP_00117562.1		indolepyruvate ferredoxin oxidoreductase family protein	17079.54997	7.284519183	0.302208552	24.04883801	2.22E-128	8.95E-126	95.0411942
ABUW_R508700	ABUW_1917	NZ_CP008706.1	1932461	1933605	+	WP_000185517.1		hypothetical protein	4077.391826	7.2777549	0.355672235	20.46197084	4.70E-93	4.30E-91	90.3661612
ABUW_R505450	ABUW_1114	NZ_CP008706.1	1133350	1140499	+	WP_000383010.1		amino acid permease	1396.508443	7.275472236	0.278756478	26.09974232	3.67E-10	2.1E-107	116.6751933
ABUW_R51110	ABUW_2603	NZ_CP008706.1	2608716	2608731	+	WP_001188962.1		four-helix bundle copper-binding protein	7279.868477	7.258137784	0.456681059	15.89322165	7.06E-57	1.97E-55	54.70574326
ABUW_R51330	ABUW_2536	NZ_CP008706.1	2526527	2528629	+	WP_000808292.1	paaz	phenylacetyl-acyl degradation hydrolase family protein PaaZ	4627.007606	7.247496011	0.401460749	18.0671462	5.78E-73	2.77E-71	70.55747754
ABUW_R51050	ABUW_2604	NZ_CP008706.1	2597339	2599192	-	WP_001121974.1		5-oxopolypentenolone amide-oxylase family protein	1196.678075	7.218804156	0.32890423	19.9583239	8.46E-97	1.62E-94	103.7898452
ABUW_R51335	ABUW_1358	NZ_CP008706.1	1385300	1385527	+	WP_000543705.1		hypothetical protein	252.1943201	7.205105183	0.342598902	21.03069857	3.44E-98	4.47E-96	95.35016903
ABUW_R51260	ABUW_2606	NZ_CP008706.1	2599873	2600737	+	WP_000466077.1		LamB/Cst family protein	1423.19541	7.199978727	0.356697949	20.9581588	1.32E-90	1.09E-88	87.96318047
ABUW_R507970	ABUW_1633	NZ_CP008706.1	1629178	1632338	+	WP_000873962.1		ribitol biosynthetic outer membrane usher protein	2618.722312	7.172419643	0.348823199	20.50284697	2.02E-93	1.90E-91	92.7017692
ABUW_R511885	ABUW_2438	NZ_CP008706.1	2426002	2426481	+	WP_000482019.1		CtA family protein	815.37107182	7.11890441	0.371824172	9.23247389	2.87E-30	1.54E-30	8.19264336
ABUW_R513040	ABUW_2688	NZ_CP008706.1	2675924	2678382	-	WP_001027310.1		hypothetical protein	1393.96074	7.144045341	0.379542165	18.82279755	4.91E-79	3.04E-77	76.5164471
ABUW_R512645	ABUW_2603	NZ_CP008706.1	2599321	2597539	+	WP_001019100.1		ATP-grp domain-containing protein	22.10.22466	7.1281914	0.3104744	22.73930093	1.83E-14	4.61E-12	111.3391085
ABUW_R509075	ABUW_1864	NZ_CP008706.1	1859752	1860705	+	WP_000210290.1		oxidoreductase	306.7263758	7.111834	0.3819749	18.66356504	9.80E-78	5.81E-76	75.23615847
ABUW_R512015	ABUW_1637	NZ_CP008706.1	1615777	1615108	+	WP_000106125.1		flavin reductase family protein	519.5381652	7.045196625	0.601027941	11.72190043	9.85E-32	1.06E-30	92.9248233
ABUW_R51055	ABUW_2605	NZ_CP008706.1	2599155	2599961	+	WP_000276200.1		putative hydro-lyase	769.471035	7.008264273	0.37924015	16.47915462	3.01E-76	1.7E-74	73.7081612
ABUW_R503180	ABUW_0646	NZ_CP008706.1	651474	651917	-	WP_001107685.1		VOC family protein	6234.266871	6.979197532	0.349874747	19.94764069	1.57E-88	1.22E-86	85.91454675
ABUW_R511845	ABUW_2434	NZ_CP008706.1	2422589	2423002	+	WP_000988336.1		hypothetical protein	38.632602481	6.863807197	0.1048105	6.560964911	5.35E-11	1.66E-10	9.78004277
ABUW_R51290	ABUW_2528	NZ_CP008706.1	2519516	2521654	-	WP_001010574.1		3-hydroxyacyl-CoA dehydrogenase	16.15.155009	6.822419744	0.239439945	28.49323975	1.42E-178	1.94E-175	97.84181899
ABUW_R508085	ABUW_1659	NZ_CP008706.1	1652339	1652770	+	WP_000720299.1		hypothetical protein	280.6847332	6.768474395	0.50449487	14.81635755	4.85E-41	8.14E-40	39.08929887
ABUW_R506270	ABUW_1286	NZ_CP008706.1	1306198	1306541	+	WP_001833061.1		hypothetical protein	504.7512917	6.742962461	0.574473147	11.77363447	8.17E-32	9.07E-31	40.24272023
ABUW_R508045	ABUW_1649	NZ_CP008706.1	1645128	1645378	+	WP_001197474.1		hypothetical protein	1723.800466	6.690832276	0.323562482	20.67854063	5.39E-95	5.57E-93	92.2530683
ABUW_R511845	ABUW_2455	NZ_CP008706.1	2424667	2444658	+	WP_000419320.1		acetylpropiophionylthioester-CoA carboxylase subunit alpha	3837.508829	6.65108859	0.291495979	22.54802717	1.66E-110	3.46E-111	

ABUW_RS05225	ABUW_1064	NZ_CP008706.1	1074526	1075776	-	WP_00032526.1		glycosyltransferase family 2 protein	1291.489325	5.206480662	0.25834546	20.15558448	2.405E-90	1.906E-88	87.7243310
ABUW_RS10335	ABUW_2885	NZ_CP008706.1	2675287	2675631	-	WP_001004876.1		hypothetical protein	78.10128252	5.095193038	0.48445673	10.50952324	7.81E-26	6.10E-25	24.2487203
ABUW_RS1460	ABUW_3587	NZ_CP008706.1	3645093	3646249	-	WP_001034851.1		hypothetical protein	628.7108039	5.063319788	0.301850496	16.7820853	4.17E-63	1.44E-61	60.84269778
ABUW_RS1265	ABUW_2523	NZ_CP008706.1	251493	2516276	-	WP_001017164.1		Paal family thioesterase	68.10566517	4.994107148	0.33469195	12.65319672	1.07E-36	1.53E-35	34.81647439
ABUW_RS04045	ABUW_1726	NZ_CP008706.1	172323	1724800	-	WP_01052296.1		D-amino acid dehydrogenase	5169.933625	4.960242922	0.25575537	19.4177006	5.53E-84	3.19E-82	14.0833054
ABUW_RS17400	ABUW_3575	NZ_CP008706.1	3634022	3634689	-	WP_002019090.1		serine hydroxylase family protein	565.3272485	4.96378546	0.403441094	12.30360872	8.06E-35	1.1E-33	32.16571537
ABUW_RS00995	ABUW_1911	NZ_CP008706.1	199427	200194	-	WP_001020735.1		hypothetical protein	8551.7197251	4.87132075	0.305951945	16.92168275	4.43E-57	1.27E-55	54.89565621
ABUW_RS1615	ABUW_3325	NZ_CP008706.1	3360159	3362504	-	WP_000341857.1		heavy metal translocating P-type ATPase	1178.762756	4.854944237	0.357071389	13.59956467	4.20E-42	7.42E-41	40.1036108
ABUW_RS05230	ABUW_1065	NZ_CP008706.1	1075763	1076559	-	WP_000067479.1		hypothetical protein	495.8730488	4.828579164	0.264547381	16.25221003	1.19E-74	1.01E-72	71.99424351
ABUW_RS03285	ABUW_0667	NZ_CP008706.1	673231	673680	-	WP_000100594.1		SRPBCC family protein	567.163535	4.824568075	0.271010857	17.80218742	6.80E-71	2.98E-69	68.52579103
sRNA75		no	no	no	no	no	no	no	46.15842247	4.82187473	0.4089098	11.79202539	4.29E-32	4.82E-31	30.31734287
ABUW_RS16280	ABUW_3351	NZ_CP008706.1	3387175	3388038	-	WP_000037364.1		hypothetical protein	980.7425242	4.814285334	0.425160836	11.32271133	1.00E-29	9.91E-29	28.00378646
ABUW_RS14025	ABUW_2887	NZ_CP008706.1	2894092	2894571	-	WP_000749178.1		copper resistance protein NpE	12285.46824	4.793104061	0.329229632	14.5854395	5.10E-48	1.1E-46	45.95323327
ABUW_RS1915	ABUW_2099	NZ_CP008706.1	2081980	2082762	-	WP_000095311.1		thiolase family protein	16.78188232	4.785316439	0.344809429	13.87818486	8.89E-44	1.59E-42	11.71990887
ABUW_RS09265	ABUW_1903	NZ_CP008706.1	1903508	1903933	-	WP_000706933.1		hypothetical protein	18.6996649	4.778121028	0.468536885	10.9796196	2.02E-24	1.44E-23	22.8404763
ABUW_RS1475	ABUW_3186	NZ_CP008706.1	3215372	3218296	-	WP_000470123.1		hypothetical protein	57.16706206	4.764238382	0.240480251	9.8104981	2.38E-87	1.81E-85	84.74318188
ABUW_RS07820	ABUW_1011	NZ_CP008706.1	1097650	1097868	+	WP_000351255.1		hypothetical protein	132.3187892	4.695422549	0.442321854	10.61059798	2.66E-26	2.16E-25	24.70683637
ABUW_RS07680	ABUW_1672	NZ_CP008706.1	1660275	1651645	-	WP_000701635.1		3-hydroxyacyl-CoA dehydrogenase	810.9532237	4.660692165	0.32798867	14.20991916	7.95E-46	1.58E-44	43.8012344
ABUW_RS07685	ABUW_1673	NZ_CP008706.1	1651664	1652200	+	WP_000602467.1		acyl-CoA dehydrogenase family protein	17.97166408	4.653943279	0.328098783	11.8457678	1.14E-45	2.24E-44	43.64907181
ABUW_RS11725	ABUW_2410	NZ_CP008706.1	2396784	2397410	+	WP_001055876.1	yfcF	glutathione transferase	776.3962451	4.650616096	0.256646883	16.0208004	2.16E-73	1.05E-71	70.937376
ABUW_RS11930	ABUW_2452	NZ_CP008706.1	2439044	2440216	+	WP_001051363.1		isovaleryl-CoA dehydrogenase	2343.051086	4.618727969	0.359097171	12.85848661	7.91E-38	1.61E-36	35.53916778
ABUW_RS07690	ABUW_1574	NZ_CP008706.1	1562421	1564064	-	WP_000853306.1		AMP-binding protein	1054.602328	4.606551068	0.280674983	16.4124036	1.56E-60	4.95E-59	58.30573624
ABUW_RS16440	ABUW_3383	NZ_CP008706.1	3421482	3422033	-	WP_000665665.1		phosphatase PAP2 family protein	301.0802145	4.558778825	0.265925999	17.14303542	7.09E-66	2.72E-64	63.5665374
ABUW_RS07980	ABUW_1635	NZ_CP008706.1	1633375	1634245	+	WP_000721985.1		glutathione S-transferase family protein	468.2070354	4.543159227	0.267370298	16.9933432	9.20E-65	3.34E-63	62.47837065
ABUW_RS09260	ABUW_1902	NZ_CP008706.1	1902188	1903495	-	WP_000849575.1		sorbinoside dehydrogenase family protein	1069.888758	4.541103269	0.261930579	17.3376125	2.47E-67	1.84E-66	65.00709162
ABUW_RS12720	ABUW_2524	NZ_CP008706.1	2515354	2515959	-	WP_001112269.1		carbonic anhydrase	309.64431	4.540898062	0.27863344	20.8432810	1.75E-56	2.08E-54	93.88224685
ABUW_RS10380	ABUW_3106	NZ_CP008706.1	3102650	3101033	-	WP_000522226.1	lysM	peptidoglycan-binding protein LysM	110.1512442	4.53338745	0.264521886	17.0803649	7.72E-66	2.93E-64	63.53241033
ABUW_RS11730	ABUW_2411	NZ_CP008706.1	2397444	2398304	+	WP_000825223.1	yghU	glutathione-dependent disulfide-bond oxidoreductase	1291.196473	4.525682269	0.292344005	17.93099284	6.76E-72	3.17E-70	69.49959627
ABUW_RS02200	ABUW_2143	NZ_CP008706.1	2129710	2129874	-	WP_000846293.1		hypothetical protein	28.121597864	4.524388711	0.33717117	14.8167014	4.70E-41	7.92E-40	49.1205411
ABUW_RS10010	ABUW_2561	NZ_CP008706.1	2642754	2643221	-	WP_001104786.1		hypothetical protein	1239.2777022	4.519362277	0.306081837	11.76195629	2.58E-49	5.80E-48	47.23654758
ABUW_RS16140	ABUW_3322	NZ_CP008706.1	3357551	3357882	-	WP_000553610.1		hypothetical protein	926.5169002	4.493459174	0.40118414	11.20022173	4.07E-29	3.89E-28	27.4097529
ABUW_RS16615	ABUW_3217	NZ_CP008706.1	3249351	3250346	+	WP_000623034.1	add	adenosine deaminase	516.2517894	4.492679084	0.410499	10.86502991	1.69E-27	1.44E-26	25.83610207
ABUW_RS12900	ABUW_2658	NZ_CP008706.1	2654223	2654996	-	WP_002031934.1		DUF4882 family protein	375.148168	4.476776975	0.217789707	20.55503303	8.87E-94	6.89E-92	91.1810044
ABUW_RS04330	ABUW_2044	NZ_CP008706.1	2030665	2030773	-	WP_001370435.1		FdhF/YnfP family oxidoreductase	111.842605	4.454445205	0.249432576	17.85831177	2.49E-71	1.1E-69	68.19272629
ABUW_RS10170	ABUW_2317	NZ_CP008706.1	2310091	2310245	+	WP_000469288.1		hypothetical protein	770.2935559	4.427254674	0.360774247	12.27183741	1.29E-34	1.64E-33	32.7859884
ABUW_RS08390	ABUW_1723	NZ_CP008706.1	1721401	1721897	-	WP_0007071649.1		hypothetical protein	89.8443327	4.399628724	0.423965522	10.37732669	3.14E-25	2.35E-24	32.62802323
ABUW_RS08140	ABUW_1523	NZ_CP008706.1	152271	1522714	-	WP_000058166.1		hypothetical protein	1082.899022	4.380991183	0.340637951	12.8610649	7.45E-38	1.09E-36	35.16071958
ABUW_RS09270	ABUW_1904	NZ_CP008706.1	1904447	1904743	-	WP_001027736.1		antibiotic biosynthesis monooxygenase	316.8657159	4.377616716	0.255756248	17.1833883	1.10E-65	4.22E-64	63.3749894
ABUW_RS03990	ABUW_0628	NZ_CP008706.1	629273	629914	-	WP_000175332.1		peroxiredoxin	16.161628	4.372688664	0.369177551	11.84440383	2.30E-32	2.62E-31	30.28020999
ABUW_RS07985	ABUW_1936	NZ_CP008706.1	1934269	1935030	-	WP_000155428.1		SDR family NAD(P)-dependent oxidoreductase	390.9343749	4.369198494	0.312566724	13.97832258	2.11E-44	3.98E-43	42.00498332
ABUW_RS1340	ABUW_2128	NZ_CP008706.1	2102872	2104275	-	WP_000182742.1	lpdA	dihydrodipicolyl dehydrogenase	665.6628746	4.348781741	0.45863658	9.53954377	1.43E-21	1.82E-21	20.04943318
ABUW_RS1345	ABUW_2097	NZ_CP008706.1	2079357	2079998	-	WP_000103583.1		CoA transferase subunit B	733.8216324	4.340461122	0.340078339	12.7631912	2.63E-37	3.79E-36	45.21169006
ABUW_RS10345	ABUW_2529	NZ_CP008706.1	2114286	2116821	-	WP_000128728.1		2-oxo acid dehydrogenase subunit E2	634.8421235	4.296120047	0.425572659	10.09493433	5.82E-24	4.05E-23	32.30231912
ABUW_RS07425	ABUW_1621	NZ_CP008706.1	1606545	1607912	-	WP_000599794.1		sorbinoside dehydrogenase family protein	781.4867356	4.291166695	0.242663246	17.86362848	5.61E-70	2.35E-68	67.8283529
ABUW_RS07160	ABUW_1237	NZ_CP008706.1	125242	125931	-	WP_001045996.1	aspZ	aquaporin Z	671.712677	4.21912315	0.286866209	11.3671984	1.16E-50	2.83E-49	48.54820294
ABUW_RS16170	ABUW_3124	NZ_CP008706.1	3144782	3145975	-	WP_001099213.1		MP3 transporter	835.9190838	4.290600877	0.282742661	15.9732292	5.34E-52	1.31E-50	49.88241841
ABUW_RS09275	ABUW_1905	NZ_CP008706.1	1904783	1905424	-	WP_000201064.1		hydrolase	833.8059485	4.275247419	0.201233645	21.24492804	3.67E-100	5.10E-98	97.26222165
ABUW_RS13200	ABUW_2720	NZ_CP008706.1	2710743	2710748	+	WP_000002450.1		KTCS domain-containing protein	164.8343324	4.268872369	0.384201657	11.1102175	1.11E-28	1.03E-27	26.98742583
ABUW_RS12805	ABUW_2639	NZ_CP008706.1	2637592	2638434	-	WP_0010382436.1		universal stress protein	40.85148318	4.25757136	0.267613302	15.90942442	5.45E-57	1.54E-55	54.8164393
ABUW_RS16720	ABUW_10885	NZ_CP008706.1	107406	1081448	+	WP_019394543.1		lp-like domain-containing protein	50008.24393	4.242340585	0.204407659	20.75431233	1.10E-95	1.29E-93	92.88937362
ABUW_RS1825	ABUW_2451	NZ_CP008706.1	2438282	2438899	-	WP_000102693.1		TetR/KdcR family transcriptional regulator	3967.166207	4.220232038	0.253217916	16.66640378	2.30E-62	7.66E-61	60.1681842
ABUW_RS17105	ABUW_2561	NZ_CP008706.1	2564334	2564664	+	WP_000207459.1		MerR family transcriptional regulator	624.2330037	4.191450701	0.324275308	12.92559317	3.23E-38	4.82E-37	36.31723631
sRNA27		no	no	no	no	no	no	no	240.0879551	4.164393293	0.264363096	15.72551954	6.60E-56	1.80E-54	53.74574994
ABUW_RS03655	ABUW_0742	NZ_CP008706.1	743342	744103	-	WP_000307140.1		hypothetical protein	81.24272504	4.15879523	0.314487687	13.0251986	2.19E-39	3.34E-38	37.86327771
ABUW_RS10220	ABUW_1206	NZ_CP008706.1	123701	1232327	-	WP_000104166.1		hydrolase	42.10259722	4.195187815	0.218343227	11.80183495	7.34E-79	4.48E-77	76.34887371
ABUW_RS05235	ABUW_1066	NZ_CP008706.1	1076659	1077399	-	WP_001186266.1		hypothetical protein	389.360916	4.092066761	0.307421379	13.9393573	2.00E-40	3.22E-39	38.49160648
ABUW_RS16180	ABUW_2096	NZ_CP008706.1	2078651	2079355	+	WP_001045567.1		CoA transferase subunit A	2383.311861	4.085665224	0.327059843	12.4922557	8.23E-36	1.19E-34	33.39079305
ABUW_RS16790	ABUW_3252	NZ_CP008706.1	3281966	3282304	-	WP_001181746.1	raiA	ribosome-associated translation inhibitor RaiA	3509.359416	4.082504302	0.23816855	17.1442148	6.94E-66	2.89E	

ABUW_RS00340	ABUW_0069	NZ_CP008706.1	73148	73780	-	WP_000781235.1	maIA	maleylacetoacetate isomerase	4447.188804	3.597026838	0.373814328	9.622495887	6.43E-22	4.1E-21	20.3862595
ABUW_RS1610	ABUW_2092	NZ_CP008706.1	207400	2074885	-	WP_00093854.1		3-hydroxybutyrate dehydrogenase	900.341006	3.5693327 E	0.28790411	12.39776041	2.69E-35	3.6 E-34	33.44220823
ABUW_RS20180	no	NZ_CP008706.1	897527	897621	+			hypothetical protein	15.972919	3.564872802	1.293832055	2.75522486	0.00586448	0.00829093	2.05408391
ABUW_RS10330	ABUW_210	NZ_CP008706.1	210702	210230	-	WP_000642315.1		2,3-bisubstrate dehydrogenase	32.7140566	3.548460314	0.23819345	16.9026026	3.23E-50	7.58E-49	48.0056284
ABUW_RS08570	ABUW_1959	NZ_CP008706.1	1750437	1756615	+	WP_00126404.1		58 family peptidase	892.6827832	3.546704966	0.90760512	18.59244838	3.70E-77	2.10E-75	17.84761847
ABUW_RS10335	ABUW_2107	NZ_CP008706.1	210260	210245	+	WP_000238445.1		acetoacetyl reductase	222.5993803	3.542298023	0.377724906	9.37798374	6.72E-21	4.0 E-20	19.36437399
ABUW_RS00335	ABUW_0068	NZ_CP008706.1	72582	73100	-	WP_001919415.1		VOC family protein	24.8016693	3.525651062	0.35376472	9.966059799	2.8E-23	1.46E-22	21.83419325
ABUW_RS16240	ABUW_3343	NZ_CP008706.1	337684	3377493	+	WP_000507882.1		hypothetical protein	447.097713	3.512700492	0.368877913	9.522819091	1.69E-21	1.04E-20	19.98100381
ABUW_RS08095	ABUW_1651	NZ_CP008706.1	654682	655515	-	WP_00109442.1		universal stress protein	8100.689663	3.50803882	0.279361469	12.5573467	3.62E-36	5.07E-35	34.29512322
ABUW_RS07430	ABUW_1622	NZ_CP008706.1	1507940	1508392	+	WP_00186567.1		GNA1 family N-acyltransferase	306.4889197	3.464987081	0.316005481	10.99973554	3.83E-28	3.44E-27	26.4635621
ABUW_RS07990	ABUW_1637	NZ_CP008706.1	1635040	1635723	+	WP_000920714.1		SCR family NAD(P)-dependent oxidoreductase	232.5891353	3.451241218	0.310507718	11.00849046	3.48E-28	3.10E-27	26.0380331
ABUW_RS10310	ABUW_2122	NZ_CP008706.1	2104169	2107774	-	WP_000421072.1		TGRIQ144 family phosphatase	345.7110745	3.445531086	0.336404933	10.24221331	1.28E-24	9.33E-24	23.03019449
ABUW_RS06065	ABUW_1241	NZ_CP008706.1	1282739	1283191	-	WP_0008315608.1		DUFGD2 domain-containing protein	639.0061519	3.444710771	0.261828239	13.1788098	1.16E-39	1.80E-38	37.74453373
ABUW_RS12615	ABUW_2986	NZ_CP008706.1	2989891	2990541	-	WP_001033098.1		TerR/AcrI family transcriptional regulator	211.873828	3.443952042	0.888683641	3.875340878	0.000190476	0.000197782	3.703812432
ABUW_RS00345	ABUW_0070	NZ_CP008706.1	73767	735074	-	WP_000435854.1	fehA	fumarylacetoacetate	12787.00428	3.443108944	0.36710021	9.37910021	6.65E-21	3.98E-20	9.40051069
ABUW_RS03650	ABUW_1741	NZ_CP008706.1	742953	743345	-	WP_001056569.1		hypothetical protein	63.87815953	3.433048452	0.307409503	11.6166588	6.32E-29	5.96E-28	27.22480407
ABUW_RS08375	ABUW_0720	NZ_CP008706.1	178317	178865	-	WP_000195718.1	tusD	sulfurtransferase complex subunit TusD	3942.661732	3.427514941	0.32446003	10.56374954	4.39E-26	3.47E-25	24.45927633
ABUW_RS07525	ABUW_1642	NZ_CP008706.1	1628462	1629241	+	WP_000772583.1		transglutaminase family protein	115156353.2	3.423952122	0.229933641	16.89072129	3.79E-50	8.83E-49	48.05406978
ABUW_RS10315	ABUW_2123	NZ_CP008706.1	2071784	2104749	+	WP_000465449.1		MBL fold metallo-hydrolase	127.5235342	3.419234105	0.347156766	9.20344182	9.20E-23	6.4E-22	21.17659191
ABUW_RS00540	ABUW_1953	NZ_CP008706.1	1740233	1749526	+	WP_000589660.1		hypothetical protein	493.58747	3.407180102	0.31025167	10.90209641	1.15E-27	9.76E-27	26.01609955
ABUW_RS08885	ABUW_1962	NZ_CP008706.1	1793948	1790790	+	WP_001032848.1		PQQ-dependent sugar dehydrogenase	2276.90416	3.401970547	0.85304992	18.35879361	2.81E-75	1.49E-73	72.82701724
ABUW_RS16100	ABUW_3314	NZ_CP008706.1	334780	3348997	+	WP_00186468.1		Re/Si-specific NAD(P)-transhydrogenase subunit alpha	1445.827742	3.401942025	0.321618044	17.50533678	3.87E-26	3.08E-25	24.51643336
ABUW_RS18995	ABUW_2405	NZ_CP008706.1	2457318	2457896	-	WP_000608703.1		3-oxoacid CoA-transferase subunit A	34.0498084	3.400314456	0.471887791	7.204242393	5.84E-13	2.10E-12	11.67434803
ABUW_RS18405	ABUW_3780	NZ_CP008706.1	3840038	3841195	-	WP_00180676.1		acyl-CoA dehydrogenase family protein	683.9599488	3.391922273	0.329946785	10.27704955	8.88E-25	6.50E-24	23.8746073
ABUW_RS12970	ABUW_2672	NZ_CP008706.1	2656073	2666017	-	WP_001046072.1		hypothetical protein	70.7652231	3.385734366	0.55138648	6.14277497	8.03E-10	2.31E-09	8.63703243
ABUW_RS04365	ABUW_0869	NZ_CP008706.1	886151	886588	-	WP_000668782.1		universal stress protein	10098.074839	3.354193268	0.223127841	10.92899866	4.70E-51	1.01E-49	48.94810092
ABUW_RS18475	ABUW_3784	NZ_CP008706.1	3857039	3857416	-	WP_001078111		ribonuclease E-Inhibitor ReaB	1647.514358	3.342572243	0.793010734	4.26036295	2.50E-05	4.99E-05	4.205210768
ABUW_RS18285	ABUW_1923	NZ_CP008706.1	1388369	1388941	+	WP_000043384.1		TerR/AcrI family transcriptional regulator	492.5632001	3.334910218	0.328315339	10.5770847	3.06E-24	2.8E-23	22.66221031
ABUW_RS19145	ABUW_3524	NZ_CP008706.1	3580463	3580869	+	WP_000687235.1		hypothetical protein	3336.22511	3.326664416	0.325794222	10.29318051	1.77E-24	1.27E-23	22.88694840
ABUW_RS08380	ABUW_0721	NZ_CP008706.1	178751	1787758	+	WP_000504789.1		SCR family NAD(P)-dependent oxidoreductase	2742.627338	3.290145749	0.232500599	14.806358	1.92E-45	3.76E-44	43.42543452
ABUW_RS00720	ABUW_1651	NZ_CP008706.1	1648054	1650417	+	WP_000300711		hypothetical protein	311.4948929	3.285953316	0.218671861	16.40744519	1.46E-53	1.54E-53	51.62535953
ABUW_RS04415	ABUW_0910	NZ_CP008706.1	907091	908008	+	WP_000868053.1	glyD	glycerol-3-phosphate dehydrogenase	1006.051678	3.289053838	0.280220394	15.6194351	3.22E-55	8.7 E-54	53.05982767
ABUW_RS16145	ABUW_2373	NZ_CP008706.1	238678	2386950	-	WP_000108119.1		amidohydrolase	403.0680618	3.257905058	0.21997818	14.8161547	1.26E-49	2.87E-48	47.54225935
ABUW_RS12445	ABUW_2519	NZ_CP008706.1	2509039	2509665	-	WP_000707328.1		hypothetical protein	97.6040661	3.240286495	0.363074341	18.902915323	5.48E-19	2.89E-18	47.53845532
ABUW_RS10000	ABUW_0895	NZ_CP008706.1	1204035	1204168	+	WP_000040098.1		catalsase family protein	566.8886024	3.23972623	0.235233928	10.72235954	3.74E-43	6.79E-42	41.07046802
ABUW_RS03605	ABUW_0732	NZ_CP008706.1	738071	739546	+	WP_00105676.1	hchA	protein deglycylase HchA	387.2567347	3.233772878	0.245609388	10.16324338	1.37E-39	2.10E-38	37.67436796
ABUW_RS06595	ABUW_1552	NZ_CP008706.1	1565002	1565961	-	WP_000783000.1		NdYgYgYdYel family stress tolerance protein	5721.840566	3.209058693	0.30092705	10.68316065	1.00E-26	1.23E-25	24.9122825
ABUW_RS14760	ABUW_3041	NZ_CP008706.1	3087141	3088559	-	WP_001012848.1		phosphonotransferase/hydrophobicity	2323.712966	3.204636418	0.163701966	15.57604112	2.48E-85	1.78E-83	42.9439819
ABUW_RS12405	ABUW_2554	NZ_CP008706.1	2544862	2545296	-	WP_000780057.1		DUF333 domain-containing protein	3964.162147	3.203265314	0.299853637	10.6827629	1.23E-26	1.0E-25	24.944385
ABUW_RS09525	ABUW_1658	NZ_CP008706.1	1659771	1662757	+	WP_000162636.1		DEAD/DEAH box-like coiled-coil family protein	1472.424893	3.200304839	0.162378004	16.6355029	3.86E-62	1.26E-60	59.8886717
ABUW_RS08385	ABUW_1923	NZ_CP008706.1	178751	1787758	+	WP_000184768.1	tumC	class I fumarylhydrolase	3943.018996	3.193768678	0.175249741	17.8142695	5.16E-71	2.29E-69	68.63982226
ABUW_RS18690	ABUW_3473	NZ_CP008706.1	3521127	3521622	-	WP_000053846.1		glutathione S-transferase family protein	1229.673908	3.185760073	0.17916748	17.7890577	9.94E-71	4.30E-69	68.36066559
ABUW_RS09490	ABUW_1651	NZ_CP008706.1	165288	1653076	+	WP_075874782.1		hypothetical protein	92.77509314	3.171260172	0.278566602	11.38420481	5.01E-30	5.06E-29	28.26682239
ABUW_RS05480	ABUW_1920	NZ_CP008706.1	194571	1947357	+	WP_000196831.1		BapA prete-like domain-containing protein	4525.440612	3.167835357	0.20449162	15.40619539	1.47E-53	3.70E-52	51.43197584
ABUW_RS02875	ABUW_0885	NZ_CP008706.1	885851	882819	+	WP_000194101.1		HAMP domain-containing histidine kinase	4044.784549	3.146625186	0.219410553	10.29761401	7.36E-34	9.02E-33	32.04420078
ABUW_RS10365	ABUW_2103	NZ_CP008706.1	2119327	2120466	+	WP_000307591.1		transcriptional regulator	796.4408741	3.14240718	0.223183914	14.08197281	4.91E-45	9.34E-44	43.02964191
ABUW_RS05215	ABUW_1602	NZ_CP008706.1	1617198	1617203	-	WP_000744219.1		hypothetical protein	573.6837466	3.127498198	0.193738409	16.14289186	1.27E-58	3.76E-57	56.42307621
ABUW_RS14870	ABUW_3054	NZ_CP008706.1	309587	3092412	-	WP_000100012.1		EcS family protein	5.98.01149	3.102722029	0.232637527	13.3371589	1.41E-40	2.30E-39	38.63909965
ABUW_RS00714	ABUW_1516	NZ_CP008706.1	1504540	1505268	+	WP_000848611.1		aspartate/glutamate acetylase family protein	152.624967	3.092291004	0.239064417	12.90178734	4.06E-38	5.99E-37	36.22221018
ABUW_RS04635	ABUW_0945	NZ_CP008706.1	953162	953843	+	WP_000187642.1	fehD	formate dehydrogenase accessory sulfuryltransferase FehD	96.06323002	3.05975443	0.328628482	9.100179392	1.27E-20	7.50E-20	9.4172441
ABUW_RS09195	ABUW_1888	NZ_CP008706.1	1889590	1890057	+	WP_000180179.1		saccharopine dehydrogenase NADP-binding domain-containing protein	397.5036773	3.058861547	0.288238477	10.6122589	2.61E-26	2.10E-25	24.67393183
ABUW_RS05116	ABUW_1642	NZ_CP008706.1	1650072	1650482	+	WP_001042571.1		GFA family protein	393.729252	3.038804026	0.249481465	10.1804825	3.95E-34	4.96E-33	34.00774846
ABUW_RS12750	ABUW_2628	NZ_CP008706.1	2624476	2625780	-	WP_000659371.1		MF-S transporter	81.1163445	3.016042712	0.289799144	10.40735549	2.30E-25	1.73E-24	23.76073009
ABUW_RS12720	ABUW_2620	NZ_CP008706.1	2618026	2618454	-	WP_000468271.1		GNA1 family N-acyltransferase	95.6377502	3.015192109	0.284682251	10.59091738	3.28E-26	2.62E-25	24.88085779
ABUW_RS10170	ABUW_0339	NZ_CP008706.1	361932	362507	-	WP_00184385.1		superoxide dismutase family protein	1022.173678	2.988825062	0.242080401	12.3482292	5.91E-35	6.68E-34	33.17537001
ABUW_RS00115	ABUW_0023	NZ_CP008706.1	2176	27319	+	WP_001876301.1		methionine/alanine import family NSS transporter small subunit	778.9216626	2.985606862	0.197299441	13.521505	9.94E-52	2.43E-50	49.61090509
ABUW_RS12215	ABUW_2516	NZ_CP008706.1	2505452	2505643	-	WP_002017791.1		hypothetical protein	93.7842307	2.958834542	0.845452886	3.499704468	0.000465774	0.00080795	3.093236981
ABUW_RS10770	ABUW_2216	NZ_CP008706.1	2201452	2202107	-										

ABUW_N14030	ABUW_2888	N2_CP008706.1	2894635	2896239	-	WP_000214787.1		isocitrate lyase	10.548 13035	2.637876399	0.25559038	10.32360023	5.51E-25	4.08E-24	23.38919734
sRNA77	no	no	no	no	no	no	no		229.3661001	1.636647131	0.374886812	7.03085574	2.05E-12	7.16E-12	11.14580923
ABUW_N19750	ABUW_3525	N2_CP008706.1	3808992	3582410	-	WP_000003544.1		poliphosphate--AMP phosphotransferase	23.91475916	2.63233481	0.93356824	10.5990016	4.06E-42	7.24E-41	40.3045253
ABUW_N06816	ABUW_597	N2_CP008706.1	1602372	1602569	-	WP_000004893.1			95.34859244	2.631884484	0.47044235	5.59446644	2.21E-08	5.70E-08	7.243777807
ABUW_N06965	ABUW_5975	N2_CP008706.1	193311	192500	+	WP_000002965.1	acs	acetyl-CoA ligase	1603.182053	2.628810465	0.21951311	12.0820091	134E-33	1.64E-32	31.7862507
ABUW_N08916	ABUW_832	N2_CP008706.1	1927466	1928599	+	WP_000001760.1		CoA transferase subunit B	94.29614725	2.62348854	0.341532593	7.688270676	149E-14	5.96E-14	13.22467776
ABUW_N00106	ABUW_0022	N2_CP008706.1	12685	2713	+	WP_000002725.1		sodium-dependent transporter	10886.94454	2.616905874	0.18810649	6.56810518	124E-54	3.28E-53	52.48422627
ABUW_N19760	ABUW_3320	N2_CP008706.1	3354427	3355329	-	WP_000002677.1		copper resistance c protein B	833.9744303	2.609614148	0.30216157	8.636772105	5.78E-18	2.84E-17	16.54701409
ABUW_N07419	ABUW_1618	N2_CP008706.1	1603894	1604400	-	WP_000009437.1		GNA71 N16 acetyltransferase	25.36516504	2.608734616	0.606876436	4.298625651	1.72E-05	3.46E-05	4.460505755
ABUW_N09485	ABUW_1950	N2_CP008706.1	1950563	1952100	+	WP_000003298.1		DHA2 efflux efflux MFS transporter permease subunit	22.36980705	2.60623859	0.437074667	5.962910863	2.48E-09	6.91E-09	8.16030533
ABUW_N10360	ABUW_2102	N2_CP008706.1	211813	211819	+	WP_000003645E.1	lpA	lipoyl synthase	500.7776	2.598855686	0.33899323	7.666394063	1.77E-14	7.02E-14	13.1534503
ABUW_N1820	ABUW_3865	N2_CP008706.1	3933639	3943181	+	WP_000964180.1		NAD(P)H-dependent oxidoreductase	78.15208805	2.596524594	0.256007187	10.14238947	3.58E-24	2.51E-23	22.61016561
sRNA74	no	no	no	no	no	no	no		67.06418988	2.590606551	0.15750289	8.20460548	2.31E-16	1.04E-15	14.98089935
ABUW_N0750	ABUW_0357	N2_CP008706.1	380432	380740	+	WP_0004571408.1		hypothetical protein	96.23606246	2.57516263	0.400306002	6.432985311	125E-10	3.78E-10	9.421974166
ABUW_N02060	ABUW_1918	N2_CP008706.1	191241	191381	+	WP_0007710264.1		hypothetical protein	87.01932377	2.565862391	0.450893979	5.69061041	127E-08	3.32E-08	21.77527705
ABUW_N00280	ABUW_0057	N2_CP008706.1	162104	162943	-	WP_0000034950.1		formate/nitrite transporter family protein	48.12045499	2.54891853	0.26564582	5.95951083	8.38E-22	5.32E-21	20.27433632
ABUW_N1830	ABUW_3857	N2_CP008706.1	3868042	3869199	-	WP_000009759.1	ppC	2-methylerythrose synthase	37813.52569	2.547370647	0.274420827	9.28271611	1.65E-20	9.73E-20	16.0181886
ABUW_N07450	ABUW_826	N2_CP008706.1	152529	152532	-	WP_000758190.1		hypothetical protein	9337.75093	2.543960007	0.392582011	6.480074316	9.17E-11	2.81E-11	9.551465563
ABUW_N02965	no	N2_CP008706.1	2564072	266616	-			transposase	93.44318025	2.53561819	0.389335341	6.510842098	7.38E-11	2.27E-11	9.643962341
ABUW_N16240	ABUW_1939	N2_CP008706.1	1939373	1944508	-	WP_0007214344.1		hypothetical protein	488.2637773	2.532916994	0.218287491	11.55054377	7.33E-31	7.77E-30	29.0506206
ABUW_N16500	ABUW_3395	N2_CP008706.1	3438237	3439439	+	WP_000234600.1		acetate kinase	893.1925919	2.527859025	0.272651919	9.270691029	185E-20	1.09E-19	18.96445886
ABUW_N11010	ABUW_2701	N2_CP008706.1	2685712	2685765	-	WP_0000025373.1		lysine family transporter	259.1475051	2.524867677	0.287403393	8.785100463	1.56E-18	7.96E-18	10.96272609
ABUW_N10205	ABUW_2611	N2_CP008706.1	2464021	2465226	+	WP_0009310806.1		3-oxoacyl-CoA thioesterase	59.41984803	2.524604774	0.36619343	6.895013797	5.39E-12	1.83E-11	10.7379053
ABUW_N10816	ABUW_2901	N2_CP008706.1	2900451	2900888	-	WP_0004419056.1		SRP40CC domain-containing protein	83.12930379	2.519452824	0.228404562	11.02628073	2.85E-28	2.58E-27	26.58766866
ABUW_N08825	ABUW_1966	N2_CP008706.1	195359	196126	-	WP_000731729.1		putative porin	57522.15981	2.506792607	0.237416004	10.5889622	4.63E-26	3.66E-25	24.43674852
ABUW_N19105	ABUW_2700	N2_CP008706.1	2684807	2685101	-	WP_000825869.1		hypothetical protein	74.1676478	2.5040103	0.223078024	11.231031	2.87E-29	2.77E-28	27.5580414
ABUW_N02360	ABUW_0480	N2_CP008706.1	492078	492641	+	WP_000988414.1		DUF4256 domain-containing protein	222.223919	2.502755026	0.30891016	8.1018741	5.41E-16	2.38E-15	14.62292311
ABUW_N00516	ABUW_0194	N2_CP008706.1	116513	116809	+	WP_0004218563.1		alpha/beta fold hydrolase	928.8868829	2.499319197	0.173809579	14.37964014	6.95E-47	1.42E-45	44.8471667
ABUW_N0330	ABUW_068	N2_CP008706.1	101100	101153	+	WP_000636740.1		DUF962 domain-containing protein	252.1909256	2.495358711	0.201555506	12.36280099	2.86E-35	3.81E-34	33.41862482
ABUW_N10505	ABUW_2698	N2_CP008706.1	2683223	2684445	+	WP_0000032335.1		exocysteine/tyrosine kinase subunit	319.4959929	2.494997762	0.200889234	12.41675833	2.04E-35	2.76E-34	33.51050558
ABUW_N1160	ABUW_2294	N2_CP008706.1	2296800	2291987	+	WP_0002442890.1		OsmC family protein	341.7051892	2.494456523	0.32851638	7.593210496	3.12E-14	1.22E-13	12.9259624
ABUW_N18665	ABUW_3874	N2_CP008706.1	3944234	3942750	+	WP_0007214778.1		hypothetical protein	641.807049	2.487053533	0.30194762	8.256998612	1.47E-16	6.76E-16	16.17931673
ABUW_N11450	ABUW_2354	N2_CP008706.1	2336883	2337728	-	WP_000535318.1		AnsC family transcriptional regulator	652.4444155	2.485264076	0.234195471	10.56610607	4.28E-26	3.39E-25	24.48946881
ABUW_N03470	ABUW_0705	N2_CP008706.1	176524	171695	+	WP_000181534.1		patatin-like phospholipase family protein	575.5789825	2.469170565	0.18471919	13.36719035	9.40E-41	1.56E-39	38.8071869
ABUW_N06040	ABUW_848	N2_CP008706.1	143194	1444829	+	WP_0003445328.1		mechanosensitive ion channel	73.1472863	2.46191918	0.224368773	10.17261091	5.18E-28	4.59E-27	26.3371028
ABUW_N09885	ABUW_2056	N2_CP008706.1	2035907	2036884	+	WP_000719470.1		DUF482 family protein	429.064283	2.454316733	0.300435734	8.1898156	3.09E-16	1.38E-15	14.5891451
ABUW_N18485	ABUW_3796	N2_CP008706.1	3858104	3859005	-	WP_0004218563.1		DUF1003 domain-containing protein	608.690774	2.444816205	0.17708159	3.610103564	0.000305228	0.000432	3.26504052
ABUW_N08080	ABUW_1994	N2_CP008706.1	1400021	1401307	-	WP_000565562.1		hypothetical protein	32.44965767	2.441640749	0.332322589	7.346526836	2.03E-13	7.54E-13	12.1271021
ABUW_N18106	ABUW_3702	N2_CP008706.1	3759865	3761095	+	WP_000291628.1		DUF2735 domain-containing protein	455.4398762	2.437167174	0.21958091	11.38937842	4.72E-30	4.77E-29	28.32161431
ABUW_N18916	ABUW_083	N2_CP008706.1	1678646	1679080	-	WP_0001615006.1		acyl-CoA thioesterase	193.5828837	2.426937505	0.194575952	12.1676479	4.62E-34	5.75E-33	32.24059811
ABUW_N08620	ABUW_098	N2_CP008706.1	1602669	1602760	-	WP_0001615006.1		hypothetical protein	34.2834144	2.424221069	0.420959357	3.763850723	8.22E-09	2.20E-08	7.657670619
ABUW_N02519	ABUW_2297	N2_CP008706.1	2284943	2285191	-	WP_0001668550.1		hypothetical protein	351.17311027	2.422744212	0.195260351	12.40776328	2.37E-35	3.20E-34	33.49531401
ABUW_N1830	ABUW_3777	N2_CP008706.1	3836763	3838116	-	WP_0001615286.1		MkG family MFS transporter	209.0296393	2.422597579	0.272464305	8.885495739	3.36E-19	1.77E-18	17.47302323
ABUW_N07530	ABUW_0431	N2_CP008706.1	1925958	1929992	-	WP_000230477.1		proteasome-type protease	1088.181169	2.419409361	0.198550499	12.10860999	5.03E-34	6.23E-33	32.2057103
ABUW_N0755	ABUW_0398	N2_CP008706.1	380776	382101	+	WP_000160948.1		S8 family serine peptidase	272.4169303	2.416624582	0.260742351	11.68422711	1.53E-31	1.68E-30	29.77180782
ABUW_N19235	ABUW_4042	N2_CP008707.1	24797	25180	+	WP_00054348.1		hypothetical protein	367.3845986	2.394568165	0.329779947	7.26100018	3.84E-13	1.40E-12	11.85233874
ABUW_N09165	ABUW_870	N2_CP008706.1	1668296	1670758	-	WP_000003930.1		penicillin acylase family protein	550.6877036	2.390818007	0.252397941	9.471475481	2.76E-21	1.68E-20	19.77350616
ABUW_N19040	ABUW_4003	N2_CP008706.1	4174	2566	+	WP_000208411.1		zeta toxin family protein	195.2898929	2.39011978	0.257003515	9.217836343	1.72E-20	1.01E-19	18.95933382
ABUW_N1020	ABUW_2470	N2_CP008706.1	2462483	2464006	+	WP_0002210505.1		3-hydroxyacyl-CoA dehydrogenase	147.5478132	2.382831601	0.267161707	8.912389234	4.19E-19	2.65E-18	17.57598476
ABUW_N07895	ABUW_1618	N2_CP008706.1	161108	1614905	-	WP_000714022.1	eutC	ethanolanine ammonia-lyase subunit EutC	61.95516749	2.379520359	0.269205263	8.839023044	9.66E-19	5.01E-18	17.29987078
ABUW_N19775	ABUW_2354	N2_CP008706.1	2843149	2843508	-	WP_000744506.1		hypothetical protein	388.7433293	2.378030842	0.280667731	7.954344668	1.80E-15	7.65E-15	14.11660108
ABUW_N18200	ABUW_3335	N2_CP008706.1	3368532	3368792	-	WP_000709879.1		hypothetical protein	144.3185675	2.364862289	0.406207073	3.182838235	NA	NA	11.87161
ABUW_N19170	ABUW_2460	N2_CP008706.1	245198	2453300	-	WP_001151921.1		acyl-CoA dehydrogenase C-terminal domain-containing protein	54.7320161	2.358286179	0.260185826	9.063853397	126E-19	6.98E-19	18.5623685
ABUW_N09190	ABUW_087	N2_CP008706.1	1888336	1889574	-	WP_000602283.1		NADH flavin oxidoreductase/NADH oxidase family protein	188.036111	2.356218943	0.27310918	8.627738334	6.28E-18	3.07E-17	15.92380304
ABUW_N09495	ABUW_1952	N2_CP008706.1	1953073	1954559	+	WP_0004841503.1		GHz1 auxin-responsive promoter family protein	68.41637747	2.351871847	0.249475748	9.427255618	4.12E-21	2.54E-20	19.59533969
ABUW_N18360	ABUW_2234	N2_CP008706.1	2221020	2223885	-	WP_0000010661.1		malate synthase G	92.15426337	2.345054195	0.178517251	10.18503565	107E-39	1.67E-38	37.7772488
sRNA8	no	no	no	no	no	no	no		975.7787727	2.343471184	0.29414668	7.967015612	1.63E-15	6.92E-15	14.15971019
sRNA63	no	no	no	no	no	no	no		84.75956052	2.344031825	0.182226349	7.333582857	193E-13	7.16E-13	12.14319371
ABUW_N19160	ABUW_0359	N2_CP008706.1	382230	382661	-	WP_000008069.1		hypothetical protein	1058.8017139	2.330525628	0.23				

ABUW_RS1805	ABUW_2447	NZ_CP008706.1	2432924	2434362	+	WP_000781142.1		SGN/HGDSL hydrolase family protein	105.7350975	1.884677343	0.305222033	6.17480686	6.62E-10	1.92E-09	8.716673854
ABUW_RS1825	ABUW_2430	NZ_CP008706.1	2418995	2419606	+	WP_000885227.1		LydE family translocator	145.627038	1.880060953	0.275905593	6.1035010	9.50E-12	3.16E-11	10.50184737
ABUW_RS0860	ABUW_3607	NZ_CP008706.1	1406888	1407317	+	WP_001223091.1		hypothetical protein	95.68876101	1.875604926	0.280555295	6.89935109	2.09E-11	6.74E-11	10.1719315
ABUW_RS17435	ABUW_3582	NZ_CP008706.1	3641996	3641994	-	WP_001082025.1		DUF1311 domain-containing protein	1594.544604	1.873399094	0.232928016	8.042824235	8.78E-16	8.30E-15	11.9838466
ABUW_RS05895	ABUW_1944	NZ_CP008706.1	176194	1763507	-	WP_002021140.1		GDHGF domain-containing protein	967.1258172	1.872800466	0.202288642	9.258060041	2.08E-20	1.25E-19	9.91647186
ABUW_RS1465	ABUW_3388	NZ_CP008706.1	3428111	3429424	-	WP_001038448.0		alpha-beta hydrolase	1657.712899	1.868900922	0.196653255	9.503534161	2.03E-21	1.25E-20	19.90310205
ABUW_RS17060	ABUW_3507	NZ_CP008706.1	3554228	3554566	-	WP_000434938.1		RNA-binding protein	11917.9733	1.867790709	0.207440649	9.002677708	2.85E-19	1.95E-18	17.32618764
ABUW_RS04920	ABUW_003	NZ_CP008706.1	1018106	1019341	+	WP_000383695.1		multidrug efflux MFS transporter	768.161367	1.86119367	0.160922929	12.33356902	5.97E-35	7.76E-34	33.1095932
ABUW_RS14755	ABUW_3040	NZ_CP008706.1	3066228	3067126	-	WP_001015419.1	argB		2394.345585	1.86106051	0.179076102	10.39259686	2.68E-25	2.02E-24	23.09427995
ABUW_RS14395	ABUW_2965	NZ_CP008706.1	2978751	2978951	+	WP_000705177.1		hypothetical protein	1338.562044	1.858118053	0.616385797	3.014537425	0.002573715	0.00406001	23.9463246
ABUW_RS08825	ABUW_1914	NZ_CP008706.1	1808186	1810852	+	WP_000952702.1	cipA	ATP-dependent GTPase ATP-binding subunit CipA	15141.19663	1.849116734	0.176191885	10.49489726	9.12E-26	7.06E-25	24.10592161
sRNA50	no	no	no	no	no	no	no	no	157.5167563	1.84195445	0.199352265	9.25976188	2.05E-20	1.95E-19	18.92276174
ABUW_RS05875	ABUW_003	NZ_CP008706.1	1238496	1242185	+	WP_000960544.1		M1 family metallophosphatase	1010.060745	1.838359875	0.242731916	7.5736411	1.63E-14	1.42E-13	12.84190874
ABUW_RS05920	ABUW_3567	NZ_CP008706.1	1958626	1959366	-	WP_000193120.1		HD domain-containing protein	165.059345	1.83239116	0.219056634	8.364919728	6.02E-17	2.80E-16	15.55254085
ABUW_RS06775	ABUW_089	NZ_CP008706.1	1386617	1386997	-	WP_000150791.1		hypothetical protein	68.00861665	1.830699375	0.229878423	7.044445458	1.86E-12	6.50E-12	11.8702521
ABUW_RS07325	ABUW_3602	NZ_CP008706.1	1488252	1489919	+	WP_002017678.1		MCE family protein	1068.249486	1.827103005	0.204569105	8.9314710871	4.20E-19	2.24E-18	17.49195983
ABUW_RS02160	ABUW_0440	NZ_CP008706.1	1421400	1454335	-	WP_001184905.1		TRAP transporter/large permease subunit	1082.852946	1.825724608	0.219765103	8.307565078	9.77E-17	4.51E-16	15.34548773
ABUW_RS01600	ABUW_0325	NZ_CP008706.1	147427	1484548	-	WP_001184549.1		lipase secretion chaperone	975.0243139	1.825008695	0.296967637	6.147500179	7.67E-10	2.26E-09	8.645637767
ABUW_RS07765	ABUW_090	NZ_CP008706.1	3880740	3881904	+	WP_001191432.1		outer membrane protein assembly factor	38714.655882	1.824761287	0.145192579	12.57306466	2.97E-36	4.46E-35	54.37843481
ABUW_RS06765	ABUW_087	NZ_CP008706.1	1498106	1498321	-	WP_001293264.1		hypothetical protein	78.5555108	1.82000691	0.241921925	7.523116955	5.35E-14	2.06E-13	12.65552322
ABUW_RS03720	ABUW_0758	NZ_CP008706.1	1752840	1753025	+	WP_001271405.1		hypothetical protein	25.83921457	1.81951055	0.395302652	4.600301434	4.22E-06	8.98E-06	5.046764405
ABUW_RS16660	ABUW_2963	NZ_CP008706.1	2178563	2179846	+	WP_170319961.1		acryl-CoA dehydrogenase family protein	300.2371946	1.818288993	0.187654265	9.689462076	3.34E-22	2.16E-21	20.66517693
ABUW_RS14480	ABUW_267	NZ_CP008706.1	1292465	1299990	-	WP_000605213.1		GFA family protein	72.482608	1.814269452	0.395219054	4.590541456	4.42E-06	9.40E-06	5.026893756
ABUW_RS06190	ABUW_054	NZ_CP008706.1	1492468	1529271	-	WP_000171852.1		hypothetical protein	23.44660944	1.810193556	0.429234035	4.224230621	2.40E-05	4.76E-05	4.322091874
ABUW_RS02995	ABUW_909	NZ_CP008706.1	919252	9193932	-	WP_0020276394.1		hypothetical protein	96.21628281	1.810447732	0.227326007	8.719200937	1.55E-15	6.61E-15	14.1799241
ABUW_RS18870	ABUW_3875	NZ_CP008706.1	3842024	3843164	-	WP_000173305.1		hypothetical protein	2956.891631	1.81026734	0.146836725	5.223129478	1.76E-07	4.20E-07	63.73710683
ABUW_RS1375	ABUW_2105	NZ_CP008706.1	1212186	1212215	+	WP_000177555.1		GDHGF domain-containing protein	1162.248537	1.808897193	0.204174597	8.859560024	8.03E-19	4.49E-18	17.37819163
ABUW_RS19010	ABUW_875	NZ_CP008706.1	1875004	1875924	-	WP_001010819.1	catA	catechol 1,2-dioxygenase	9114.65310	1.808106764	0.248877074	7.265180084	3.73E-13	1.37E-12	11.86383456
ABUW_RS18515	ABUW_876	NZ_CP008706.1	1669306	1670190	+	WP_001091732.1		hypothetical protein	503.746396	1.807130489	0.165028043	10.93848555	7.54E-28	6.58E-27	26.1846666
ABUW_RS06225	ABUW_076	NZ_CP008706.1	1020204	1020339	-	WP_001278405.1		hypothetical protein	26.61920741	1.805123642	0.36610706	4.930589542	8.20E-07	1.86E-06	5.71312193
ABUW_RS12330	ABUW_254	NZ_CP008706.1	2507164	2507444	-	WP_000338857.1		hypothetical protein	240.4946575	1.799693393	0.618460099	2.63862566	0.008253476	0.01224666	19.1916506
ABUW_RS10670	ABUW_295	NZ_CP008706.1	281189	282412	-	WP_000993541.1		alkane 1-monooxygenase	236.1812265	1.799185906	0.258914035	6.951877812	3.16E-12	1.24E-11	10.36551841
ABUW_RS13055	ABUW_2781	NZ_CP008706.1	2776038	2777177	+	WP_001015439.1		acryl-CoA dehydrogenase family protein	158.858032	1.798089358	0.343491862	5.234688859	1.65E-07	3.95E-07	6.403742143
ABUW_RS14335	ABUW_2963	NZ_CP008706.1	2197320	21987335	-	WP_000118514.1		non-heme iron oxygenase ferredoxin subunit	45.0306163	1.79511475	0.446536162	4.028042923	5.62E-05	0.00017443	3.98821947
ABUW_RS16915	ABUW_149	NZ_CP008706.1	1410687	1411097	-	WP_0003333634.1		hypothetical protein	0.72746027	1.793166847	1.90162662	0.434390388	0.345634673	0.392933529	0.405671913
ABUW_RS02395	ABUW_0488	NZ_CP008706.1	1503331	1501184	+	WP_000175501.1		enoyl-CoA hydratase/isomerase family protein	171.7710424	1.792710784	0.323078547	5.549024828	2.87E-08	7.34E-08	7.18407188
ABUW_RS03355	ABUW_921	NZ_CP008706.1	919200	9202260	-	WP_000196178.1		MFS transporter	284.8587641	1.790148464	0.32174211	8.141562537	3.94E-17	1.85E-16	15.73232929
ABUW_RS06970	ABUW_1431	NZ_CP008706.1	1423557	1423880	-	WP_0001673007.1		hypothetical protein	216.941004	1.788217092	0.232744995	7.68319126	1.55E-14	6.19E-14	13.20824027
ABUW_RS15595	ABUW_3210	NZ_CP008706.1	3243718	3245400	-	WP_001056249.1		MFS transporter	11.68467794	1.78673445	0.306581889	5.627918109	5.61E-09	1.52E-08	7.817682454
ABUW_RS05885	ABUW_005	NZ_CP008706.1	143172	1444974	-	WP_000199940.1		aminopyruvate P family protein	284.5521922	1.786252617	0.171259767	10.43007737	1.81E-25	1.37E-24	23.86202192
ABUW_RS02920	ABUW_908	NZ_CP008706.1	1906839	1910207	+	WP_000109348.0		cation protein antiporter	1244.787161	1.774190409	0.195836071	9.059128079	13.1E-19	7.28E-18	18.8081875
ABUW_RS1295	ABUW_2738	NZ_CP008706.1	2728902	2728927	-	WP_001026236.1		ONAF family N1-acetyltransferase	231161862	1.772143916	0.220370189	8.0416688	8.86E-16	8.84E-15	14.8120052
ABUW_RS18340	ABUW_087	NZ_CP008706.1	140571	140585	+	WP_000108714.1		hypothetical protein	53.1146116	1.77176557	0.592090441	2.989360798	0.0027195618	0.004392958	2.337242923
ABUW_RS02885	ABUW_0598	NZ_CP008706.1	133239	133432	-	WP_000148560.1		hypothetical protein	925.3991735	1.771675882	0.378885195	4.70078952	2.59E-06	5.61E-06	5.230982568
ABUW_RS09500	ABUW_963	NZ_CP008706.1	1564456	1565984	+	WP_000177758.1		TafA family protein	41.91988663	1.771627574	0.318285045	5.60164755	2.18E-08	5.50E-08	7.25971018
ABUW_RS08335	ABUW_1752	NZ_CP008706.1	1748882	1749118	+	WP_000523043.1		hypothetical protein	214.245982	1.76848851	0.332303874	5.321901878	1.03E-07	2.50E-07	6.602342824
ABUW_RS10445	ABUW_0254	NZ_CP008706.1	269194	269345	-	WP_001465967.1		ONAF family N1-acetyltransferase	132.5616885	1.766619554	0.270252493	5.53692376	6.28E-11	1.94E-10	9.72474079
ABUW_RS07870	ABUW_1611	NZ_CP008706.1	1605654	1606307	-	WP_0003619034.1	nhb	oxygen-insensitive NADPH/H1 nitroductase	284.9970096	1.760089809	0.30419709	9.793932876	6.88E-09	1.85E-08	7.73813674
ABUW_RS01620	ABUW_0329	NZ_CP008706.1	350974	351834	-	WP_0010180517.1		BamA family transporter	2711627174	1.765919742	0.164679289	10.72333839	7.91E-27	6.60E-26	25.1905806
ABUW_RS10600	ABUW_2072	NZ_CP008706.1	2051777	2053852	-	WP_000202696.1	ppk1	polyphosphate kinase 1	1655.564748	1.763897068	0.240217881	7.874317705	3.43E-15	1.44E-14	13.8422773
ABUW_RS14345	ABUW_2767	NZ_CP008706.1	2758907	2759994	-	WP_000483430.1		NAD(P)FAD-dependent oxidoreductase	169.7110024	1.763325999	0.26892752	5.658891677	5.49E-11	1.70E-10	9.76851889
ABUW_RS03705	ABUW_0755	NZ_CP008706.1	751684	752240	+	WP_000826377.1		hypothetical protein	612.6176621	1.75938437	0.31628386	5.61220629	1.95E-08	5.06E-08	7.29581937
ABUW_RS15575	ABUW_2795	NZ_CP008706.1	2793499	2793837	-	WP_0001671321.1		hypothetical protein	37.71235294	1.759162302	0.608796479	2.899907174	0.003742382	0.00579248	2.23818681
ABUW_RS19125	ABUW_2085	NZ_CP008706.1	2066159	2067106	-	WP_00014328.1		transporter	47.6862662	1.757619339	0.31789197	5.601264456	2.19E-08	5.50E-08	7.259988365
ABUW_RS02430	ABUW_0750	NZ_CP008706.1	178784	1788951	+	WP_000104769.1		hypothetical protein	67.1245056	1.754227171	0.305961903	5.831719001	5.31E-09	1.44E-08	7.841180713
ABUW_RS06975	ABUW_1432	NZ_CP008706.1	1423885	1424109	+	WP_0001050407.1		hypothetical protein	318.6014445	1.75425194	0.229886241	7.630953168	2.33E-14	9.16E-14	10.0382534
ABUW_RS02025	ABUW_2391	NZ_CP008706.1	2379969	2380193	-	WP_000174981.1		hypothetical protein	256.478999	1.753744225	0.407750764	4.31020083	1.70E-05	3.43E-05	4.46591738
ABUW_RS10055	ABUW_2487	NZ_CP008706.1	2459376	2460530	-	WP_000167392.1		acryl-CoA dehydrogenase family protein	89.06641786	1.75187497	0.350653399	4.995216373			

ABUW_RS17640	ABUW_3623	NZ_CP008706.1	3681056	3682105	+	WP_000722631.1				hypothetical protein	3.12	595684	164.68	173	0.173506085	9.45883416	3.1E-21	1.90E-20	19.72234805
ABUW_RS08850	ABUW_1910	NZ_CP008706.1	1814373	1816397	+	WP_000001168.1				NAD(P)-dependent 2,4-dienoyl-CoA reductase	73.18025046	164.152557	0.31858806	5.124933028	2.57E-07	6.05E-07	6.02E-07	6.18205343	
ABUW_RS10210	ABUW_2488	NZ_CP008706.1	2460842	2466300	+	WP_000006289.1				enoyl-CoA hydratase	27.81031659	13629365	0.40854088	4.00521007	6.20E-05	0.000119724	3.328397345		
ABUW_RS10580	ABUW_2232	NZ_CP008706.1	2222003	222416	+	WP_000525676.1				biopolymer transporter ExbD	44.9901905	163148046	0.341663256	4.775102424	1.80E-06	3.94E-06	5.404326253		
ABUW_RS10615	ABUW_2025	NZ_CP008706.1	230706	231650	+	WP_00091276.1				LyxR family transcriptional regulator	558.8023826	28988139	0.163883162	9.945397039	2.64E-23	1.80E-22	2.17445911		
ABUW_RS00920	ABUW_0166	NZ_CP008706.1	207147	209314	+	WP_00108472.1	batT			choline BCTT transporter BatT	7935.009942	162675431	0.54561747	9.83201462	8.20E-23	5.69E-22	212607875		
ABUW_RS00590	ABUW_0109	NZ_CP008706.1	163753	164190	+	WP_00071912.1				DUF2147 domain-containing protein	4566.120197	162670207	0.202769778	8.022413343	1.04E-15	4.47E-15	14.34988775		
ABUW_RS02830	ABUW_0576	NZ_CP008706.1	573257	573526	-	WP_000571491.1				phage holin family protein	12.89085996	1624312196	0.369500408	2.852125305	0.004342798	0.0066605	2.176493189		
ABUW_RS12195	ABUW_2506	NZ_CP008706.1	2501453	2502391	-	WP_000123655.1				hydroxymethylglutaryl-CoA lyase	129.9730593	1622811096	0.233196873	9.957688035	3.46E-12	1.19E-11	10.52266403		
ABUW_RS16075	ABUW_3309	NZ_CP008706.1	3343675	3344469	+	WP_000532989.1				TlMael protein	1687.958601	1620672364	0.210117952	7.719187339	1.23E-14	4.90E-14	13.04025023		
ABUW_RS10835	ABUW_2229	NZ_CP008706.1	2218907	2219623	+	WP_000525882.1				energy transducer TonB	67.88272193	116102203	0.263585689	6.123329515	9.16E-10	5.62E-09	13.58101218		
ABUW_RS10840	ABUW_2230	NZ_CP008706.1	2219664	2220545	+	WP_00201828.1				MoA/Tox/ExbB protein channel family protein	155.5740238	161929229	0.20260816	7.960781358	1.17E-15	7.27E-15	14.13827675		
ABUW_RS12320	ABUW_2738	NZ_CP008706.1	2727699	2728505	+	WP_001237336.1				peptidoglycan Di-metalloendopeptidase family protein	5311551463	1609889883	0.120486727	7.857428502	3.92E-15	1.63E-14	13.7872816		
ABUW_RS13035	ABUW_1352	NZ_CP008706.1	1378003	1379646	+	WP_0000447790.1				MF5 transporter	530.9016642	1607193857	0.309850188	5.19871237	2.14E-07	5.07E-07	6.29501301		
ABUW_RS09475	ABUW_1648	NZ_CP008706.1	1647325	1648785	+	WP_000063670.1	isaH			indokasin etamide hydrolase	167.1563057	1606175103	0.269471842	5.962598293	2.48E-09	6.92E-09	8.19766944		
ABUW_RS06220	ABUW_1275	NZ_CP008706.1	1019599	1021008	-	WP_000066269.1				hypothetical protein	16.43154467	1605473796	0.429933753	3.734235296	0.000186286	0.000341861	3.64553233		
ABUW_RS14305	ABUW_2847	NZ_CP008706.1	2861714	2862937	-	WP_000064049.1				MF5 transporter	137.87189748	1603197123	0.285969649	5.61039445	2.01E-08	5.19E-08	7.284623088		
ABUW_RS02390	ABUW_0487	NZ_CP008706.1	499163	500320	-	WP_000617016.1				acyl-CoA dehydrogenase family protein	363.2200255	1602630106	0.288493173	5.555174442	2.77E-08	7.10E-08	7.14860315		
ABUW_RS12480	ABUW_0261	NZ_CP008706.1	271948	2719425	+	WP_000221198.1				aminotransferase class 1b pyridoxal phosphate-dependent enzyme	363.1634572	1597487444	0.240249566	6.649283365	2.99E-11	9.35E-11	10.02914441		
ABUW_RS14830	ABUW_3056	NZ_CP008706.1	3062659	3063474	+	WP_00084343.1				arginyltransferase	1457.722263	159420605	0.14291608	11.15330851	6.75E-29	6.35E-29	27.1971894		
ABUW_RS14515	ABUW_2989	NZ_CP008706.1	3007583	3008527	+	WP_000505079.1				4-ethylpyridoxate synthase family protein	48.86902462	1592184404	0.389852709	4.084066543	4.43E-05	8.84E-05	4.06857727		
ABUW_RS10115	ABUW_2083	NZ_CP008706.1	2063558	2064592	+	WP_00185615.1	antC			anthranilate 12-dioxygenase elctron transfer component AntC	9149319446	1588403195	0.164149337	6.03215848	1.62E-09	5.1E-09	8.291924287		
ABUW_RS06880	ABUW_1411	NZ_CP008706.1	1408162	1408941	-	WP_000066269.1				hypothetical protein	1410416862	1587256653	0.438839654	3.161893902	0.000299106	0.000330977	3.749223911		
ABUW_RS02975	ABUW_0605	NZ_CP008706.1	605411	605451	-	WP_00102342.1				acyl-CoA dehydrogenase C-terminal domain-containing protein	4097.43123	1586092737	0.198263398	7.88744398	1.89E-16	8.60E-16	15.06545693		
ABUW_RS07995	ABUW_1638	NZ_CP008706.1	1635001	1636358	+	WP_000932085.1				chlorinate mutase	262.1662094	1584671052	0.229493895	6.90585861	5.02E-12	1.17E-11	10.7618374		
ABUW_RS02435	ABUW_1754	NZ_CP008706.1	175411	175167	+	WP_001001967.1				hypothetical protein	118.3019125	1584488059	0.385689471	4.168196308	3.99E-05	7.75E-05	4.10682944		
ABUW_RS10490	ABUW_2778	NZ_CP008706.1	2771967	2772706	+	WP_002040866.1				p-hydroxyinnamoyl-CoA hydratase/lyase	2146.60844	1578635588	0.296144457	5.196288915	1.06E-07	2.58E-07	6.589912751		
ABUW_RS04830	ABUW_0985	NZ_CP008706.1	997995	1000436	+	WP_000800799.1				CSLRase domain-containing protein	1770.14582	1577409611	0.208311436	7.572322596	3.66E-14	1.43E-13	12.8452521		
ABUW_RS10690	ABUW_1343	NZ_CP008706.1	135274	135658	+	WP_000744750.1				hypothetical protein	729.958419	1577556455	0.208146611	7.569512876	3.75E-14	1.44E-13	12.8365941		
ABUW_RS02455	ABUW_0273	NZ_CP008706.1	101482	101637	+	WP_001001967.1				hypothetical protein	14.1436135	1570391739	0.32116525	2.95121762	0.003155237	0.00493527	2.036659043		
ABUW_RS10495	ABUW_2778	NZ_CP008706.1	2772444	2773595	+	WP_001181903.1				aldehyde dehydrogenase	2253.35167	1570146787	0.280407763	5.599512548	2.15E-08	5.54E-08	7.25010544		
ABUW_RS06165	ABUW_0259	NZ_CP008706.1	195540	1956306	-	WP_000929117.1				hypothetical protein	8.68069186	1569991842	0.508207968	3.089250938	0.00206619	0.00320317	2.48442722		
ABUW_RS10845	ABUW_2231	NZ_CP008706.1	2220561	2220983	+	WP_000525884.1				biopolymer transporter ExbD	59.88990406	1567505994	0.23718736	6.11029167	3.18E-11	1.20E-10	9.920188014		
ABUW_RS10650	ABUW_1291	NZ_CP008706.1	1219421	1219723	+	WP_00185715.1				hypothetical protein	532.521793	1560572519	0.285421974	5.467612993	4.56E-08	1.14E-07	6.19415351		
ABUW_RS10870	ABUW_1469	NZ_CP008706.1	1453508	14537464	+	WP_000064284.1	katG			catalase/peroxidase HPI	2277.771277	1557145333	0.197840484	8.868734998	3.64E-15	1.52E-14	10.81973873		
ABUW_RS11780	ABUW_2835	NZ_CP008706.1	2844057	2845301	-	WP_000707986.1				NADH flavin oxidoreductase/NADH oxidase family protein	509.2274023	1556941984	0.181928268	5.558042438	1.15E-17	5.53E-17	16.25706671		
ABUW_RS10605	ABUW_3712	NZ_CP008706.1	376248	3772108	-	WP_000001967.1				23S ribosomal RNA	85868.376714	1548485113	0.56455647	2.742734735	0.000092988	0.009159944	2.038197176		
ABUW_RS11735	ABUW_2412	NZ_CP008706.1	2398342	2399262	-	WP_000357081.1				LyxR family transcriptional regulator	209.6247886	1545665327	0.226384089	6.827300212	8.65E-12	2.88E-11	10.54071486		
ABUW_RS10210	ABUW_2466	NZ_CP008706.1	2461660	2464241	+	WP_000101937.1				SDR family oxidoreductase	31.71218262	1542478705	0.41028312	3.751890955	0.000197872	0.000319759	3.495197777		
ABUW_RS06070	ABUW_1888	NZ_CP008706.1	1986138	1986620	-	WP_000873308.1				hypothetical protein	57.42626167	1541296167	0.265088776	5.814710284	6.07E-09	1.64E-08	7.783918762		
ABUW_RS06870	ABUW_1409	NZ_CP008706.1	1407736	1408392	+	WP_000826376.1				hypothetical protein	64.29293198	1540665856	0.277801982	5.545915845	2.92E-08	7.47E-08	7.05521261		
ABUW_RS10805	ABUW_3255	NZ_CP008706.1	3284472	3287364	+	WP_000183084.1				23S ribosomal RNA	8602.37311	1537740978	0.554043203	2.775489291	0.005518711	0.008129811	2.079363797		
ABUW_RS10420	ABUW_2527	NZ_CP008706.1	2547614	2547473	+	WP_001007559.1				epoxyguanosine oxidase GshH	2542.090483	1535891241	0.319447656	4.807962689	1.52E-06	3.38E-06	5.471433332		
ABUW_RS02050	ABUW_0975	NZ_CP008706.1	1018442	1018925	-	WP_000401355.1				hypothetical protein	39.98401755	1533545503	0.455017832	3.373804981	0.000741069	0.00148735	2.903296599		
ABUW_RS0315	ABUW_1708	NZ_CP008706.1	1707738	1710011	+	WP_000998542.1				methylglutemyl-dependent oxidoreductase	4.421819185	1531482934	0.200945632	7.839049511	2.21E-14	8.69E-14	10.06077204		
sRNA9	no	no	no	no	no	no	no	no	no	no									
sRNA5	no	no	no	no	no	no	no	no	no	no									
ABUW_RS18335	ABUW_3868	NZ_CP008706.1	3939316	3937907	-	WP_000001967.1				23S ribosomal RNA	8562.01419	153264229	0.55818201	2.74613826	0.006030767	0.00907375	2.024024072		
ABUW_RS10600	ABUW_3102	NZ_CP008706.1	3125141	3126522	-	WP_001856861.1				DUF2167 domain-containing protein	12.0149465	1532590354	0.174201478	8.797803383	1.40E-18	7.14E-18	16.140364		
ABUW_RS09310	ABUW_1912	NZ_CP008706.1	1914091	1914009	+	WP_002035810.1				TerR/ActR family transcriptional regulator	91.51165441	1531422638	0.635519185	2.417314673	0.016634772	0.022210141	1653414705		
ABUW_RS04745	ABUW_0967	NZ_CP008706.1	977483	977804	-	WP_001078074.1				HlyD family secretion protein	967.0311775	1530724722	0.182938089	11.93109973	8.1E-33	9.5E-32	31.02182338		
ABUW_RS07770	ABUW_1693	NZ_CP008706.1	1683217	1687722	+	WP_000852508.1				translocation-assembly module TamB domain-containing protein	6799.971211	1527188617	0.17206184	11.1064284	8.34E-29	7.81E-28	10.27116988		
ABUW_RS12380	ABUW_2547	NZ_CP008706.1	2538800	2539903	+	WP_001258339.1				FAD-binding oxidoreductase	61.01490195	1527189531	0.350154184	4.363496428	1.28E-05	2.62E-05	4.592495966		
ABUW_RS10950	ABUW_1485	NZ_CP008706.1	1453892	1453453	+	WP_00184522.1				DMT family protein	497.964594	1527239082	0.277457372	5.064409821	3.70E-08	9.36E-08	7.08856754		
ABUW_RS06675	ABUW_1568	NZ_CP008706.1	1583405	1584865	+	WP_001016533.1				aminooxy- histidine dephosphatase	1030.403716	1526825866	0.195483024	3.231580572	1.85E-16	8.42E-16	15.07454896		
ABUW_RS09370	no	NZ_CP008706.1	3041499	3041858	-		ssaA			transfer-messenger RNA	4								

ABLW_R0307	ABLW_0756	NZ_CP008706.1	722237	722620	+	WP_000807875.1	hypothetical protein	32	93 920 961	14445740.7	0.30872935	4.678574578	2.886	0.6	6.235e	1.207002471
ABLW_R0300	ABLW_0751	NZ_CP008706.1	722620	7230731	+	WP_000930308.1	ABC transporter ATP-binding protein	107	88396 096	1424239.97	0.97258032	2.006	23.2	17.23	1.0388387	
ABLW_R08440	ABLW_0753	NZ_CP008706.1	7370234	737343	+	WP_00037070.1	PAS domain-containing protein	930	239 2424	144 96339.0	0.786854	8.064803859	7.346	9.	3.96	5.44953308
ABLW_R08230	ABLW_890	NZ_CP008706.1	688764	687437	+	WP_000579811.1	FMN-binding glutamate synthase family protein	157	1237 3201	144085003.0	0.858883	7.71812524	9.16	9.	3.76	0.34074929
ABLW_R0350	ABLW_2841	NZ_CP008706.1	2533891	2533262	+	WP_000203777.1	APC family permease	918800	9307	143988848	0.29966 0	4.804874795	1.556	0.6	3.42E	0.64610794
ABLW_R0460	ABLW_4996	NZ_CP008707.1	58930	59 86	+	WP_00 87 807.8.1	hypothetical protein	84	25733039	14396771.0	0.94283593	3.475 60499	0.005 0662	0.00879631	3.05569494	
ABLW_R06260	ABLW_4998	NZ_CP008707.1	592566	594 08	+	WP_00 90 7729.1	NAD(P)FAD-dependent oxidoreductase	524	254710	143989579	0.880726	7.646428 9	2.075	4.	8.66	1.4088 09
ABLW_R0330	ABLW_2592	NZ_CP008706.1	296703	2967302	+	WP_000847096.1	hypothetical protein	51273338	18	1437672521	0.3895346	3.66893385	0.002243584	0.00047478	3.35957 067	
ABLW_R0160	ABLW_2397	NZ_CP008706.1	234886	2398504	+	WP_00024546.1	malonate decarboxylase hcp-ABC synthase	177	855566	143642577.07	0.28855 98	4.7905 078	0.625	0.7	8.82	0.284332
ABLW_R0785	ABLW_808	NZ_CP008706.1	600401	604025	+	WP_000070779.1	mAb	2650	287	143505769	0.263802	6.6349351	3.286	1.	103E	0.98535744
ABLW_R0380	ABLW_2678	NZ_CP008706.1	288763	288882	+	WP_000020811.1	HisE/HisU family protein	244	190 145	14331974	0.35250883	6.03042687	1.1E	0.9	3.5E	0.80 14587
ABLW_R0375	ABLW_2830	NZ_CP008706.1	2836264	28373 0	+	WP_00 980954.1	RHS repeat-associated core domain-containing protein	51518498	143303342	0.210423	6.790093 129	1.02E	1.1	3.68E	1.0	6.424 874
ABLW_R0360	ABLW_2810	NZ_CP008706.1	2809273	282609	+	WP_00368893.1	ATP-binding protein	430	4302525	143045025	0.94262286	8.723704585	1.65E	9.	135E	7.869919
ABLW_R0610	ABLW_5007	NZ_CP008706.1	3036	3306	+	WP_00 981304.1	BlaA antitoxin family protein	734	666793	143940878	0.20566988	6.962 97476	3.35E	2.	1.96E	0.3507388
ABLW_R0515	ABLW_2911	NZ_CP008706.1	2920756	292 448	+	WP_0010805.1	ABC transporter ATP-binding protein	200	259135	143395045	0.20058789	7.00867 805	9.97E	13.	3.66E	0.14490 97
ABLW_R0490	ABLW_3798	NZ_CP008706.1	3859808	3860509	+	WP_00 903528.1	Siderocalyx NAD(P)-dependent oxidoreductase	290	239791	14273865	0.75780825	188357 447	0.05622967	0.07802629	0.17232408	
ABLW_R0245	ABLW_3051	NZ_CP008706.1	6978	751	+	WP_00128484.1	hypothetical protein	219	65506	142687404	0.24680044	0.77768437	7.61E	0.9	0.47E	6.6802432
ABLW_R04750	ABLW_3209	NZ_CP008706.1	305535	306697	+	WP_008080283.1	GNA1 family N-acyltransferase	83	9556 04	14256 0739	0.56690776	3.56225 106	8.50E	0.8	2.09E	0.6803350
ABLW_R0515	ABLW_2783	NZ_CP008706.1	2778966	2779602	+	WP_00745290.1	DUF3237 domain-containing protein	23	860961	142454661	0.95656962	2.392 97 861	0.067904	0.02370945	1.64 06E	0.9616
ABLW_R0510	ABLW_3326	NZ_CP008706.1	336278	336368	+	WP_000898220.1	copper resistance protein CopC	71	11505836	142357559	0.30017793	3.74244827	2.1E	0.6	4.60E	0.33737454
sRNA19	no	no	no	no	no	no	no	305	773355	142357559	0.243089	5.88002969	3.85E	0.9	1.06E	0.79760 858
sRNA19	no	no	no	no	no	no	no	305	773355	142357559	0.243089	5.88002969	3.85E	0.9	1.06E	0.79760 858
ABLW_R0885	ABLW_820	NZ_CP008706.1	8 9649	8 9678	+	WP_00 07 9433.1	nuclear transfer factor 2 family protein	15	26 7437	14864389	0.2458485	8.88430 12	3.95E	0.9	1.06E	0.796 707
ABLW_R0890	ABLW_2240	NZ_CP008706.1	222999	223035	+	WP_00 90 9278.1	DUF 649 domain-containing protein	304	378 367	148 1957	0.14929482	5.0570 149	2.06E	2.1	1.27E	2.209 8614
ABLW_R0390	ABLW_3573	NZ_CP008706.1	363205	363347	+	WP_00020272.1	fadA	5429	80509	14804853	0.27879722	5.50398672	3.70E	0.8	9.36E	0.70285744
ABLW_R08140	ABLW_871	NZ_CP008706.1	66344	66344	+	WP_000409843.1	tal	483	726 706	147342395	0.99228854	7.089 9838	135E	4.	1.27E	0.10279 96
ABLW_R0760	ABLW_2210	NZ_CP008706.1	220026	220098	+	WP_08592089.1	glutathione S-transferase N-terminal domain-containing protein	368	3282	148470947	0.97 862439	9.0127823	2.0E	1.	1.5E	8.795303 9
ABLW_R0565	ABLW_1823	NZ_CP008706.1	18884	18995	+	WP_00068943.1	hypothetical protein	48	5955034	1408874002	0.23186626	6.0944 059	1.0E	0.9	3.5E	0.80447 548
ABLW_R0705	ABLW_2617	NZ_CP008706.1	2608081	262952	+	WP_00008 1475.1	RHS domain-containing protein	5454	602	140842631	0.98005459	7.80835 43	1.6E	1.	1.3E	0.3838951
ABLW_R0425	ABLW_2911	NZ_CP008706.1	83 3015	83 1015	+	WP_004042311.1	CopD family outer membrane protein	404	4827998	140726243	0.98089833	3.447646567	7.90E	0.6	1.45E	0.74802247
ABLW_R0035	ABLW_3301	NZ_CP008706.1	332005	333378	+	WP_000862841.1	SRD family oxidoreductase	708	0228595	1403876309	0.80223458	7.789 02562	6.75E	5.	2.78E	1.50643507
ABLW_R0085	ABLW_0308	NZ_CP008706.1	62092	63303	+	WP_00 923507.1	alpha-beta hydrolase	454	225 48	139304848	0.90394986	8.724097909	2.68E	9.	135E	7.80739878
ABLW_R0850	ABLW_0377	NZ_CP008706.1	40200	40300	+	WP_00 91846 94.1	oxygen-dependent copper-binding cytochrome oxidase	38	627 263	139801829	0.30907 425	6.85858995	3.45E	1.	1.06E	0.96087 1
ABLW_R0919	ABLW_2660	NZ_CP008706.1	265555	265664	+	WP_00 90852.1	right-handed parallel-beta-helix repeat-containing protein	934	9873343	139 982239	0.20097 428	6.62595235	3.45E	1.	1.06E	0.96982026
ABLW_R0250	ABLW_3749	NZ_CP008706.1	3805847	38065 9	+	WP_000625445.1	glutathione S-transferase	138	97 935	139096633	0.9134083	8.622524878	6.53E	9.	3.9E	7.44655742
ABLW_R0125	ABLW_2390	NZ_CP008706.1	2378950	2379954	+	WP_000566431.1	cybB	98	105 175	139037676	0.32309052	3.2187 408	0.0018904	0.00239522	2.66605 95	
ABLW_R0385	ABLW_2573	NZ_CP008706.1	3629099	3632062	+	WP_000898942.1	fadB	6097	177	13899 878	0.83833255	4.90474424	9.55E	0.7	1.06E	0.5678853
ABLW_R0150	ABLW_3274	NZ_CP008706.1	326880	236 666	+	WP_00 943298.1	hydrolase	277	700689	13883840	0.87 9794	8.0770258	6.50E	6.	2.88E	5.4030555
ABLW_R0530	ABLW_2579	NZ_CP008706.1	2573456	2573456	+	WP_00 066523.1	tacC	4946	0799 5	1387537394	0.2649976	5.24406801	157E	0.7	3.75E	0.62478366
ABLW_R0845	ABLW_838	NZ_CP008706.1	83801	834526	+	WP_000390 85.1	pcaH	17	768344	138666029	0.7202375	5.12467832	2.86E	0.7	1.47E	0.1775005
ABLW_R0910	ABLW_2782	NZ_CP008706.1	2777259	2778509	+	WP_00004 032.1	OspY family protein	52	476482	138333021	0.95838369	3.97326889	8.23E	0.5	0.62E	0.3818884
ABLW_R08830	ABLW_8 5	NZ_CP008706.1	8 9066	8 9128	+	WP_00 88603.1	YnfA family protein	956	407309	13847087	0.220327	6.29059345	3.3E	0.	9.35E	0.93002844
ABLW_R0820	ABLW_3757	NZ_CP008706.1	381340	381377	+	WP_000483007.1	DoxC family protein	80	620673	138054249	0.62303951	5.66237964	9.26E	1.	164E	0.74426973
ABLW_R04750	ABLW_0681	NZ_CP008706.1	67867	980 04	+	WP_00192047.1	ToC family protein	907	00678	1380272382	0.935 925	5.2138951	5.42E	4.	2.06E	0.26005 37
ABLW_R0395	ABLW_2888	NZ_CP008706.1	288842	288964	+	WP_00708728.1	uase accessory protein UreI	457	302331	137 075297	0.7380595	4.9264327	3.67E	1.89E	0.6	5.723 1075
ABLW_R0075	ABLW_4011	NZ_CP008706.1	6469	6684	+	WP_00 910347.1	hypothetical protein	523	0526961	137 095249	0.27558256	4.97526669	6.52E	0.7	1.49E	0.86704665
ABLW_R0085	ABLW_3310	NZ_CP008706.1	3345204	3346025	+	WP_000897823.1	SRD family NAD(P)-dependent oxidoreductase	276	0305649	136916846	0.297427	6.230734559	6.48E	0.9	1.35E	0.89755078
ABLW_R0895	ABLW_2241	NZ_CP008706.1	2230382	2230682	+	WP_000205997.1	integration host factor subunit beta	6062	8194	136632925	0.3061268	0.4608756	1.3E	0.5	1.00E	24 39888 14
ABLW_R0660	no	NZ_CP008706.1	309461	309894	+	no	no	20002	8512	136896305	0.33684701	4.0478014	9.35E	0.5	0.0001942	3.9933534
ABLW_R0919	ABLW_2862	NZ_CP008706.1	287 943	287 984	+	WP_007082321.1	RNase P RNA component class A	27801	4666	135747416	0.88884750	4.69894352	6.62E	0.6	5.66E	0.24762805
ABLW_R02040	ABLW_0779	NZ_CP008706.1	764738	764889	+	WP_00 923490.1	hypothetical protein	242	0239509	135679641	0.31850776	6.80853598	4.34E	0.5	8.35E	0.4704395
ABLW_R0390	ABLW_2778	NZ_CP008706.1	125257	125462	+	WP_00 184645.1	trypsinogen synthase subunit beta	682	3 9405	135470495	0.14639351	10.8264771	6.45E	4.	27E	2.3499504
ABLW_R0285	ABLW_2843	NZ_CP008706.1	289591	2896842	+	WP_000735778.1	aspartate dehydrogenase	62	5045 874	13586533	0.49032 939	3.870730495	0.0008481	0.0002032	3.69607 17	
ABLW_R0775	ABLW_3638	NZ_CP008706.1	365711	368557	+	WP_00 984577.1	pfpG	8048	07775	134032367	0.8234809	8.6274828	107E	9.	5.5E	9.2 2585677
ABLW_R03260	ABLW_0662	NZ_CP008706.1	688299	688405	+	WP_00 90963.1	NADH flavin oxidoreductase/NADH oxidase	3052	889033	1345843794	0.247777371	5.442648437	5.25E	0.8	13.6E	0.82686462
ABLW_R0475	ABLW_2087	NZ_CP008706.1	206779	2068955	+	WP_00 95238.1	hypothetical protein	53	9691036	134487925	0.32346703	4.9737 039	3.95E	0.5	6.9E	0.52067366
ABLW_R0310	ABLW_3390	NZ_CP008706.1	343374	343722	+	WP_00 072702.1	NADP-dependent glyoxylate:3-phosphate dehydrogenase	7930	820363	134277655	0.7559251	6.7332082	2.94E	1.	9.02E	1.40489962
ABLW_R06235	ABLW_078	NZ_CP008706.1	102178	103367	+	WP_000356498.1	hypothetical protein	54	7149927	134 437641	0.2824363	4.79510872	2.04E	0.6	4.55E	0.5330354
ABLW_R0495	ABLW_0916	NZ_CP008706.1	92249	922495	+	WP_000250932.1	lytic domain repeat protein	22638	85735	134070562	0.9845 074	7.22942545	4.85E	1.	1.76E	0.17399547
ABLW_R006	ABLW_2073	NZ_CP008706.1	2054 69	2055940	+	WP_03 8045811.1	bifunctional metallophosphatase/5'-nucleotidase	55	514876	1340322 04	0.96945458	8.605497318	10E	1.1	3.35E	0.4772866
ABLW_R09020	ABLW_053	NZ_CP008706.1	84044	85057	+	WP_00104515.1	SRD family oxidoreductase	427	810335	1337330661	0.72240945	7.765462847	8.3E	5.	3.35E	0.47475304
ABLW_R0035																

ABUW_RS1760	ABUW_3533	NZ_CP008706.1	3590643	3592025	+	WP_000764528.1		1685.951427	12768043	0.14928296	8.55 W 4223	1.22E-17	5.85E-17	16.233 65097
ABUW_RS04735	ABUW_0965	NZ_CP008706.1	975261	976332	-	WP_000657699.1		36.6000776	127626607	0.183634355	6.94988236	3.65E-12	1.26E-11	10.9006085
ABUW_RS03890	ABUW_0793	NZ_CP008706.1	773502	773801	+	WP_000335868.1		2287.631394	1274610438	0.188150432	6.774422048	1.25E-11	4.09E-11	10.3884285
ABUW_RS16885	ABUW_3472	NZ_CP008706.1	3520481	3521158	+	WP_000232196.1		394.3406979	1272387443	0.19575529	8.45090849	2.91E-17	1.37E-16	16.86200541
ABUW_RS16355	ABUW_3368	NZ_CP008706.1	1407402	1407773	-	WP_001081565.1		10642.48459	1271877899	0.179585892	7.082286835	1.42E-12	5.02E-12	11.29292476
ABUW_RS16355	ABUW_3732	NZ_CP008706.1	1728754	1730247	-	WP_000089272.1	glnD	1941608035	1270381014	0.172619111	7.359488554	1.85E-13	6.90E-13	12.1615972
ABUW_RS10300	ABUW_2324	NZ_CP008706.1	2307851	2308774	-	WP_001041738.1		2779.404583	1268946310	0.279381688	4.539196708	5.76E-06	12.1E-05	4.97229543
ABUW_RS07825	ABUW_1602	NZ_CP008706.1	6197969	6198673	+	WP_000923629.1		491.9674852	1262335437	0.232451902	5.430523182	5.62E-08	1.40E-07	6.854665782
ABUW_RS06570	ABUW_1847	NZ_CP008706.1	935661	9360530	+	WP_000197593.1		434.2580702	1262324919	0.238949401	5.282435894	1.27E-07	3.08E-07	6.51055184
ABUW_RS16670	ABUW_3429	NZ_CP008706.1	3474605	3476053	+	WP_001088252.1		3045.317383	1261045655	0.28802164	4.37932921	1.19E-05	2.44E-05	4.610453302
ABUW_RS06670	ABUW_1567	NZ_CP008706.1	1382851	1383234	+	WP_000735997.1		656.8044979	1260426209	0.194710369	6.473338911	9.59E-11	2.93E-10	9.533736495
ABUW_RS05195	ABUW_1658	NZ_CP008706.1	1067320	1068366	-	WP_000005193.1		663.2602768	1257504196	0.220757999	5.096301834	1.22E-08	3.22E-08	7.492199294
ABUW_RS06165	ABUW_1261	NZ_CP008706.1	1295906	1296121	+	WP_000560785.1		1504.379185	1257200771	0.164067754	7.062692638	1.82E-14	7.21E-14	10.4230083
ABUW_RS11005	ABUW_2325	NZ_CP008706.1	2308990	2309550	+	WP_000037185.1		124.0720834	1256400383	0.453373147	2.7170479	0.005584189	0.008435958	2.073885602
ABUW_RS20240	no	NZ_CP008706.1	2508189	2508305	+	WP_000514392.1		198.0471592	1254826122	0.468806145	2.676641794	0.007436409	0.01035467	1.957209287
ABUW_RS16025	ABUW_0372	NZ_CP008706.1	395481	395735	-	WP_000018719.1		10848.91057	1253600348	0.591938888	2.1045553	0.033906748	0.045988433	1.73701783
ABUW_RS10805	ABUW_2282	NZ_CP008706.1	2207544	2208866	+	WP_000953841.1		861.5937482	1252285563	0.100168688	7.819029864	5.32E-15	2.20E-14	10.65718905
ABUW_RS06265	ABUW_1265	NZ_CP008706.1	1208155	1208589	+	WP_000375508.1		8170001761	1252181963	0.387589255	3.230618527	0.00125227	0.00202306	2.636193965
ABUW_RS17305	ABUW_3556	NZ_CP008706.1	3614094	3615804	+	WP_000753277.1		668.3662979	1251209107	0.123385859	9.380370257	6.57E-21	3.94E-20	19.40437847
ABUW_RS18910	ABUW_3883	NZ_CP008706.1	395103	3952395	-	WP_001052448.1		5109.302874	1250994407	0.141445102	8.843730349	9.26E-19	4.81E-18	17.3749534
ABUW_RS101820	ABUW_0371	NZ_CP008706.1	394311	395411	+	WP_000110468.1		462.184785	1250100527	0.187434272	6.869701409	2.56E-11	8.16E-11	10.0881033
ABUW_RS16180	ABUW_3393	NZ_CP008706.1	3365795	3366208	-	WP_000732830.1		253.8775604	1248101446	0.395475897	3.15394819	0.00199773	0.00258336	2.587815002
sRNA84	no	no	no	no	no	no	no	1020.21865	1244287621	0.246097797	5.066069718	4.28E-07	9.95E-07	6.02702129
ABUW_RS15500	ABUW_2798	NZ_CP008706.1	2795178	2796641	+	WP_0000442089.1		696.6580092	1244114185	0.358694228	3.488453259	0.000821464	0.000090527	3.455033955
ABUW_RS09100	ABUW_1655	NZ_CP008706.1	1057263	1058234	+	WP_012300601.1		57.6401812	1243087687	0.290333006	4.27861424	1.88E-05	3.77E-05	4.24419711
ABUW_RS19905	no	NZ_CP008706.1	2870712	2870896	+		satS	102171106	1242983716	0.245616757	5.060663328	4.16E-07	9.73E-07	6.01020964
ABUW_RS08865	ABUW_1622	NZ_CP008706.1	1617655	1618749	+	WP_000051050.1		516.0213924	1242712933	0.193768752	9.12344697	8.08E-20	4.54E-19	18.3432706
ABUW_RS08935	ABUW_1836	NZ_CP008706.1	1832006	1833361	+	WP_000168123.1		911959398	1241225419	0.320167612	3.876798812	0.00010584	0.000196692	3.70621298
ABUW_RS16100	ABUW_2088	NZ_CP008706.1	2061070	2061420	+	WP_000664154.1		1014078222	1240319395	0.406025866	3.054779339	0.00252262	0.00357178	2.447186556
ABUW_RS10245	ABUW_2475	NZ_CP008706.1	2468454	2469454	+	WP_001186958.1		45.78291473	1239956391	0.3167905	3.370317679	0.00750819	0.00162524	2.988754756
ABUW_RS06930	ABUW_1422	NZ_CP008706.1	1412317	1415840	+	WP_000093892.1		1638272322	1239483373	0.498425056	2.53252556	0.01034411	0.01367026	1.75502409
ABUW_RS04400	ABUW_2768	NZ_CP008706.1	2760339	2760993	+	WP_000834590.1		47.0978195	1239069693	0.358595023	3.451916072	0.00056623	0.000594718	3.120214681
ABUW_RS04840	ABUW_0987	NZ_CP008706.1	1010095	1010125	+	WP_001016705.1		1042.719193	12387770808	0.201675051	6.165471005	7.87E-10	2.29E-09	8.64021898
ABUW_RS08835	ABUW_1816	NZ_CP008706.1	1819555	1821170	+	WP_000993005.1		905625454	1237848101	0.170406424	7.264879754	3.74E-13	1.37E-12	11.8628229
ABUW_RS07365	ABUW_1510	NZ_CP008706.1	1495500	1496762	+	WP_000681841.1		53.32132785	1235003628	0.424870368	2.10677731	0.005851731	0.005544428	2.2476110291
ABUW_RS09630	ABUW_1980	NZ_CP008706.1	1985528	1986901	+	WP_001051828.1		1020.13176	1234533279	0.21853892	5.799903593	6.64E-09	1.76E-08	7.746434366
ABUW_RS117175	ABUW_3530	NZ_CP008706.1	3586588	3588190	+	WP_000858585.1		437.5036187	1234362245	0.141072186	7.498625958	2.14E-18	1.08E-17	16.98772249
ABUW_RS20460	ABUW_1624	NZ_CP008706.1	1414827	1414937	+	WP_000702347.1		1014180041	1234195303	0.679095054	1.817411708	0.069154096	0.089675524	10.04256076
ABUW_RS17455	ABUW_3588	NZ_CP008706.1	3645367	3645864	+	WP_000996189.1		405.3375644	123296703	0.10009895	6.846053399	7.59E-12	2.54E-11	9.25692168
ABUW_RS03716	ABUW_0757	NZ_CP008706.1	752595	752774	+	WP_000066269.1		1414490936	1231211962	0.426196802	2.88340553	0.003934006	0.00658991	2.217052425
ABUW_RS07270	ABUW_1491	NZ_CP008706.1	1476869	1479367	+	WP_000063294.1	csuD	970.5711689	1230428449	1.126997506	108996297	NA	NA	!VALUE
ABUW_RS10510	ABUW_2595	NZ_CP008706.1	2589493	2589904	+	WP_000912261.1		201559478	1229628019	0.210622658	5.838061454	5.28E-09	1.44E-08	7.425209558
ABUW_RS14015	ABUW_2885	NZ_CP008706.1	2892495	2893370	+	WP_001071965.1		67.33718625	1229245221	0.284776116	4.193532031	1.58E-05	3.20E-05	4.84419947
ABUW_RS04175	ABUW_0851	NZ_CP008706.1	83103	832101	+	WP_001177681.1		1038.029615	1228991959	0.173619216	7.078226693	1.46E-12	5.15E-12	11.28501454
ABUW_RS18745	ABUW_3243	NZ_CP008706.1	3272162	3273307	+	WP_000370427.1		503.1014285	1225987726	0.89496271	7.233105668	4.72E-19	1.76E-18	11.7845604
ABUW_RS08205	ABUW_1685	NZ_CP008706.1	1680469	1681917	+	WP_089520732.1		1020.889561	1225578476	0.177901639	6.889883056	5.62E-12	1.90E-11	12.72104338
ABUW_RS08335	ABUW_1710	NZ_CP008706.1	1710049	1710272	+	WP_0003709986.1		923.311446	122518304	0.164031954	7.953943226	1.81E-15	7.60E-15	14.1665465
ABUW_RS14110	ABUW_2910	NZ_CP008706.1	2929023	2930752	+	WP_001045157.1		1035.140224	1224145622	0.123936271	9.208518801	3.31E-20	1.90E-19	18.72121818
ABUW_RS08285	ABUW_1702	NZ_CP008706.1	1698654	1699244	+	WP_001025253.1		32.76561499	121976831	0.33916403	3.190293199	0.000330306	0.000584969	3.32887402
ABUW_RS14295	ABUW_2945	NZ_CP008706.1	2960308	2961102	+	WP_000988810.1		49.58316409	12170665	0.357194579	3.401816992	0.00066941	0.00115501	2.944471421
sRNA40	no	no	no	no	no	no	no	2.421647124	1217482076	1.140581805	1.0674297	0.285781332	0.338193005	0.479003651
ABUW_RS12765	no	NZ_CP008706.1	2628331	2629679	+			168.165964	1216069974	0.254419904	4.775957427	1.79E-06	3.92E-06	5.44641069
ABUW_RS20485	ABUW_4191	NZ_CP008707.1	6270	6410	+	WP_0000091026.1		69.58426426	1214624745	0.435919375	2.786390177	0.005320867	0.008085194	2.09231391
ABUW_RS15445	ABUW_2769	NZ_CP008706.1	2766066	2767859	+	WP_000811587.1		45.75772442	1214210179	0.305268103	3.977870692	6.96E-05	0.00019184	3.880610545
ABUW_RS15255	ABUW_2878	NZ_CP008706.1	2871422	2871925	+	WP_000616319.1		7035.970453	1213237463	0.243558849	4.977555304	6.44E-07	1.47E-06	10.51874101
ABUW_RS15055	ABUW_3161	NZ_CP008706.1	3124581	3125141	+	WP_000716116.1		474.4625995	1211776575	0.167264161	7.705375197	1.30E-14	5.24E-14	10.28053271
ABUW_RS18745	ABUW_3850	NZ_CP008706.1	3910997	3915057	+	WP_000732887.1		903.688375	1208949052	0.222052144	5.442838916	5.24E-08	1.31E-07	6.882849652
ABUW_RS18985	ABUW_3899	NZ_CP008706.1	3968537	3969535	+	WP_000592161.1		771.6166579	1208387879	0.163638022	7.895161647	3.69E-16	1.54E-14	13.81274981
ABUW_RS12375	ABUW_0576	NZ_CP008706.1	2536659	2538799	+	WP_000616330.1		36.8866973	1206477353	0.367728444	3.285359219	0.00198024	0.000196958	2.77319165
ABUW_RS19530	ABUW_1110	NZ_CP008706.1	169525	170232	+	WP_000733532.1	tbcD	103.8727321	1205669974	0.256553921	4.69947982	2.61E-06	5.64E-06	5.248432036
ABUW_RS03010	ABUW_4650	NZ_CP008706.1	4671862	4684703	+	WP_000108875.1		454.3176849	120451475	0.413196427	8.41625732	1.04E-17	1.90E-16	15.72202083
ABUW_RS12145	ABUW_2498	NZ_CP008706.1	2491831	2493300	+	WP_001033063.1		803.8615638	1201645					

ABUW_RS1000	ABUW_2466	NZ_CP008706.1	2458034	245937	-	WP_000208930.1		MF5 transporter	63.15319237	1.54959859	0.29397609	3.929556192	8.51E-05	0.00015933	3.79170175
ABUW_RS07605	ABUW_558	NZ_CP008706.1	646276	154805	-	WP_000106102.1	pgaB	poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgaB	63.03239142	1.64957472	0.248018981	4.656730165	3.21E-06	6.91E-06	5.76070096
ABUW_RS06016	ABUW_231	NZ_CP008706.1	672825	1274309	-	WP_000156408.1		MF5 transporter	95.9554626	1.63919363	0.18342671	6.294040004	3.16E-10	9.30362079	
ABUW_RS1025	ABUW_329	NZ_CP008706.1	212039	213335	+	WP_00514545.1		hypothetical protein	86.12516401	1.60292053	0.43233237	2.660666035	0.007789827	0.0165197	193733508
ABUW_RS02685	ABUW_0465	NZ_CP008706.1	477246	477819	+	WP_000792527.1		lytic transglycosylase domain-containing protein	2965.951109	1.84663548	0.1215621	9.87620638	2.64E-21	1.61E-20	10.791901
ABUW_RS0585	ABUW_2817	NZ_CP008706.1	291808	282302	-	WP_000482851.1		type VI secretion system pilin protein VsgG	3702.319214	1.18708325	0.22222535	5.16510204	2.60E-07	6.67E-07	623453379
ABUW_RS02330	ABUW_0656	NZ_CP008706.1	663238	683669	+	WP_000202555.1	macL	large conductance mechanosensitive channel protein MacL	42.01846486	1.14782391	0.182499551	6.2857718547	3.20E-10	6.61E-10	9.07057074
ABUW_RS016	ABUW_4107	NZ_CP008707.1	67345	67845	+	WP_0001058570.1	kepB	signal peptidase I	84.35772592	1.145106193	0.276681821	4.10895057	3.49E-05	6.82E-05	6.46848786
ABUW_RS02730	ABUW_0555	NZ_CP008706.1	656947	557147	-	WP_000100085.1		TarD/Cla4 C4-type zinc finger protein	34.91035448	1.141822444	0.449103063	2.542352865	0.011610895	0.05946404	1173737244
ABUW_RS09735	ABUW_2004	NZ_CP008706.1	2000651	2000935	-	WP_000050492.1		DUF2523 domain-containing protein	8.5104264	1.141095716	0.522896814	2.182257924	0.020905052	0.039757618	1400578989
ABUW_RS03725	ABUW_0759	NZ_CP008706.1	753018	753365	+	WP_0001024261.1		hypothetical protein	29.75884587	1.136187262	0.322145151	3.526941954	0.000420389	0.000733541	3.134575475
ABUW_RS1805	ABUW_2840	NZ_CP008706.1	2850997	2852142	-	WP_000227832.1		LyfM peptidoglycan-binding domain-containing protein	810.430189	1.13361024	0.140816789	8.050559756	8.24E-16	3.58E-15	14.446338
ABUW_RS19080	ABUW_4012	NZ_CP008707.1	6689	7185	+	WP_0000861205.1		therمونase family protein	110.227772	1.134004054	0.207172374	5.47080883	4.48E-08	1.02E-07	6.549010013
ABUW_RS08970	ABUW_843	NZ_CP008706.1	183999	1841428	+	WP_000004228.1		glucosyl/quinolate/hikimate family membrane-bound PQQ-dependent dehydrogenase	70.8244522	1.131617609	0.196272865	5.765532624	8.14E-09	2.18E-08	7.661912943
ABUW_RS06855	ABUW_3605	NZ_CP008706.1	1406546	1406911	+	WP_000154887.1		hypothetical protein	54.76696799	1.12677005	0.256289645	4.396459351	1.10E-05	2.26E-05	6.445765444
ABUW_RS19140	ABUW_0023	NZ_CP008707.1	12161	1924	+	WP_000724805.1		PasA family protein	3454.018065	1.126008962	0.199505896	5.643988395	1.06E-08	4.33E-08	7.3637718004
ABUW_RS00255	ABUW_4052	NZ_CP008706.1	57716	58452	-	WP_000100767.1		dienelactone hydrolase family protein	902.252445	1.1466017	0.257494332	3.460934042	1.30E-05	2.64E-05	4.577851925
ABUW_RS09660	ABUW_941	NZ_CP008706.1	936306	937537	+	WP_000104701.1		right-handed parallel-beta-helix repeat-containing protein	55.7402156	1.14262612	0.2743045	4.09851963	4.16E-05	8.06E-05	4.059710927
ABUW_RS04870	ABUW_0993	NZ_CP008706.1	1004910	1006790	+	WP_000058386.1	toIB	Tol-Pal system beta-proteol repeat protein TolB	5559.546463	1.14118864	0.293339891	5.523843098	3.34E-08	8.47E-08	7.017934869
ABUW_RS16495	ABUW_2160	NZ_CP008706.1	2140911	2142017	+	WP_000373497.1		porin	310.0805955	1.0167222	0.181645993	6.164954206	7.05E-10	2.03E-09	8.979782026
ABUW_RS01615	ABUW_053	NZ_CP008706.1	129216	1292456	-	WP_000100085.1		hypothetical protein	40.20597402	1.116216784	0.350799448	3.18108885	0.001465708	0.002375438	2.624255629
ABUW_RS10255	ABUW_2314	NZ_CP008706.1	2299784	2299963	-	WP_000100569.1		hypothetical protein	18.5471678	1.117109248	0.63105265	1.076895881	0.07094464	0.08981467	100444194
ABUW_RS03190	ABUW_0648	NZ_CP008706.1	635328	635843	+	WP_000447151.1		GspE/FltF family pseudopilin	794.1026907	1.116852866	0.212718068	5.261464274	1.52E-07	3.64E-07	6.438303469
ABUW_RS19175	ABUW_2715	NZ_CP008706.1	2698499	2698962	+	WP_000381295.1		aromatic acidH+ symported lytic MF5 transporter	40.8189957	1.11682419	0.357334477	3.125430683	0.001775449	0.002856603	2.544302242
ABUW_RS00500	ABUW_0510	NZ_CP008706.1	12476	1480	+	WP_0001021535.1		hypothetical protein	102.4015563	1.1140276	0.242024381	4.593455251	4.35E-06	9.26E-06	5.033541698
ABUW_RS04605	ABUW_0939	NZ_CP008706.1	146349	1466914	+	WP_000154887.1		helicum-helic transcriptional regulator	38.2051044	1.11854477	0.399419583	2.7183675423	0.005374879	0.008143862	2089186544
ABUW_RS00675	ABUW_043	NZ_CP008706.1	184655	185656	-	WP_000095188.1	mIB	lytic murein transglycosylase B	81.6730951	1.109225593	0.203005985	5.487437793	4.57E-08	1.14E-07	6.841294718
ABUW_RS1720	ABUW_3238	NZ_CP008706.1	3265780	3266406	-	WP_0002000136.1		CoA-glycosylphosphatase	6.787795029	1.10211276	0.223871029	4.954705594	7.24E-07	1.65E-06	5.782552806
ABUW_RS1900	no	NZ_CP008706.1	2443390	2443401	+			glutathione S-transferase	1413320599	1.10684413	0.242049893	4.572792526	4.81E-06	1.02E-05	4.991861069
ABUW_RS0830	ABUW_2228	NZ_CP008706.1	2218083	2218797	+	WP_000371944.1		glutathione-dependent receptor	624.6149448	1.105759533	0.136655232	7.656777688	1.40E-14	5.56E-14	13.25225895
ABUW_RS03895	ABUW_0754	NZ_CP008706.1	77380	774268	+	WP_000271493.1		helicum-helic domain-containing protein	2209.486695	1.1055707	0.206326091	5.538407497	8.40E-08	2.06E-07	6.65531596
ABUW_RS07375	ABUW_610	NZ_CP008706.1	1497172	1498771	+	WP_000195800.1		class I SAM-dependent methyltransferase	132.118501	1.10329119	0.237434647	3.37551609	0.00077389	0.00442059	2.056517758
ABUW_RS16120	ABUW_2084	NZ_CP008706.1	2055042	2056100	+	WP_0001071630.1		AraC family transcriptional regulator	187.0903886	1.104837721	0.212320453	5.180309618	2.21E-07	5.23E-07	6.28120135
ABUW_RS09665	ABUW_2052	NZ_CP008706.1	203816	2031848	+	WP_000371819.1		lytic fibrinolytic protein	65.5745857	1.10456514	0.590502801	1.870704954	0.06188988	0.06030047	1095284201
ABUW_RS1905	ABUW_3071	NZ_CP008706.1	3099162	3099242	-			rRNA	77.25231979	1.10414435	0.405190142	2.720236423	0.006523526	0.00977623	2.016771953
ABUW_RS06605	ABUW_054	NZ_CP008706.1	106078	130806	+	WP_000841565.1		GHKL domain-containing protein	102.4015563	1.103286674	0.187342162	5.889057326	3.88E-09	1.06E-08	7.973103197
ABUW_RS05325	ABUW_085	NZ_CP008706.1	109601	110064	+	WP_0002320489.1		CYH and CHAD domain-containing protein	184.121132	1.10997724	0.18978149	6.847912443	8.89E-11	2.72E-10	9.56471018
ABUW_RS19155	ABUW_0291	NZ_CP008707.1	1058	1115	+	WP_0001067227.1		hypothetical protein	118.9104617	1.100781033	0.371441848	2.96353609	0.003041064	0.004756697	2.322684475
ABUW_RS19145	ABUW_4089	NZ_CP008706.1	2069797	2071647	+	WP_000198647.1		dienelactone hydrolase family protein	38.94643016	1.099811065	0.176278827	2.92286277	0.003468293	0.00532802	2.268991694
ABUW_RS07140	ABUW_0465	NZ_CP008706.1	1454699	1456296	+	WP_0001058570.1		amino acid permease	61.15931571	1.09918674	0.276602921	3.973637269	7.08E-05	0.00133765	3.873568921
ABUW_RS01300	ABUW_2086	NZ_CP008706.1	2067158	2067688	-	WP_000373658.1		flavin reductase family protein	16.32622668	1.097423596	0.500233197	2.183224402	0.028248036	0.038658742	14.0752282
ABUW_RS09720	ABUW_2000	NZ_CP008706.1	198517	1988723	+	WP_000147909.1		hypothetical protein	335.06638	1.096833015	0.205201963	5.54516243	9.03E-08	2.21E-07	6.655371672
ABUW_RS1480	ABUW_2560	NZ_CP008706.1	2557064	2550545	-	WP_0002001416.1	tsaH	type VI secretion system ATPase TsaH	952.755043	1.095103292	0.11262759	9.755271751	1.75E-22	1.9E-21	20.3909018
ABUW_RS18660	ABUW_3873	NZ_CP008706.1	3941343	3942210	-	WP_0001033587.1		alpha/beta hydrolase	802.0312726	1.092932717	0.154410404	7.077395992	1.46E-12	5.17E-12	11.26841196
ABUW_RS09716	ABUW_999	NZ_CP008706.1	998188	1008406	+	WP_0002074156.1		hypothetical protein	90.21440549	1.092754472	0.333383819	3.273299998	6.001662997	0.00759972	2.754823333
sRNA26	no	no	no	no	no	no	no	no	23.391639348	1.092153491	0.135535555	3.402190725	0.000559983	0.000600073	3.019165637
ABUW_RS04895	ABUW_0998	NZ_CP008706.1	1009126	1010660	+	WP_0002716836.1		amido hydrolase	45.06488192	1.091754215	0.240965818	4.530742772	5.88E-08	1.23E-05	4.309291533
ABUW_RS11145	ABUW_2291	NZ_CP008706.1	2278307	2279503	-	WP_000669300.1		phosphodiesterase glycosylase family protein	732.344295	1.091423291	0.210667178	5.180794183	2.21E-07	5.23E-07	6.218736793
ABUW_RS01810	ABUW_0369	NZ_CP008706.1	39216	393378	+	WP_00010283716.1		putative DNA modification/repair radical SAM protein	430.4182933	1.091282593	0.1891020916	6.452671688	1.10E-10	3.34E-10	9.476708991
sRNA93	no	no	no	no	no	no	no	no	52.9196025	1.09117172	0.4011712	2.718989219	0.005481974	0.0097846	2.009241275
ABUW_RS00350	ABUW_090	NZ_CP008706.1	110738	110812	+	WP_00010216684.1	csy2	type I-F CRISPR-associated protein Csy2	26.67155353	1.090418032	0.13264446	8.221048378	2.02E-16	9.16E-16	5.0384412
ABUW_RS10470	ABUW_2388	NZ_CP008706.1	2105472	2106917	-	WP_0004719778.1		capsule assembly Wzd family protein	73.8123107	1.090062938	0.19761575	5.1500235	3.47E-08	8.79E-08	7.055902755
ABUW_RS14310	ABUW_2948	NZ_CP008706.1	296280	2964191	+	WP_000418172.1		FAD-dependent oxidoreductase	98.40976079	1.089529446	0.329008483	3.311054469	0.000927791	0.00143382	2.811626263
ABUW_RS19710	ABUW_3489	NZ_CP008706.1	3538557	3538855	-	WP_0001008920.1		ABC transporter	1676.547017	1.08850581	0.200562843	5.581901233	2.38E-08	6.15E-08	7.215740008
ABUW_RS07360	ABUW_009	NZ_CP008706.1	1484532	1485503	+	WP_000303270.1		acyl-CoA desaturase	82.10500026	1.08783288	0.368750912	2.95021633	0.001377517	0.004025051	2.3051915425
ABUW_RS16200	ABUW_3347	NZ_CP008706.1	332825	3336347	-	WP_0001548985.1		TadA family hydrolase	435.8104991	1.086322889	0.226543896	4.716188223	1.63E-06	3.58E-06	4.545881009
ABUW_RS16610	ABUW_3216	NZ_CP008706.1	3247773	3248948	+	WP_0000431791.1		zinc-binding dehydrogenase	187.216119	1.084198989	0.304056946	3.56688071	0.000362913	0.000638236	3.195025307
ABUW_RS10270	ABUW_2861	NZ_CP008706.1	2871422	2871635	-	WP_0001166305.1		hypothetical protein	83.3449449	1.083418304	0.301870389				

ABUW_RS12385	ABUW_2548	NZ_CP008706.1	2539900	2540832	-	WP_0008595678.1		4-hydroxyproline epimerase	75.59996242	1.022100619	0.285966207	3.574200708	0.000351299	0.000619696	3.207821439
ABUW_RS03195	ABUW_0649	NZ_CP008706.1	654223	655284	+	WP_000777885.1		OmpA family protein	530404.6495	1.019148507	0.209087054	4.874278377	1.095E-06	2.44E-06	5.62307418
ABUW_RS1975	ABUW_2319	NZ_CP008706.1	2302706	2304121	+	WP_000378386.1		cytosine permease	585.107479	1.01920958	0.269033213	3.783625624	0.0005456	0.000282542	3.548918404
ABUW_RS03665	ABUW_0744	NZ_CP008706.1	744323	744514	-	WP_001076118.1		hypothetical protein	58.99241438	1.01767895	0.28455848	3.576341081	0.000348437	0.000615185	3.21099411
ABUW_RS02160	ABUW_0438	NZ_CP008706.1	450223	451008	+	WP_000049106.1		hypothetical protein	2001.125999	1.018842854	0.254453555	3.96339747	6.43E-05	0.000122026	3.91547789
ABUW_RS12445	ABUW_2562	NZ_CP008706.1	2551291	2551959	-	WP_010322205.1		ankyrin repeat domain-containing protein	42.65708618	1.016010155	0.325330244	3.324535764	0.001793612	0.000288365	2.540055198
ABUW_RS08110	ABUW_0664	NZ_CP008706.1	1656266	1656709	+	WP_000221476.1		RDD family protein	346.9522201	1.015563371	0.277420871	3.660653775	0.000251573	0.000450282	3.346515037
ABUW_RS06215	ABUW_1274	NZ_CP008706.1	1910555	1910966	+	WP_000801877.1		hypothetical protein	29.03694474	1.015129126	0.318178053	2.658254691	0.007854651	0.01782613	1.934563966
ABUW_RS16365	ABUW_3772	NZ_CP008706.1	3829811	3831586	-	WP_002042386.1		acyl-CoA dehydrogenase	60.77439026	1.014967629	0.264247825	3.840968717	0.00012255	0.000226388	3.645160029
ABUW_RS09380	ABUW_1922	NZ_CP008706.1	1920270	1921082	-	WP_000095626.1		amidohydrolase family protein	118.1866527	1.014309668	0.297559885	3.408758093	0.000652593	0.001109408	2.954908527
ABUW_RS20330	no	NZ_CP008706.1	3870899	3871033	+			hypothetical protein	5.514458729	1.01078394	0.1020677636	0.990306738	0.32024214	0.368707935	0.433315716
ABUW_RS09975	ABUW_2054	NZ_CP008706.1	2032229	2034787	+	WP_001124963.1		fmbrl biogenesis outer membrane usher protein	1242.003872	1.00761698	0.418114761	2.42488819	0.015457103	0.02198817	1.057614492
ABUW_RS05595	ABUW_1343	NZ_CP008706.1	1186865	1189290	+	WP_000080869.1		YhdD/YJX family protein	919.5373678	1.007361538	0.3089078	3.216142739	0.001100033	0.001827676	2.738100782
ABUW_RS13385	ABUW_2757	NZ_CP008706.1	2747075	2748625	-	WP_000256739.1		NAQ(P)FAD-dependent oxidoreductase	177.1489627	1.006313965	0.27463152	3.664233315	0.000248081	0.000444427	3.352189436
ABUW_RS14475	ABUW_2981	NZ_CP008706.1	2997394	2997993	-	WP_002000381.1		biliverdin-producing enzyme	78.74481981	1.006162726	0.339791549	2.761191932	0.003065232	0.0004792324	2.91453843
ABUW_RS1890	ABUW_2403	NZ_CP008706.1	2390433	2391620	+	WP_000941172.1		MFS transporter	122.9605987	1.001491183	0.290535842	3.447048649	0.000566747	0.000969619	3.013387976
ABUW_RS1715	ABUW_2822	NZ_CP008706.1	2826369	2828399	-	WP_000205086.1		NADPH-dependent 2,4-dienoyl-CoA reductase	335.0568808	1.001334181	0.273076381	3.666864848	0.000245542	0.000404688	3.356085832

Table S4. RNA-seq data: Absolute and relative expression (ESP/MEP > 2-fold down)

ABUW_RS16495	ABUW_3394	NZ_CP008706.1	3435621	3437474	-	WP_000365488.1		phosphogluconate dehydratase	3986.957411	-1.000995018	0.271541661	-3.868340481	0.000227502	0.000409016	3.388259498
ABUW_RS16335	ABUW_3766	NZ_CP008706.1	3819796	3818743	-	WP_001288049.1		4'-phosphopantetheinyltransferase superfamily protein	568.5876529	-1.001183396	0.302829202	-3.305510086	0.000948027	0.01573795	2.803019508
ABUW_RS1216	ABUW_2306	NZ_CP008706.1	2290588	2292046	+	WP_000204465.1	queG	RNA epoxycyclooxime(34) reductase QueG	388.2119102	-1.003234738	0.201974016	-4.823846547	1.14E-06	3.13E-06	5.050520862
ABUW_RS00770	ABUW_0155	NZ_CP008706.1	170215	172932	+	WP_000086433.1	aceE	pyruvate dehydrogenase (acetyl-transfering), homodimeric type	4190.87234	-1.004879683	0.238838735	-4.20651903	2.58E-05	5.13E-05	4.89727062
ABUW_RS17585	ABUW_3612	NZ_CP008706.1	3670615	3671454	-	WP_001302011.1		hypothetical protein	900.922334	-1.004887465	0.111653873	-9.004862381	2.16E-19	1.16E-19	1.82912108
ABUW_RS09935	ABUW_2046	NZ_CP008706.1	2026511	2026714	+	WP_000301760.1		hypothetical protein	230.2948979	-1.005272234	0.261963142	-3.837456571	0.00014315	0.000229544	3.63913268
ABUW_RS06365	ABUW_1005	NZ_CP008706.1	1318955	1319398	+	WP_000204017.1		hypothetical protein	79.48119486	-1.006213492	0.300556868	-3.347815041	0.00092443	0.001362648	2.856516328
ABUW_RS00180	ABUW_0037	NZ_CP008706.1	45270	46382	+	WP_00119029.1	dnaJ	molecular chaperone DnaJ	7454.718853	-1.006593568	0.205036295	-4.909343334	9.14E-07	2.06E-06	5.886530306
ABUW_RS16335	ABUW_2188	NZ_CP008706.1	2172182	2173615	-	WP_000083876.1		SidA/LcdP-pdA family monooxygenase	1174.867092	-1.006949764	0.547757902	-1.183311708	0.066016487	0.08588325	1.060919529
ABUW_RS15920	ABUW_3278	NZ_CP008706.1	3311628	3312188	+	WP_000897689.1		hypothetical protein	20722.67108	-1.0084265	0.340620571	-2.960556662	0.003070836	0.004799224	2.91828982
ABUW_RS00175	ABUW_0036	NZ_CP008706.1	44788	45165	+	WP_000529425.1		hypothetical protein	935.8497236	-1.009958352	0.203370612	-4.966097808	6.83E-07	1.56E-06	5.807040835
ABUW_RS03275	ABUW_0665	NZ_CP008706.1	671436	672146	+	WP_000850475.1		DsbC family protein	79.48119486	-1.006213492	0.300556868	-3.347815041	0.00092443	0.001362648	2.856516328
ABUW_RS15845	ABUW_3263	NZ_CP008706.1	3293552	3293929	+	WP_000266123.1		DUF4951 domain-containing protein	391.5292085	-1.012540903	0.197734992	-5.10696595	3.04E-07	7.14E-07	6.146368291
ABUW_RS15935	ABUW_2269	NZ_CP008706.1	2255156	2256193	+	WP_001174011.1		fructose-bisphosphate aldolase class II	11851.2851	-1.015289822	0.173772639	-5.842632068	5.14E-09	1.40E-08	7.854538533
ABUW_RS15975	ABUW_2257	NZ_CP008706.1	2242421	2243182	+	WP_000680692.1	kdsB	3-deoxy-manno- octulosonate cyclidyltransferase	2396.503528	-1.015854163	0.069000088	-11.17550254	5.37E-29	5.16E-28	17.2928517
ABUW_RS00210	ABUW_0643	NZ_CP008706.1	50718	51020	+	WP_000843074.1		LysR family transcriptional regulator	450.1460253	-1.017040874	0.114471848	-8.88467832	6.41E-19	3.39E-18	1.74042087
ABUW_RS02600	ABUW_0658	NZ_CP008706.1	533776	534029	+	WP_000006558.1	coaCB	l-phosphopantetheinyltransferase decarboxylase (phosphopantetheinyltransferase- γ -cysteine ligase)	2468.931887	-1.019205124	0.182621829	-5.828185843	2.39E-08	6.13E-08	7.124484685
ABUW_RS02190	ABUW_0446	NZ_CP008706.1	460144	460220	+			RNA-ase	6179.354584	-1.019656959	0.359760193	-8.234268437	0.00453073	0.00701497	2.13974756
ABUW_RS16050	ABUW_3304	NZ_CP008706.1	3337161	3337179	+	WP_00121265.1		3'-5' exonuclease	765.7650293	-1.020350501	0.169602591	-6.110125668	1.79E-09	5.02E-09	8.299679993
ABUW_RS08755	ABUW_1758	NZ_CP008706.1	1719342	1719350	-	WP_000134203.1		Rieske (2Fe-2S) protein	2155.927229	-1.020749894	0.18019871	-6.374114631	1.84E-10	5.52E-10	9.257683342
ABUW_RS16755	ABUW_2212	NZ_CP008706.1	2199040	2199972	+	WP_001222564.1		Dyp-type peroxidase	1163.264251	-1.022870511	0.164045197	-6.235296923	4.51E-10	1.32E-09	8.179950552
ABUW_RS01455	ABUW_0296	NZ_CP008706.1	316635	316717	+	WP_001193997.1	anbB	3-dehydroquinate synthase	3338.954343	-1.023850105	0.112483705	-9.12228087	8.85E-20	4.95E-19	8.10512582
ABUW_RS17340	ABUW_3563	NZ_CP008706.1	3620599	3621372	+	WP_001019361.1		transcriptional regulator	1188.109425	-1.024714639	0.179383737	-5.172416563	1.11E-08	2.94E-08	7.330608607
ABUW_RS17855	ABUW_3617	NZ_CP008706.1	3725597	3726031	+	WP_001275666.1	anrC	aspartate reductase (glutaredoxin)	440.2054857	-1.024716702	0.148927179	-6.180051962	5.95E-12	2.01E-11	10.69726192
ABUW_RS00375	ABUW_0076	NZ_CP008706.1	81024	81899	+	WP_000571167.1		HsdR family protein	722.0750193	-1.02690222	0.256694841	-4.000478844	6.32E-05	0.000120081	3.92052715
ABUW_RS08825	ABUW_1999	NZ_CP008706.1	1402955	1403446	+	WP_001055215.1		hypothetical protein	409.5987489	-1.030378187	0.205928351	-5.003624597	5.63E-07	1.29E-06	5.888119566
ABUW_RS03415	ABUW_0694	NZ_CP008706.1	698755	698830	+			RNA-Vai	184.1079502	-1.031862143	0.272097701	-3.793222187	0.000149245	0.000273254	3.654312874
ABUW_RS10905	ABUW_2243	NZ_CP008706.1	2232619	2233303	+	WP_000218021.1		(c)GMP kinase	9883.166561	-1.032223659	0.184996053	-5.159774506	2.14E-08	6.18E-08	7.208990792
ABUW_RS17810	ABUW_3657	NZ_CP008706.1	3718629	3717488	+	WP_000104553.1		ATP-binding protein	490.5948937	-1.032533538	0.150477101	-6.861073083	8.40E-08	2.29E-08	10.64018906
ABUW_RS15510	ABUW_2183	NZ_CP008706.1	2143315	2144184	+	WP_000422835.1		DUF2797 domain-containing protein	1892.445785	-1.035895252	0.233539777	-4.435626626	9.18E-09	1.90E-05	4.721799561
ABUW_RS10990	ABUW_2697	NZ_CP008706.1	2682890	2682986	+			RNA-Met	1582.975219	-1.037854847	0.040458723	-2.567947722	0.010230257	0.014896172	1.688252535
ABUW_RS15980	ABUW_2179	NZ_CP008706.1	2160924	2161262	+	WP_000006591.1		hypothetical protein	35.20787341	-1.039512952	0.370278699	-2.807373012	0.004984737	0.007611118	2.185516572
ABUW_RS07055	ABUW_1567	NZ_CP008706.1	1555114	1556202	+	WP_000648007.1	prfA	peptide chain release factor 1	1943.94872	-1.039934783	0.18082657	-5.751006514	8.87E-09	2.37E-08	7.62579359
ABUW_RS15200	ABUW_3131	NZ_CP008706.1	3154562	3155365	+	WP_000420180.1		sulfite exporter TsaU/SaUe family protein	401.0489636	-1.041947013	0.175808566	-5.924893408	3.13E-08	8.67E-08	9.401912906
ABUW_RS15020	ABUW_2185	NZ_CP008706.1	2145619	2147748	+	WP_001025119.1		TnrdB-dependent selenophore receptor	834.1485064	-1.043293969	0.35647085	-2.92674551	0.003425292	0.005328323	2.2735752
ABUW_RS04145	ABUW_0846	NZ_CP008706.1	826186	828226	+	WP_000547891.1		site-specific ribonuclease	2124.79079	-1.044727357	0.193312567	-7.836675719	4.63E-15	1.92E-14	11.7723447
ABUW_RS09150	ABUW_1679	NZ_CP008706.1	1678602	1679396	+	WP_001228544.1		hypothetical protein	473.0116094	-1.046777238	0.176650216	-5.92570596	3.11E-09	8.63E-09	8.063767616
ABUW_RS16205	ABUW_3740	NZ_CP008706.1	3796249	3797088	+	WP_000490209.1		zinc ABC transporter substrate-binding protein	769.847544	-1.046886234	0.153586539	-6.18914049	9.30E-12	3.09E-11	10.50974359
ABUW_RS07080	ABUW_1453	NZ_CP008706.1	1444515	1445525	+	WP_000836263.1	tsaD	IA (adenosine(37)-N6)-theonylcarbamoyltransferase complex transferase subunit Tt	870.1710368	-1.047813944	0.192832296	-5.433941919	5.51E-08	1.37E-07	5.682719712
ABUW_RS14400	ABUW_2966	NZ_CP008706.1	2979062	2979577	+	WP_001142469.1		acyl CoA thioesterase	855.3062096	-1.049396862	0.19796482	-5.837458335	5.30E-09	1.44E-08	7.8142258
ABUW_RS19300	ABUW_4056	NZ_CP008707.1	33741	346277	+	WP_025464697.1	aph(3')-Ib	aminoglycoside O-6-phosphotransferase APH(3')-Ib	857.1987749	-1.049519614	0.44336523	-2.367100608	0.01925197	0.025234291	1.59601885
ABUW_RS15570	ABUW_3409	NZ_CP008706.1	3456860	3457139	+	WP_000106771.1	rdgB	RdgB/HAM1 family non-canonical protein NTP phosphorylase	504.24295	-1.049885325	0.20102262	-5.214607104	1.83E-07	4.37E-07	6.05954532
ABUW_RS18890	ABUW_3879	NZ_CP008706.1	3946285	3946225	+	WP_001062607.1	dnaK	molecular chaperone DnaK	6657.18589	-1.051747659	0.230095698	-4.570919404	4.86E-06	1.03E-05	4.488220908
ABUW_RS18990	ABUW_3900	NZ_CP008706.1	3966631	3967129	+	WP_001145511.1	dmeF	CDF family Cys(II)/His(II) zinc transporter DmeF	115.278941	-1.053172763	0.266299317	-3.957318704	7.58E-05	0.000142568	3.488220908
ABUW_RS19215	ABUW_3742	NZ_CP008706.1	3797686	3798474	+	WP_001102011.1	znuC	zinc ABC transporter ATP-binding protein ZnuC	124.710048	-1.054456391	0.52595965	-6.893856033	5.43E-12	1.84E-11	10.7349151
ABUW_RS16575	ABUW_3410	NZ_CP008706.1	3457512	3458387	+	WP_001196409.1		hypothetical protein	473.8246607	-1.054357101	0.161445037	-5.531866685	6.50E-11	2.00E-10	9.08814354
ABUW_RS03480	ABUW_0707	NZ_CP008706.1	73265	73461	+	WP_002546470.1	sbmA	peptide antibiotic transporter SbmA	779.436600	-1.055070535	0.17943895	-6.530187965	3.20E-08	8.14E-08	1.092285731
ABUW_RS04260	ABUW_0868	NZ_CP008706.1	848304	848705	+	WP_001848631.1	sdhC	succinate dehydrogenase, cytochrome b558 subunit	1004.04957	-1.055897022	0.179261465	-5.890193435	3.86E-09	1.06E-08	1.07567891
ABUW_RS06030	ABUW_0234	NZ_CP008706.1	277293	278120	+	WP_001089419.1	nap	type I methionylaminoacyltransferase	3213.46047	-1.054549442	0.149788008	-7.050026166	1.75E-12	6.16E-12	1.21072768
ABUW_RS06745	ABUW_082	NZ_CP008706.1	934785	935240	+	WP_001177595.1		histidine phosphatase family protein	677.337208	-1.056773959	0.124253626	-8.504974843	1.82E-17	8.67E-17	16.061953
ABUW_RS01010	ABUW_0267	NZ_CP008706.1	284168	286185	+	WP_001275655.1		efflux RND transporter periplasmic adaptor subunit	447.285127	-1.058369351	0.19339149	-6.248210849	4.15E-07	1.22E-09	8.145552033
ABUW_RS08250	ABUW_1694	NZ_CP008706.1	1691695	1692761	+	WP_000511728.1		MF3 transporter	384.8726578	-1.061202056	0.19104344	-5.677037510	2.01E-08	5.21E-08	7.282978357
ABUW_RS09230	ABUW_1895	NZ_CP008706.1	1896238	1896805	+	WP_00011378.1		TeiR/ACR family transcriptional regulator	60.659587	-1.061145186	0.332160347	-3.194718894	0.001099671	0.002272984	2.643435338
ABUW_RS000370	ABUW_0075	NZ_CP008706.1	80575	81027	+	WP_001118319.1	hucC	histidine utilization repressor	941.759814	-1.06129505	0.217106244	-4.888018262	1.02E-08	2.92E-08	5.440884152
ABUW_RS14350	ABUW_2956	NZ_CP008706.1	2959082	2959663	+	WP_000074494.1		nicotianamine monooxidase transporter	235.7718941	-1.062450269	0.205933638	-5.159194552	2.48E-07	5.84E-07	6.233321329
ABUW_RS01025	ABUW_0250	NZ_CP008706.1	265280	265913	+	WP_000194096.1	hdsB	imidazole glycerol-phosphate dehydratase HdsB	487.816356	-1.063042197	0.155406832	-6.838006051	8.03E-12	2.88E-11	10.5721368
ABUW_RS05555	ABUW_1035	NZ_CP008706.1	1035210	1035611	+	WP_001042511.1	glcA	lactoylglutamate lyase	2624.570661	-1.063965109	0.17943895	-5.929323147	3.04E-09	8.45E-09	8.07031608
ABUW_RS16															

ABUW_RS04265	ABUW_0869	NZ_CP008706.1	848705	848070	+	WP_000833672.1	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	16 54 74351	-1.07513743	0.218620443	-4.958652088	7.10E-07	1.62E-06	5.790879077
ABUW_RS05055	ABUW_0214	NZ_CP008706.1	238703	239623	+	WP_000423185.1		LyrR family transcriptional regulator	924 5323259	-1.075607778	0.218645848	-4.918406279	8.68E-07	1.96E-06	5.707642233
ABUW_RS06025	ABUW_2399	NZ_CP008706.1	333308	333178	-	WP_001200131.1		ComE family DNA-binding protein	356.6664925	-1.076834283	0.17183545	-6.290524504	3.16E-10	9.33E-10	9.303023864
ABUW_RS03960	ABUW_0809	NZ_CP008706.1	789187	788556	+	WP_000433820.1			61153287307	-1.076967685	0.379883739	-2.834982854	0.004582871	0.007007937	2.564794176
ABUW_RS03855	no	NZ_CP008706.1	768870	769238	+	WP_000533744.1		hypothetical protein	825.4653478	-1.077403841	0.28655501	-3.765043942	0.000398929	0.003008192	5.319168484
ABUW_RS0385	ABUW_2396	NZ_CP008706.1	288243	286276	-	WP_000636785.1		transposase	8446.096965	-1.079333712	0.571931488	-1.887173086	0.059370409	0.077484881	1.182229
ABUW_RS0720	ABUW_3845	NZ_CP008706.1	3914103	3914780	+	WP_001847027.1		TerR-like family transcriptional regulator	8012597828	-1.080187001	0.879722978	-5.746505499	9.18E-09	2.43E-08	7.614749083
ABUW_RS06735	ABUW_076	NZ_CP008706.1	1390336	1390581	+	WP_000181639.1		sulfurtransferase TusA family protein	4515797026	-1.080216056	0.28540364	-3.784778669	0.000193845	0.000283663	5.950732617
ABUW_RS07305	ABUW_1698	NZ_CP008706.1	1484261	1485475	+	WP_000792929.1		TerR-like family transcriptional regulator	69.5916107	-1.082650372	0.4523681	-2.60730828	0.009525716	0.03384605	187339445
ABUW_RS05620	ABUW_023	NZ_CP008706.1	1034032	1035162	+	WP_001025859.1	mgk	endocytic tyrosine cyclase MGK	107.695259	-1.084084579	0.18163369	-9.180548808	4.29E-20	2.45E-19	8.61252491
ABUW_RS06000	ABUW_028	NZ_CP008706.1	1269959	1270972	-	WP_0001289259.1	lpA	lipoyl synthase	12276.76082	-1.086428391	0.198817802	-7.770316211	7.83E-15	3.21E-14	10.49364410
ABUW_RS0650	ABUW_0197	NZ_CP008706.1	151872	153620	+	WP_001837407.1		LysM/peptidoglycan-binding domain-containing protein	1546.931972	-1.087597429	0.27193389	-4.000900064	6.31E-05	0.00018924	3.52195433
ABUW_RS01185	ABUW_2295	NZ_CP008706.1	228141	228329	-	WP_000210681.1	tk	transketolase	1854.120729	-1.088828921	0.186428283	-7.98069165	1.45E-15	6.20E-15	14.2078418
ABUW_RS06160	ABUW_048	NZ_CP008706.1	1289200	1290105	-	WP_000128669.1		ABC transporter ATP-binding protein	902.9774036	-1.089926405	0.241292341	-4.517036879	6.27E-06	1.38E-05	4.882566127
ABUW_RS03975	ABUW_0282	NZ_CP008706.1	789693	790199	-	WP_000172390.1		hypothetical protein	1546.005810	-1.090784894	0.27714621	-3.935816242	8.29E-05	0.00055382	3.808800378
ABUW_RS0380	ABUW_238	NZ_CP008706.1	122912	124003	+	WP_000918444.1	aroC	chorismate synthase	3087.526888	-1.09219793	0.800314210	-5.738414266	9.95E-09	2.54E-08	7.594906864
ABUW_RS0640	ABUW_3829	NZ_CP008706.1	3895617	3896747	-	WP_000832259.1	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	25396.66454	-1.093187483	0.1252881	-8.724484178	2.67E-18	1.34E-17	16.8718211
ABUW_RS0430	ABUW_3377	NZ_CP008706.1	3204292	3244543	+	WP_001924502.1	nobC	NADH:quinone oxidoreductase subunit A	5871537667	-1.09718771	0.256910727	-4.270735293	1.95E-05	3.90E-05	4.440242963
ABUW_RS0665	ABUW_3498	NZ_CP008706.1	3473800	3474402	+	WP_000056698.1		TerR-like family transcriptional regulator	93.6336649	-1.098228894	0.13822642	-8.86935103	7.36E-19	3.85E-18	17.4465028
ABUW_RS07300	ABUW_3555	NZ_CP008706.1	361091	361247	+	WP_000095865.1		pyrimidine/nucleoside phosphorylase	2164.914021	-1.09855414	0.181659305	-6.795272972	1.08E-11	3.57E-11	10.44694977
ABUW_RS03680	ABUW_0747	NZ_CP008706.1	747339	748100	+	WP_024432496.1		helle-tum-helle domain-containing protein	1298.390510	-1.099669526	0.192224686	-8.509951856	1.74E-17	8.32E-17	16.0800636
ABUW_RS06005	ABUW_0205	NZ_CP008706.1	127169	1272581	+	WP_000117505.1	sthA	Ss-specific RNA (DIPV)/transhydrogenase	7499.586491	-1.102721023	0.194816333	-8.179493392	2.85E-16	1.28E-15	14.86268982
ABUW_RS06090	ABUW_046	NZ_CP008706.1	1587621	1588433	+	WP_000110172.1	queF	NADPH-dependent L-cysteine-2-deazaaminoglutathione reductase QueF	934.4186764	-1.103288564	0.181090854	-6.848819109	7.44E-12	2.41E-11	10.60361467
ABUW_RS02315	ABUW_0471	NZ_CP008706.1	428883	431740	+	WP_001019438.1		23S rRNA (adenine(2030)-N6)-methyltransferase RnuJ	2194.126044	-1.105040002	0.128544486	-8.579759489	9.91E-18	4.60E-17	16.3687472
ABUW_RS0270	ABUW_073	NZ_CP008706.1	1087096	1087884	+	WP_000706554.1		rRNA large subunit pseudouridine synthase E	217.077231	-1.107400888	0.12861637	-5.888955502	8.83E-18	4.33E-17	16.3635186
ABUW_RS07590	ABUW_3610	NZ_CP008706.1	3671463	3672230	-	WP_000897420.1		uroporphyrinogen-III synthase	582.9689972	-1.107774055	0.189601226	-5.842652376	5.16E-09	1.40E-08	7.854318533
ABUW_RS0455	ABUW_116	NZ_CP008706.1	115365	116336	+	WP_001231896.1		substrate-kinase domain-containing protein	699.7235461	-1.109170254	0.269376893	-4.175441973	3.83E-05	7.46E-05	4.12727253
ABUW_RS0550	ABUW_3819	NZ_CP008706.1	3884097	3884972	-	WP_000591427.1	galJ	UTP--glucose-1-phosphate uridyltransferase GalJ	7967.34234	-1.110323262	0.1262638	-8.563891896	1.09E-17	5.27E-17	6.87585423
ABUW_RS00470	ABUW_0095	NZ_CP008706.1	16252	167373	+	WP_001011089.1		bifunctional 3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase	8709.716093	-1.110730452	0.21588649	-5.27348425	1.33E-07	3.2E-07	6.493011862
ABUW_RS05710	ABUW_1863	NZ_CP008706.1	1941301	1941661	+	WP_000161888.1	bauf	acetylcholine phosphatase protein BauF	152.351609	-1.10844772	0.477186104	-2.332059775	0.016955548	0.027652822	15.965075327
ABUW_RS02550	ABUW_059	NZ_CP008706.1	129273	129767	+	WP_000083505.1		DUF4442 domain-containing protein	1619.969282	-1.11481003	0.21693146	-5.122476447	3.02E-07	7.08E-07	6.149962451
ABUW_RS06720	ABUW_077	NZ_CP008706.1	1090566	1091068	+	WP_000106912.1		cold-shock protein	36787.18034	-1.115418407	0.238272469	-4.318698347	1.57E-05	3.19E-05	4.468542996
ABUW_RS0425	ABUW_2971	NZ_CP008706.1	2985182	2986624	+	WP_001028103.1	betB	betaine-aldehyde dehydrogenase	4266.030248	-1.118504187	0.392692894	-2.840652848	0.004502129	0.00688581	2.162000547
ABUW_RS09920	ABUW_2043	NZ_CP008706.1	2024376	2024579	+	WP_000301760.1		hypothetical protein	236.4085257	-1.118978944	0.246673797	-4.524188186	6.07E-08	1.27E-05	4.896397673
ABUW_RS0360	ABUW_2752	NZ_CP008706.1	2742488	2742887	+	WP_000735756.1		hypothetical protein	2959.544335	-1.11891943	0.204437784	-5.46335617	4.67E-08	1.97E-07	6.93184125
ABUW_RS01885	ABUW_2361	NZ_CP008706.1	2347619	2348458	+	WP_001841768.1		rRNA methyltransferase	1044.55969	-1.117700812	0.18651449	-5.992568269	2.07E-09	5.79E-09	8.237221668
ABUW_RS0425	ABUW_4089	NZ_CP008706.1	54366	55391	+	WP_000188464.1		IS30-like element ISBa5 Q2 family transposase	4088.57338	-1.118281103	0.199747873	-7.000287976	2.55E-12	8.86E-12	10.05235128
ABUW_RS0595	ABUW_2393	NZ_CP008706.1	3326394	3326663	+	WP_000567533.1		HP family phosphatase protein	127.674933	-1.118892754	0.180788431	-6.189349317	6.04E-10	1.76E-09	8.755431047
ABUW_RS0310	ABUW_0301	NZ_CP008706.1	35208	354140	+	WP_000077841.1	serA	phosphoglycerate dehydrogenase	93382.22402	-1.120140943	0.166268993	-7.17648673	7.7E-13	2.88E-12	10.58770975
ABUW_RS07865	ABUW_3669	NZ_CP008706.1	3725416	3726889	+	WP_000670216.1		arsenate reductase ArsC	954.6205399	-1.12182006	0.2777415	-4.03905055	5.37E-05	0.000102673	3.988545694
ABUW_RS0625	ABUW_3420	NZ_CP008706.1	3467497	3468339	+	WP_000103170.1	thyA	thymidylate synthase	1475.032186	-1.122163736	0.192301401	-8.535442339	5.36E-09	1.46E-08	7.836971525
ABUW_RS0550	ABUW_3811	NZ_CP008706.1	3872632	3873438	-	WP_001813019.1	ddl	D-lactate dehydrogenase	1286.212284	-1.124657666	0.25859004	-4.34919607	1.37E-05	2.78E-05	4.555667002
ABUW_RS03220	ABUW_0605	NZ_CP008706.1	619387	619860	+	WP_000052467.1		DUF5231 domain-containing protein	10569.9481	-1.126777982	0.305510333	-3.688844255	0.000225996	0.000403638	3.391501371
ABUW_RS0345	ABUW_2955	NZ_CP008706.1	2968768	2969007	+	WP_000937181.1			15.0120602	-1.127718032	0.237647876	-4.745337959	2.08E-06	4.54E-06	5.343097257
ABUW_RS0725	ABUW_3440	NZ_CP008706.1	3486644	3486644	+	WP_000022499.1	topA	type I DNA topoisomerase	1448.138710	-1.130078883	0.165467882	-7.31972623	2.64E-13	9.75E-13	12.0186310
ABUW_RS0405	ABUW_3378	NZ_CP008706.1	3416258	3416550	+	WP_000095254.1	haS	histidine--rRNA ligase	7952.0118	-1.130702371	0.18197416	-6.980719021	2.94E-12	1.02E-11	10.99226886
ABUW_RS09970	ABUW_222	NZ_CP008706.1	1626895	1626197	+	WP_001878588.1		6S rRNA (uracil(4688)-N3)-methyltransferase	6782.618475	-1.130720685	0.17824373	-3.343495483	2.25E-10	6.69E-10	9.174362467
ABUW_RS05050	ABUW_049	NZ_CP008706.1	105784	1058531	+	WP_001833637.1	raiD	EamA family phosphatase RaiD	1531106576	-1.13148882	0.189010468	-6.694430295	2.17E-11	6.95E-11	10.5795186
ABUW_RS01855	ABUW_2273	NZ_CP008706.1	2258391	2258984	+	WP_000081866.1	maf	septum formation protein Maf	7648.761404	-1.132540013	0.154004293	-8.395106922	4.65E-17	2.18E-16	16.66252875
ABUW_RS0630	ABUW_3260	NZ_CP008706.1	3291904	3292002	+	WP_000027359.1	glaA	RobiA family phosphatase GlaA	8062.807685	-1.133553502	0.14218435	-9.12548108	7.14E-20	4.03E-19	9.394695236
ABUW_RS00015	ABUW_0003	NZ_CP008706.1	2753	3835	+	WP_000550807.1	recF	DNA replication/repair protein RecF	2757.918768	-1.134023656	0.28426578	-5.008362386	5.49E-07	1.28E-06	5.88930711
ABUW_RS0595	ABUW_3820	NZ_CP008706.1	3884884	3886858	-	WP_000071144.1		polysaccharide biosynthesis protein	25.119174524	-1.13523312	0.10272243	-4.9402753963	5.32E-21	3.18E-20	9.49599527
ABUW_RS0570	ABUW_2195	NZ_CP008706.1	2156453	2156971	+	WP_000939377.1	cobU	ictional adenosylcobamide kinase/adenosylcobamide-phosphate guanlyltransferase	450.2899254	-1.136709192	0.167621763	-7.21812593	5.53E-10	2.02E-12	11.69749732
ABUW_RS07330	ABUW_3331	NZ_CP008706.1	3617805	3618011	-	WP_000053613.1		DUF1854 domain-containing protein	72.37942173	-1.138802368	0.295236318	-8.357257141	0.000146607	0.000212262	3.673224547
ABUW_RS07720	ABUW_3637	NZ_CP008706.1	3696203	3697402	+	WP_000063593.1		threonine synthase	9449.82652	-1.139037191	0.197355687	-5.77149304	7.86E-09	2.19E-08	7.674761205
ABUW_RS02920	ABUW_0604	NZ_CP008706.1	619206	6192881	+	WP_0000721907.1		glycylseryltransferase family 25 protein	10645.833668	-1.140743849	0.178205514	-6.630216551	3.24E-11	1.03E-10	9.988261988
ABUW_RS08750	ABUW_0797	NZ_CP008706.1	1790798	1791916	+	WP_000751306.1		DUF1449 family protein	3917.914501	-1.14082249					

ABUW_R503860	ABUW_0787	NZ_CP008706.1	769195	769638	+	WP_002039534.1		hypothetical protein	93.7914595	-1.97459874	0.243192275	-4.882802608	1.055-06	2.34E-06	5.62986639
ABUW_R503970	ABUW_2876	NZ_CP008706.1	2885001	2887019	+	WP_000801654.1	mda	penicillin-binding protein 2	87.75356938	-1.9763861	0.17463326	-6.80075844	1.04E-11	3.44E-11	0.46312524
ABUW_R504785	ABUW_0976	NZ_CP008706.1	986551	989003	+	WP_004721717.1		DNA intercalation-related competence protein ComECRec2	1080.85342	-1.90525511	0.98832281	-7.051927731	1.77E-12	6.2E-12	11.20685862
ABUW_R507725	ABUW_1582	NZ_CP008706.1	695978	671797	-	WP_012305057.1	kdpB	potassium-transferring ATPase subunit KdpB	246.7248029	-1.9090781	0.96449758	-6.063142741	1.33E-09	3.78E-09	8.424975229
ABUW_R504095	ABUW_0538	NZ_CP008706.1	81464	815343	-	WP_001028717.1		valine-1- RNA ligase	178.555965	-1.93030709	0.93058174	-6.179525468	6.43E-10	1.87E-09	8.729203033
ABUW_R509885	ABUW_2036	NZ_CP008706.1	202016	202029	+	WP_000301760.1		hypothetical protein	237.8540366	-1.94494081	0.23691912	-4.984677843	5.89E-07	1.35E-06	5.68920812
ABUW_R502555	ABUW_0520	NZ_CP008706.1	529803	530291	-	WP_01018893.1		YajF family cyclic-GMP-binding protein	922.4282817	-1.94131075	0.96550556	-6.07635615	1.23E-09	3.55E-09	8.456444478
ABUW_R507305	ABUW_1537	NZ_CP008706.1	1522790	1524670	+	WP_000559187.1	mmG	RNA-uridine-5'-carboxymethylaminomethyl[34] synthesis enzyme MmmG	5273.390754	-1.96757747	0.959431648	-6.000859752	1.96E-09	5.5E-09	8.25909114
ABUW_R501885	ABUW_0242	NZ_CP008706.1	259592	260321	+	WP_01205588.1		DUF_034 domain-containing protein	355.950012	-1.97046956	0.6536141	-7.65564968	1.92E-14	7.6E-14	5.18886862
ABUW_R51446	ABUW_2969	NZ_CP008706.1	2962649	2964271	-	WP_00243371.1		BCC1 family transporter	7253.254778	-1.968027839	0.33655197	-3.55971202	0.0003706	0.000526052	3.85717959
ABUW_R51955	ABUW_3893	NZ_CP008706.1	3960729	3961889	+	WP_000823196.1		glutathionylperoxidase synthase family protein	394.666072	-1.98080626	0.237683921	-5.040684372	4.64E-07	1.07E-06	5.968955713
ABUW_R505107	ABUW_1053	NZ_CP008706.1	1016180	1063160	+	WP_010120494.1	cgtA	Ctg family GTPase CgtA	8813.541431	-1.200065878	0.89884824	-6.339697435	2.62E-10	7.77E-10	9.10971391
ABUW_R518375	ABUW_3085	NZ_CP008706.1	3102026	3102763	-	WP_000397522.1	pgeF	peptidoglycan editing factor PgeF	719.21213165	-1.200830473	0.93691036	-8.770858434	1.77E-18	9.00E-18	17.04589192
ABUW_R508475	ABUW_1740	NZ_CP008706.1	1737229	1738584	+	WP_000992588.1	relP	RIP metallopeptidase RelP	6377.630777	-1.201500072	0.93203445	-9.098762292	9.16E-20	5.1E-19	18.2914828
ABUW_R500160	ABUW_0020	NZ_CP008706.1	23706	24305	+	WP_000567889.1		glutathione-S-transferase family protein	260.8217532	-1.202605085	0.208347544	-5.77210672	7.83E-09	2.36E-08	7.678084995
ABUW_R500590	ABUW_0189	NZ_CP008706.1	134102	14458	+	WP_000877633.1		hypothetical protein	307.8347092	-1.203047906	0.280488996	-4.28939693	1.79E-05	3.60E-05	4.44371664
ABUW_R515500	ABUW_3192	NZ_CP008706.1	3222203	3222487	-	WP_000509297.1		hypothetical protein	125.1179804	-1.203307941	0.40184766	-2.994438091	0.002749508	0.004325564	2.363951249
ABUW_R519520	ABUW_3368	NZ_CP008706.1	354365	3545665	-	WP_000946653.1	purE	5-(carboxyamino)imidazole ribonucleotide mutase	2690.694099	-1.20386871	0.17870838	-5.17322821	2.33E-12	8.05E-12	11.05241498
ABUW_R500835	ABUW_1265	NZ_CP008706.1	978194	9816	+	WP_000304019.1		helic-tun-helic transcriptional regulator	9008.683356	-1.205719038	0.90570005	-6.032888889	2.50E-10	7.43E-10	9.28856564
ABUW_R502580	ABUW_0525	NZ_CP008706.1	533465	534079	-	WP_000645707.1		separation protein sepZ	809.803164	-1.206074014	0.5480029	-8.947177339	3.65E-19	1.95E-19	17.700251
ABUW_R500695	ABUW_1428	NZ_CP008706.1	141816	1418556	+	WP_000335087.1		hypothetical protein	2.714105352	-1.208527169	1.176760433	-1.020995075	0.304422783	0.35803588	0.454648481
ABUW_R500715	ABUW_1814	NZ_CP008706.1	189516	189228	+	WP_00071166.1		DUF_0737 domain-containing protein	260.5435937	-1.210431004	0.22445224	-5.406184224	6.44E-08	2.79E-08	6.79742867
ABUW_R518600	ABUW_3821	NZ_CP008706.1	3887000	388875	-	WP_000393236.1		DegT/DnaU/ErpC/HS amonotransferase family protein	9058.69027	-1.217349022	0.9222669	-7.969977071	1.28E-15	5.47E-15	11.26238035
ABUW_R519216	ABUW_3292	NZ_CP008706.1	3320241	3329763	-	WP_000219216.1	tokK	2- amino- 4- hydroxy- 6- hydroxymethylhydroxytetradine diphosphokinas	719.08342973	-1.217456966	0.91610172	-7.550534089	4.33E-18	1.68E-18	12.1744623
ABUW_R501520	ABUW_0249	NZ_CP008706.1	264663	265280	-	WP_000168730.1	hnhH	imidazole glycerol phosphate synthase subunit HnhH	1850.18041	-1.218123396	0.933627209	-7.929086269	2.21E-15	9.32E-15	9.30442255
ABUW_R516910	ABUW_3276	NZ_CP008706.1	3309597	3309923	+	WP_000127875.1	tnxA	threonine	1194.46588	-1.218878237	0.9134314	-6.650329278	2.92E-11	9.30E-11	10.032985
ABUW_R500455	ABUW_1028	NZ_CP008706.1	103991	1040140	+	WP_000048833.1		acyl-CoA thioesterase	453.7365453	-1.222179332	0.98567032	-6.10720505	7.40E-10	2.12E-09	8.670843727
ABUW_R518885	ABUW_3878	NZ_CP008706.1	3845577	384611	+	WP_010127289.1	grpE	nucleotide exchange factor GrpE	6974.534365	-1.224440318	0.221747351	-5.52179105	3.36E-08	8.52E-08	7.069542941
ABUW_R51185	ABUW_0244	NZ_CP008706.1	260787	261689	-	WP_00075489.1		DMT family transporter	103.7822783	-1.227967733	0.22617934	-5.418518555	6.08E-08	1.5E-07	6.42163464
ABUW_R516235	ABUW_3242	NZ_CP008706.1	3375650	3375648	+	WP_024432485.1	dusA	IRNA dithyridine(DO20A) synthase DusA	10.15587621	-1.230400654	0.23162313	-5.305597352	1.12E-07	2.73E-07	6.564519233
ABUW_R502335	ABUW_3639	NZ_CP008706.1	3900141	3907028	+	WP_000399393.1		hypothetical protein	37.2966104	-1.230607074	0.364901756	-3.372433687	0.000745007	0.000452905	2.940514403
ABUW_R500890	ABUW_0180	NZ_CP008706.1	198734	99534	+	WP_010123261.1		response regulator transcription factor	1185.081904	-1.232523977	0.913148198	-8.61916084	7.39E-19	3.54E-17	8.45583451
ABUW_R501105	ABUW_0226	NZ_CP008706.1	247164	247372	-	WP_010125353.1		hypothetical protein	294.4008845	-1.2331893	0.30164919	-4.096307325	4.20E-05	8.01E-05	4.089831225
ABUW_R518315	ABUW_3762	NZ_CP008706.1	381742	3811704	-	WP_000393756.1		Sif22 family protein	109.218176	-1.234782713	0.21978102	-5.618238792	1.93E-08	5.0E-08	7.300331327
ABUW_R510225	ABUW_2308	NZ_CP008706.1	2293182	2293394	-	WP_000034999.1		hypothetical protein	91.693497	-1.235673303	0.285148267	-4.329372376	1.50E-05	3.05E-05	4.584176551
ABUW_R519980	ABUW_3290	NZ_CP008706.1	3321831	3323753	-	WP_010119212.1	thrS	threonine-1-RNA ligase	22343.62419	-1.236270954	0.95631866	-7.463908658	8.40E-14	3.2E-13	12.49318469
ABUW_R500975	ABUW_0197	NZ_CP008706.1	222145	222726	+	WP_010120801.1	seb	single-strand DNA-binding protein	1041.256462	-1.238977807	0.93878469	-8.933848779	4.11E-19	2.20E-18	17.6537191
ABUW_R515330	ABUW_3199	NZ_CP008706.1	328003	3228875	-	WP_000572819.1		LysR family transcriptional regulator	136.0487013	-1.244651837	0.2685297	-4.642100431	3.45E-06	7.40E-06	5.1930527
ABUW_R511416	ABUW_2347	NZ_CP008706.1	2329339	2330061	+	WP_000741261.1		AzC family AzC-transpermease	178.881469	-1.246588423	0.93514978	-6.441825757	1.18E-10	3.58E-10	9.446607667
ABUW_R519150	ABUW_0307	NZ_CP008706.1	330021	331116	-	WP_000289091.1		bacterioferritin-associated ferredoxin	600.0857499	-1.247145168	0.73191204	-1.170455681	0.088259033	0.1022461	0.04862897
ABUW_R517955	ABUW_0388	NZ_CP008706.1	3745427	3745810	+	WP_010187001.1		hypothetical protein	622.7675729	-1.24720009	0.98335595	-7.490099902	1.27E-13	4.8E-13	12.9379164
ABUW_R5186510	ABUW_3823	NZ_CP008706.1	3888917	3889531	-	WP_000191785.1		sugar transferase	7109.381886	-1.24991421	0.95956342	-7.83324314	6.75E-15	1.97E-14	13.70581663
ABUW_R504770	ABUW_0973	NZ_CP008706.1	983495	984403	+	WP_010140078.1		Bank family transporter	97.15567457	-1.250136796	0.20061006	-6.233105732	4.57E-10	1.34E-09	8.874502171
ABUW_R502370	ABUW_0483	NZ_CP008706.1	493973	494572	-	WP_000562187.1		TsrR family transcriptional regulator	90.4889373	-1.251199319	0.253759951	-4.929687377	8.24E-07	1.87E-06	5.72972712
ABUW_R500240	ABUW_0949	NZ_CP008706.1	55409	55945	-	WP_010124411.1		MD3 family metalloprotease	381.12991273	-1.253185863	0.87202146	-6.694180366	2.19E-11	6.96E-11	10.87189194
ABUW_R505175	ABUW_1654	NZ_CP008706.1	1663176	1664309	+	WP_000573844.1		glutamate 5-kinase	9463.86901	-1.25464539	0.91742216	-6.355140399	2.08E-10	8.23E-10	9.203291271
ABUW_R519055	ABUW_3476	NZ_CP008706.1	3523132	3524244	-	WP_010184124.1		RbA family pseudouridine synthase	1290.107879	-1.254909974	0.940483337	-6.460996815	1.00E-10	3.04E-10	9.916412945
ABUW_R518335	ABUW_3057	NZ_CP008706.1	3083519	3083974	-	WP_000621643.1	mtl	ribosomal protein S16-alanine N-acetyltransferase	344.2316445	-1.255735288	0.95999863	-7.38664125	1.51E-13	5.65E-13	12.2476312
ABUW_R518210	ABUW_3337	NZ_CP008706.1	3369088	3371101	-	WP_000191572.1		hypothetical protein	1577.339983	-1.256762527	0.22188022	-5.663959846	1.48E-08	3.86E-08	7.41051028
ABUW_R510870	ABUW_2853	NZ_CP008706.1	2864190	2865011	+	WP_000129799.1		hypothetical protein	2995.901615	-1.256925111	0.225538818	-5.572978727	2.05E-08	6.42E-08	7.92320574
ABUW_R518795	ABUW_3860	NZ_CP008706.1	3927256	3928389	-	WP_000828383.1		TDI family transporter	108.482657	-1.258306549	0.96616224	-6.74276616	1.55E-11	5.05E-11	10.29677548
ABUW_R500510	ABUW_1913	NZ_CP008706.1	114543	116394	+	WP_000011219.1	psd	phosphatidylethanolamine decarboxylase	909.174178	-1.258631655	0.92710677	-7.735254202	1.03E-14	4.20E-14	13.3771059
ABUW_R519115	ABUW_3518	NZ_CP008706.1	3566252	3568339	-	WP_010185790.1	pnp	polybicyclicnucleotide nucleotidyltransferase	4.40310912	-1.259902385	0.982279181	-6.90718011	4.95E-12	1.69E-11	10.7731792
ABUW_R516745	ABUW_3444	NZ_CP008706.1	3488362	3488877	-	WP_000185733.1		SlyX family protein	554.8909223	-1.259907811	0.94406071	-6.478515059	9.36E-11	2.87E-10	9.541882073
ABUW_R511910	ABUW_2346	NZ_CP008706.1	2328749	2329219	-	WP_000471056.1		hypothetical protein	95.30149336	-1.260418897	0.920739	-6.562560509	5.50E-11	1.66E-10	9.793177809
ABUW_R518780	ABUW_3451	NZ_CP008706.1	3471962	3484840	+	WP_000862762.1	asd	aspartate-semialdehyde dehydrogenase	5789.961619	-1.261878046	0.25015482	-5.043784004	4.56E-07	1.06E-06	15.937543256
ABUW_R518950	ABUW_3892	NZ_CP008706.1	3960342	3960707	+	WP_01016728.1		hypothetical protein	390.3394552	-1.261933243	0.23446010	-5.38137064	7.39E-08	1.83E-07	6.78197352
ABUW_R514255	ABUW_2936	NZ_CP008706.1	295050												

ABUW_RS6295	ABUW_350	NZ_CP008706.1	3176635	3177258	-	WP_000463103.1		lysE family translocator	293.9569048	-1.32503926	0.203205203	-6.52056784	7.00E-11	2.9E-10	9.66605178
ABUW_RS6310	ABUW_316	NZ_CP008706.1	316446	317389	+	WP_001291249.1	ruB	23S rRNA pseudouridine(2005) synthase RuB	3305.748487	-1.32808646	0.12171978	-0.96450205	5.36E-28	4.75E-27	26.32367141
ABUW_RS6335	ABUW_0209	NZ_CP008706.1	235219	236046	+	WP_000645059.1		class I 5Ade-dependent methyltransferase	2620.15502	-1.32888945	0.166378213	-7.98787202	1.38E-15	5.91E-15	14.22871414
ABUW_RS6340	ABUW_0710	NZ_CP008706.1	81845	89203	-	WP_000819049.1		alkene reductase	910.545579	-1.33026001	0.177028928	-7.51043308	5.78E-14	2.22E-13	12.65347363
ABUW_RS6355	ABUW_0718	NZ_CP008706.1	723699	724259	+	WP_000940845.1		Mal-like protein	6513122355	-1.330539901	0.19384316	-6.941058142	3.88E-12	1.33E-11	10.70589593
ABUW_RS67750	ABUW_3507	NZ_CP008706.1	577743	578291	+	WP_0007816248.1		DUF275 domain-containing protein	349.305321	-1.330728771	0.253488105	-5.249657542	152E-07	3.66E-07	6.436595185
ABUW_RS6930	ABUW_287	NZ_CP008706.1	2170722	2172761	-	WP_000442383.1		DNA2 family efflux MFS transporter permease subunit	947.7528411	-1.331402172	0.48626205	-2.855480459	0.004297177	0.005095552	2.90748827
ABUW_RS6949	ABUW_2847	NZ_CP008706.1	2860617	2861453	+	WP_001025978.1	rmlI	RS RNA (cytidine)(M02)-2'-O)-methyltransferase	354.8597295	-1.331972637	0.162710993	-9.104514353	8.67E-20	4.86E-19	18.3130186
ABUW_RS6970	ABUW_0361	NZ_CP008706.1	383324	384190	-	WP_000355668.1		LysR family transcriptional regulator	78.1732917	-1.332878751	0.266592064	-5.009988706	5.47E-07	1.62E-06	8.595697609
ABUW_RS6340	ABUW_2748	NZ_CP008706.1	2737315	2739949	+	WP_000199457.1	alaS	alanine - RNA ligase	9488.16599	-1.33302916	0.198540935	-6.714127311	1.69E-11	6.12E-11	12.034105
ABUW_RS6505	ABUW_3300	NZ_CP008706.1	3124146	3142526	+	WP_000952665.1		aspartate 1-decarboxylase	3019.399188	-1.33357848	0.173955396	-7.666209308	1.77E-14	7.03E-14	13.6334545
ABUW_RS6750	ABUW_3597	NZ_CP008706.1	3659202	3659277	-			RNA-Trip	493.0007699	-1.33367531	0.269534292	-4.948017366	7.50E-07	1.70E-06	5.7168710883
ABUW_RS6505	ABUW_0330	NZ_CP008706.1	1042206	1043033	-	WP_000344900.1	lepB	signal peptidase I	3767.8150848	-1.335725555	0.141288074	-9.451899624	3.35E-21	2.03E-20	19.69196693
ABUW_RS6425	ABUW_3376	NZ_CP008706.1	3203088	3204285	-	WP_000878003.1		NADH-quinone oxidoreductase subunit B	8071.788965	-1.335667524	0.28918906	-6.622912999	3.78E-06	8.09E-06	5.092197538
ABUW_RS64240	ABUW_0864	NZ_CP008706.1	843829	844353	+	WP_001274941.1		YecA family protein	5164.746299	-1.337941923	0.171540575	-7.808687738	5.78E-15	2.38E-14	13.62324652
ABUW_RS6960	ABUW_0399	NZ_CP008706.1	425913	426689	-	WP_001254461.1		YfIA family ribosome hibernation GTP-binding protein	987.9180807	-1.344257703	0.156837868	-9.823720963	8.90E-23	5.96E-22	21.22520602
ABUW_RS6495	ABUW_3911	NZ_CP008706.1	3221807	3222191	-	WP_000339507.1		biological process	2810566794	-1.344331075	0.327589337	-4.103708277	4.07E-05	7.88E-05	4.10309125
ABUW_RS6450	ABUW_0907	NZ_CP008706.1	901404	902252	+	WP_001281950.1	foD	nal methyltetrahydrofolate dehydrogenase/methyltetrahydrofolate cyclohydrolase	2704.185564	-1.344802911	0.209289525	-6.425562445	13.1E-10	3.97E-10	9.401594316
ABUW_RS6905	ABUW_3507	NZ_CP008706.1	3307797	3309137	-	WP_001279275.1	ppx	ecology/morphogenesis	3047.5631219	-1.345510997	0.140422448	-11.79933989	3.98E-32	4.48E-31	20.34892401
ABUW_RS6625	ABUW_3626	NZ_CP008706.1	3992006	3993100	-	WP_001000653.1		hypothetical protein	5524.31425	-1.346176471	0.194873654	-6.907943873	4.92E-12	1.65E-11	10.7752073
ABUW_RS6420	ABUW_3375	NZ_CP008706.1	3207196	3203523	-	WP_000852150.1	nucC	NADH-quinone oxidoreductase subunit CD	30033.6877	-1.346254111	0.281649984	-4.776491910	1.78E-06	3.92E-06	5.40708282
ABUW_RS6785	ABUW_0325	NZ_CP008706.1	3610987	3610293	+	WP_000874125.1		dephospho-CoA kinase	110.649172	-1.347659281	0.182322536	-7.391622075	1.45E-13	5.45E-13	6.882464052
ABUW_RS6510	ABUW_3603	NZ_CP008706.1	3862888	3863520	-	WP_001043692.1		ISS-like element (ISaB) G family transposase	4542.838875	-1.355989886	0.220287008	-6.55660403	7.48E-10	2.95E-09	8.66642640
ABUW_RS6250	ABUW_0327	NZ_CP008706.1	267476	268990	-	WP_000095944.1		acetyl-CoA hydrolase/transferrase family protein	2906.206566	-1.356771922	0.316674931	-2.884433828	1.83E-05	3.67E-05	13.448841197
ABUW_RS6735	ABUW_3570	NZ_CP008706.1	3627409	3628323	-	WP_000598899.1	lpvO	lpdA hydrolase LpxO	4784.196585	-1.357839497	0.21917796	-6.437706383	12.1E-10	3.67E-10	9.543319035
ABUW_RS6265	ABUW_0441	NZ_CP008706.1	46483	464914	-	WP_001010889.1		hypothetical protein	651.903046	-1.358021687	0.218936603	-6.202041611	5.57E-10	1.62E-09	8.791021887
ABUW_RS63530	ABUW_0710	NZ_CP008706.1	723220	723711	+	WP_0010121007.1	meD	ndt phosphate-determining protein MeD	1215.999197	-1.358502732	0.25365461	-5.355718672	8.52E-08	2.09E-07	6.679649571
ABUW_RS6770	ABUW_0308	NZ_CP008706.1	3699236	3671275	-	WP_000093035.1	rep	DNA helicase Rep	2860.985424	-1.358694206	0.176327422	-7.705518454	1.30E-14	5.24E-14	13.80682223
ABUW_RS6360	ABUW_0622	NZ_CP008706.1	123565	124368	+	WP_000885559.1		lysothiophosphatase subunit alpha	23713.69939	-1.359344646	0.252510401	-5.383243808	7.32E-08	1.81E-07	6.74211088
ABUW_RS6215	ABUW_0447	NZ_CP008706.1	460200	460336	+			RNA-Arg	3343.385054	-1.360015002	0.351707831	-3.866894334	0.00101235	0.00024442	3.689344316
ABUW_RS6500	ABUW_2811	NZ_CP008706.1	2162783	2163076	-	WP_000198751.1		hypothetical protein	40.86691256	-1.360198999	0.497630101	-2.733722778	0.006272751	0.004912631	2.026289555
ABUW_RS6905	ABUW_0206	NZ_CP008706.1	383550	384965	+	WP_001016306.1		TolC family protein	359.0277737	-1.361281387	0.242000454	-5.551819643	2.84E-10	7.76E-09	7.109165718
ABUW_RS67720	ABUW_0581	NZ_CP008706.1	165840	1659749	+	WP_000891022.1	kdpA	potassium-transporting ATPase subunit KdpA	96.6843097	-1.361949274	0.219222123	-6.287544271	3.67E-10	1.08E-09	8.967143664
ABUW_RS6885	ABUW_0379	NZ_CP008706.1	197620	198357	+	WP_000158861.1	mauE	FMN reductase	53.42227182	-1.362141914	0.250319018	-5.442696404	5.25E-08	1.31E-07	6.882464052
ABUW_RS6160	ABUW_0327	NZ_CP008706.1	349537	350313	+	WP_000552522.1		TSP1 family transporter	490.371832	-1.362619127	0.165149668	-8.250782402	157E-16	7.20E-16	15.14293183
ABUW_RS6465	ABUW_0094	NZ_CP008706.1	105770	106240	-	WP_0010017829.1	rBfE	6,7-dimethyl-8-ribitylsuccinate synthase	6660.276249	-1.362751104	0.193103119	-7.056715073	1.70E-12	6.00E-12	11.22203243
ABUW_RS6135	ABUW_0268	NZ_CP008706.1	286175	289333	+	WP_000353983.1		CusA/CzcA family heavy metal efflux RND transporter	1617.990146	-1.3642421	0.21616029	-6.298002995	3.02E-10	8.92E-10	9.04968577
ABUW_RS6040	ABUW_0097	NZ_CP008706.1	108980	112023	+	WP_000100799.1	serB	phosphoenolpyruvate phosphatase SerB	3787.788393	-1.364563354	0.137963187	-9.890780189	4.56E-23	3.08E-22	215.0120451
ABUW_RS6180	ABUW_0321	NZ_CP008706.1	210010	2105219	-			RNA-Ser	922.9454877	-1.364802962	0.28410985	-4.832683698	1.35E-06	3.00E-06	5.523338377
ABUW_RS6380	ABUW_3371	NZ_CP008706.1	3140489	3140947	+	WP_001028560.1	secB	protein-export chaperone SecB	6508.51349	-1.36491252	0.203878772	-7.107253604	2.07E-11	6.66E-11	10.7627186
ABUW_RS6480	ABUW_0913	NZ_CP008706.1	108650	91482	-	WP_000214356.1		phosphoenolpyruvate carboxylase (GTP)	31459.07384	-1.37063513	0.202384438	-6.772433406	127E-11	4.14E-11	10.38286277
ABUW_RS68425	ABUW_930	NZ_CP008706.1	1276792	1277712	+	WP_001203785.1	argF	ornithine carbamoyltransferase	7100.903979	-1.371946261	0.154649639	-8.81731975	7.23E-19	3.75E-19	17.4218631
	sRNA5	no	no	no	no	no	no	no	92.2491262	-1.373208014	0.266533375	-5.1521053	2.58E-07	6.06E-07	6.21950774
ABUW_RS67935	ABUW_0236	NZ_CP008706.1	392378	392537	+	WP_001010594.1		5-carboxymethyl-2-lysine-5-oxopropionine Delta-isomerase	465.8701387	-1.375891504	0.146723334	-3.935755646	5.68E-21	3.41E-20	19.46775818
ABUW_RS6645	ABUW_0630	NZ_CP008706.1	3896761	3898623	-	WP_001161507.1	twbI	Vi polysaccharide biosynthesis UDP-N-acetylglucosamine C-6 dehydrogenase TwbI	6243.82637	-1.375916005	0.1833471	-7.62101237	5.42E-14	2.98E-13	12.68051917
ABUW_RS67490	ABUW_0534	NZ_CP008706.1	1520409	1521251	+	WP_001003277.1		zinc-ribon and DUF3426 domain-containing protein	15.15.990553	-1.375480581	0.192272777	-6.1748406	1.33E-26	1.65E-25	24.9604471
ABUW_RS61780	ABUW_2421	NZ_CP008706.1	2408441	2409301	+	WP_000474792.1		transport subdomain-binding domain-containing protein	276.3937333	-1.380230677	0.212316925	-6.500834438	7.99E-11	2.45E-10	9.606990738
ABUW_RS6300	ABUW_3475	NZ_CP008706.1	3522641	3523315	-	WP_000054122.1		HAD-A family hydrolase	617148888	-1.381926982	0.199841932	-8.641931587	5.53E-18	7.27E-17	16.56521285
ABUW_RS6255	ABUW_0710	NZ_CP008706.1	108185	1092464	-	WP_000667907.1		D-alanyl-D-alanine carboxypeptidase PB6B	3414.44212	-1.381882587	0.185381901	-8.355706261	6.50E-17	3.02E-16	15.5962545
ABUW_RS6245	ABUW_068	NZ_CP008706.1	67941	679623	-	WP_0001023955.1		peptidylglyoxylase	4563.332805	-1.381919244	0.200092649	-6.906396688	4.97E-12	1.69E-11	10.7127296
ABUW_RS6815	ABUW_1891	NZ_CP008706.1	1223329	1224123	+	WP_001189675.1		DUF171 family protein	476.6987832	-1.383642703	0.18552129	-7.458106012	8.78E-14	3.35E-13	12.47548891
ABUW_RS67805	ABUW_3656	NZ_CP008706.1	3718336	3718563	+	WP_000894500.1		accessory factor UbiK family protein	5905.400431	-1.383684568	0.215481195	-5.51009056	3.59E-08	9.08E-08	7.041801329
ABUW_RS6805	ABUW_018	NZ_CP008706.1	135642	134140	+	WP_000770763.1		hypothetical protein	448.5207444	-1.386921467	0.38183219	-6.339418891	0.000273254	0.000487789	3.31167784
ABUW_RS6255	ABUW_3342	NZ_CP008706.1	3189862	3189251	+	WP_000985728.1		dCTP deaminase	4998.835163	-1.387197881	0.17092465	-8.16572979	4.82E-16	9.13E-15	14.67099937
ABUW_RS6830	ABUW_900	NZ_CP008706.1	1031664	104147	+	WP_000906816.1		hella-tum-hella domain-containing protein	346.2318644	-1.387308987	0.18939604	-7.324914993	2.39E-13	8.85E-13	12.0524525
ABUW_RS69575	ABUW_2233	NZ_CP008706.1	1635336	1264472	-	WP_000100701.1	metF	methyltetrahydrofolate reductase (NADPH)	4056.026744	-1.387419733	0.21864986	-6.585236466	5.45E-11	1.42E-10	9.488480223
ABUW_RS67490	ABUW_0977	NZ_CP008706.1	989036	990019	-	WP_001985534.1		lysophospholipid acyltransferase family protein	2104.011004	-1.387594419	0.1765647	-7.858849713	3.88E-15	1.62E-14	13.79159194
ABUW_RS6808	ABUW_045	NZ_CP008706.1	1286947	1287597	+	WP_001105740.1		hypothetical protein	863.6229666						

ABUW_RS16720	ABUW_3439	NZ_CP008706.1	3482982	3483740	-	WP_00265761.1		hypothetical protein	262.334251	-1.435.95535	0.95657395	-7.73092432	1.07E-14	4.36E-14	13.3607774
ABUW_RS08445	ABUW_1374	NZ_CP008706.1	173885	1732028	-	WP_00085666.1	rmO	30S ribosomal protein S2 methyltransferase RmO	3784.765729	-1.436480642	0.14777284	-8.22362688	1.97E-16	8.97E-16	5.0472982
ABUW_RS05075	ABUW_034	NZ_CP008706.1	94548	945348	+	WP_00.98557.1		NF308.04 family lipoprotein	475.630957	-1.4400174.9	0.91920835	-7.530651249	5.05E-14	1.09E-13	12.7089989
ABUW_RS1040	ABUW_2270	NZ_CP008706.1	225619	2256557	-	WP_00.949827.1		hypothetical protein	489.796943	-1.44.9W6459	0.281476827	-5.12E5945	3.03E-07	7.1E-07	6.6323059
ABUW_RS17095	ABUW_3514	NZ_CP008706.1	356205	35632.6	+	WP_00.1051725.1		LydJ family translocator	242.7.92.03	-1.442596547	0.98705461	-8.550825156	1.22E-17	5.87E-17	9.2634206
ABUW_RS5885	ABUW_3271	NZ_CP008706.1	330428	3304787	-	WP_00050193.1		YggJ family factor	2555.557548	-1.44416798	0.1983679	-12.05064653	1.92E-33	2.33E-32	31.63420612
ABUW_RS03525	ABUW_078	NZ_CP008706.1	722376	723233	+	WP_00.198297.1	rmC	rod shape-determining protein MreC	4557.864105	-1.444.90444	0.25473204	-5.69208854	1.43E-08	3.75E-08	7.4263639
ABUW_RS14250	ABUW_2935	NZ_CP008706.1	249846	2506034	+	WP_00.028513.1		helic-tun-helic transcriptional regulator	653.5758009	-1.444369277	0.165228749	-8.6890461	3.65E-18	1.8E-17	16.74201075
ABUW_RS20100	no	NZ_CP008706.1	333874	334104	-			hypothetical protein	30.87.89952	-1.445715374	0.407266323	-3.549796027	0.00038553	0.000675641	3.17028382
ABUW_RS16420	ABUW_4087	NZ_CP008707.1	53507	54286	+	WP_000422638.1		APH37-Vit family aminoglycoside C-phosphotransferase	1897.9928	-1.450462722	0.159496859	-9.15.065706	5.62E-20	3.9E-19	8.49674868
ABUW_RS16365	ABUW_4073	NZ_CP008707.1	42564	42893	-	WP_00.0066685.1		hypothetical protein	158.7724934	-1.450475406	0.38227662	-3.794308444	0.000490506	0.000271267	3.566603321
ABUW_RS00010	ABUW_0002	NZ_CP008706.1	1590	2738	+	WP_00.0237350.1		DNA polymerase delta subunit beta	9387.10526	-1.45485.022	0.138007262	-10.54184396	5.54E-26	4.36E-25	24.3605487
ABUW_RS02185	ABUW_0445	NZ_CP008706.1	46043	46013	+			IRNA-Ser	812.33.73528	-1.455750327	0.254482957	-5.720873257	1.06E-08	2.8E-08	7.552001938
ABUW_RS17530	ABUW_3601	NZ_CP008706.1	360893	3609676	-			IRNA-Tyr	10306.87438	-1.45799888	0.32134399	-4.53035285	5.89E-06	1.23E-05	4.908549543
ABUW_RS10385	ABUW_2137	NZ_CP008706.1	2124019	2125020	-	WP_00.00410.4	pmB	50S ribosomal protein L3 N53 glutamine methyltransferase	1885.635922	-1.456489417	0.90709378	-8.059888723	7.64E-16	3.32E-16	14.4789949
ABUW_RS05025	ABUW_024	NZ_CP008706.1	935102	935711	+	WP_000470769.1		dTMP kinase	101997837	-1.456643304	0.9214439	-10.24765439	12.1E-24	8.83E-24	23.05380497
no	no	no	no	no	no	no	no	no	2666.824584	-1.458938466	0.236478986	-6.90444659	6.85E-10	1.98E-09	8.730494612
ABUW_RS10980	ABUW_2258	NZ_CP008706.1	2243192	2244202	-	WP_000050479.1		tetracycline-chamber 4'-kinase	973.5209333	-1.459.90345	0.143635953	-9.14428858	3.51E-24	2.46E-23	22.60875673
ABUW_RS9615	ABUW_3824	NZ_CP008706.1	389553	3890744	-	WP_00.924267.1		glycyltransferase family 4 protein	95564.74478	-1.459945529	0.92.923235	-9.0918798	2.22E-19	12.E-18	17.946857
ABUW_RS16400	ABUW_3183	NZ_CP008706.1	3210911	3212705	+	WP_00119540.1		ribonucleoside-diphosphate reductase subunit alpha	44.62.8993	-1.460053354	0.8556240	-7.867463399	3.62E-16	1.53E-14	13.8182846
ABUW_RS07575	ABUW_1652	NZ_CP008706.1	153589	1537889	-	WP_000307.86.1	cydB	cytochrome c ubiquinol oxidase subunit I	17504.1556	-1.4601.844578	0.28828934	-5.064991967	4.08E-07	9.5E-07	6.02.97444.96
ABUW_RS1470	ABUW_1915	NZ_CP008706.1	321253	3214536	+	WP_000025826.1		ribonucleoside-diphosphate reductase subunit beta	20891.9215	-1.46051562	0.90439169	-8.06227195	5.76E-16	2.53E-15	14.5606664
ABUW_RS17520	ABUW_3599	NZ_CP008706.1	3606092	3606766	+			IRNA-Thr	21945.73.904	-1.462295535	0.3042.843	-4.806760552	1.53E-06	3.40E-06	5.46901421
ABUW_RS1825	no	NZ_CP008706.1	372186	3721488	-			universal stress protein	439.696396	-1.462920158	0.21959271	-6.775624436	1.24E-11	4.00E-11	10.3918882
ABUW_RS02570	ABUW_0523	NZ_CP008706.1	532644	533123	-	WP_00.0175201.1		hypothetical protein	149.997578	-1.463303830	0.138603174	-10.46496839	1.25E-25	9.62E-25	24.0189576
ABUW_RS16945	ABUW_3484	NZ_CP008706.1	353620	3533774	-	WP_000278705.1	hemW	radical SAM family heme chaperone HemW	2448.618589	-1.46510.897	0.31837902	-4.601752092	4.49E-06	8.92E-06	5.04959925
ABUW_RS17525	ABUW_3600	NZ_CP008706.1	360780	3608085	-			IRNA-Gly	3504.761008	-1.465133642	0.28337443	-5.1706.2926	2.33E-07	5.5E-07	6.25883224
ABUW_RS05900	ABUW_008	NZ_CP008706.1	145788	1459297	+	WP_00.0231971.1		chitinase lyase	430.2366287	-1.467105222	0.176.98744	-8.326422689	8.33E-17	3.85E-16	5.1436165
ABUW_RS07400	ABUW_1628	NZ_CP008706.1	151779	151474	-	WP_00.0205.90.1		ABC transporter permease	2875.540059	-1.467228032	0.17698467	-8.29029193	1.0E-16	5.20E-16	5.28344378
ABUW_RS10145	ABUW_2271	NZ_CP008706.1	2256582	2257869	-	WP_00.011093.1		phosphoglycerate kinase	4507.630302	-1.46914.098	0.175667105	-8.363211201	6.10E-17	2.84E-16	5.54575013
ABUW_RS14420	ABUW_2970	NZ_CP008706.1	2946356	2945159	+	WP_00.006965.1	betI	transcriptional regulator BetI	4254.2659	-1.469293228	0.37473963	-3.920637592	8.82E-05	0.00045677	3.752765306
ABUW_RS16710	ABUW_3236	NZ_CP008706.1	3264433	3265098	-	WP_000770256.1	tsaB	adenosine (37'-ME) theophylline-adenylyltransferase complex dimerization subunit type	557.097401	-1.47033216	0.9992099	-7.4272.9046	1.1E-13	4.20E-13	0.37630374
ABUW_RS05125	ABUW_044	NZ_CP008706.1	919177	919216	+	WP_001009632.1		hypothetical protein	982.2784499	-1.478854929	0.224240517	-6.594949702	4.23E-11	1.33E-10	9.87490813
ABUW_RS14375	ABUW_2961	NZ_CP008706.1	2974807	2975148	-	WP_000072599.1		FKBP-type peptidyl-prolyl-cis to trans isomerase	779.0648107	-1.482545798	0.223483998	-6.633806405	3.27E-11	1.04E-10	9.98453773
ABUW_RS00245	ABUW_0050	NZ_CP008706.1	55993	57027	-	WP_00.011866.1	nutY	A/G-specific adenine glycosylase	600.739532	-1.48460.035	0.14774525	-8.49433595	1.99E-17	9.47E-17	16.0288232
ABUW_RS02895	ABUW_0549	NZ_CP008706.1	55319	55360	+	WP_00078678.1		helic-tun-helic transcriptional regulator	634.6227213	-1.486995102	0.234087693	-6.352842206	2.1E-10	6.33E-10	9.99441414
ABUW_RS14850	ABUW_3060	NZ_CP008706.1	3086280	3087470	-	WP_00.02196.1	tuf	elongation factor Tu	23119.7247	-1.487828262	0.214537326	-7.03608665	1.08E-12	6.89E-12	11.9166705
ABUW_RS18915	ABUW_3885	NZ_CP008706.1	3953022	3954143	-	WP_0003078.1		5-(L-tyrosylamino)imidazole ribonucleotide synthase	4797.399784	-1.48934.566	0.201093223	-7.405224548	1.30E-13	4.90E-13	12.30951895
ABUW_RS00290	ABUW_0059	NZ_CP008706.1	63022	63431	+	WP_00009.7868.1	purC	phosphoribosylamidoimidazole succinocarboxamide synthase	1032.81424	-1.489355761	0.92486987	-9.86304379	4.90E-20	2.78E-19	9.55629841
ABUW_RS17255	ABUW_3548	NZ_CP008706.1	3504299	3504383	-			IRNA-Leu	6530.85263	-1.489504183	0.342767921	-4.353108012	1.34E-05	2.74E-05	4.562829786
ABUW_RS10375	ABUW_2755	NZ_CP008706.1	2744837	2745166	-	WP_000279980.1		NCSD family protein	1374.321945	-1.491946183	0.899460535	-7.869565591	3.55E-15	1.49E-14	10.8278976
ABUW_RS18715	ABUW_3844	NZ_CP008706.1	391358	391096	+	WP_000027529.1		TetR family transcriptional regulator	956.29197	-1.49346388	0.155028781	-11.045330238	2.31E-28	2.1E-27	26.763877
ABUW_RS05005	ABUW_332	NZ_CP008706.1	943403	944095	+	WP_000160699.1	nc	ribonuclease II	2696.635898	-1.4956105.9	0.88404491	-7.338311084	2.05E-15	1.6E-15	10.0130348
ABUW_RS17975	ABUW_3693	NZ_CP008706.1	3751901	3752345	-	WP_000097792.1		timex intracellular cation channel family protein	801.097892	-1.496562984	0.234.90372	-6.3864.9639	1.70E-10	5.1E-10	9.291932489
ABUW_RS03965	ABUW_089	NZ_CP008706.1	788559	789101	+	WP_00.019703.1		hypothetical protein	738.02.9905	-1.496688652	0.27499.906	-5.532.94098	3.14E-08	8.01E-08	7.09646629
ABUW_RS16770	ABUW_3449	NZ_CP008706.1	3494075	3495361	-	WP_000787677.1	gIP	glutamate/aspartate proton symporter GIP	5622.5552.8	-1.500.847236	0.230916244	-6.900569793	8.00E-11	2.40E-10	6.609548253
ABUW_RS10990	ABUW_2260	NZ_CP008706.1	2245929	2246357	-	WP_000069684.1		biopolymer ligase Ecd	198.363632	-1.502939886	0.14466914	-10.38687042	2.85E-25	2.14E-24	23.6702491
ABUW_RS00070	ABUW_0104	NZ_CP008706.1	16160	17392	+	WP_000335555.1		tyrosine-IRNA ligase	5456.526666	-1.5032723	0.15936468	-9.432937871	3.99E-21	2.41E-20	16.816285
ABUW_RS07570	ABUW_1651	NZ_CP008706.1	1535273	1535893	-	WP_000085257.1	cyoC	cytochrome c ubiquinol oxidase subunit II	75245.56159	-1.505267157	0.255036297	-5.902863324	3.09E-09	9.9E-09	8.040060263
ABUW_RS01180	ABUW_0241	NZ_CP008706.1	258729	259679	+	WP_001189180.1		homoserine kinase	1092.207024	-1.506483308	0.969949616	-9.02104252	1.86E-19	1.02E-18	17.9922285
ABUW_RS04425	ABUW_0902	NZ_CP008706.1	888156	888880	+	WP_032088.06.1		hypothetical protein	453.7988756	-1.507923695	0.265001071	-5.690255102	1.27E-08	3.33E-08	7.477990436
ABUW_RS17370	ABUW_2825	NZ_CP008706.1	283496	283230	+	WP_00.0084863.1	pyC	dihydroantase	3065.99352	-1.509483544	0.13610301	-11.090.4917	1.40E-28	1.29E-27	26.8889857
ABUW_RS00785	ABUW_0158	NZ_CP008706.1	175584	176169	+	WP_00.150484.1		TME85 family protein	1985.723301	-1.5105.65952	0.255.84836	-5.918738825	3.24E-09	8.98E-09	8.645585861
ABUW_RS10405	ABUW_2892	NZ_CP008706.1	2898820	2901057	+	WP_000956799.1		GMDS family protein	3737.767202	-1.510790296	0.93445857	-7.809870703	5.72E-15	2.36E-14	10.6270335
ABUW_RS05855	ABUW_190	NZ_CP008706.1	193758	1934453	-	WP_00006106.1		SmrMufi family protein	9092.767785	-1.51344375	0.903278442	-8.93907.052	3.89E-19	2.08E-19	17.681047
ABUW_RS015810	ABUW_190	NZ_CP008706.1	222249	223322	-	WP_000290937.1		uniphosphorylation decarboxylase	2208.172454	-1.51450.558	0.95732463	-9.623675773	6.35E-22	4.07E-21	20.35034435
ABUW_RS16465	ABUW_3184	NZ_CP008706.1	3210981	321116	+	WP_000405010.1		hypothetical protein	167.3718477	-1.515.91995	0.21718033	-6.97888998	2.98E-12	1.03E-11	10.58625058
ABUW_RS16300	ABUW_3355	NZ_CP008706.1	33927.0	3393728	-	WP_00.0186443.1	hVC	ketol-acid reductoisomerase	33596.40446	-1.518488611	0.134999781	-11.23352.84	2.79E-29	2.70E-28	27.56916848
ABUW_RS07580	ABUW_1653	NZ_CP008706.1	1537893												

ABUW_RS1630	ABUW_3096	NZ_CP008706.1	312955	312029	+			RNAi: Gln	975.4921486	-158375964	0.276725837	-5.723208426	1056-08	2.776-08	7.557687283
ABUW_RS1940	ABUW_3885	NZ_CP008706.1	3742844	374490	+	WP_000910004.1		CyD rRNA interon membrane protein	645.8755232	-1586424758	0.23308711	-6.793856853	1096-11	3.606-11	10.44336932
ABUW_RS1795	ABUW_3554	NZ_CP008706.1	361040	361899	-	WP_00118150.1	rnbB	235 rRNA (guanosine(22)-5'-O-methyltransferase RnbB	966.915679	-1588191497	0.1672567	-8.820283828	9126-23	6.146-22	212186591
ABUW_RS1270	ABUW_2734	NZ_CP008706.1	272599	272363	-	WP_000902022.1	rnmKL	IA (guanine(2069)-N(2)-methyltransferase RnmK(235 rRNA (guanine(2445)-N(2)-methyltransferase RnmL	2486.357841	-158374993	0.164706663	-9.5765596	4966-28	4.416-27	26.3557051
ABUW_RS09619	ABUW_1676	NZ_CP008706.1	168016	16815	+	WP_000540119.1	adeC	multidrug efflux RND transporter outer membrane channel subunit AdeC	1349.9653	-1590628581	0.176631979	-9.00533846	2.566-19	1.976-19	17.9304124
ABUW_RS03519	ABUW_6710	NZ_CP008706.1	79339	720817	-	WP_000150658.1	galA	Asp-IRNA(Asu)(Glu-IRNA(Gln)amidotransferase subunit GalA	6048.94346	-1593759962	0.209297844	-7.614973361	2.646-14	1.044-13	12.95007
ABUW_RS09465	ABUW_1845	NZ_CP008706.1	184416	184670	+	WP_000019027.1		methylenehydrofolate reductase C-terminal domain-containing protein	249.894974	-1595031237	0.259851916	-6.138231893	8.346-10	2.396-09	8.621077943
ABUW_RS08399	ABUW_1724	NZ_CP008706.1	172879	172340	-	WP_00101681037.1		hypothetical protein	477.5584818	-159718316	0.249289924	-6.40693027	1485-10	4.486-10	9.348945082
ABUW_RS02445	ABUW_0498	NZ_CP008706.1	608862	509305	-	WP_000514366.1		DUF2147 domain-containing protein	977.7706001	-1600649199	0.173169377	-9.243791058	2.386-20	1.386-19	16.8609063
ABUW_RS03065	ABUW_0623	NZ_CP008706.1	624365	625261	-	WP_001071168.1		acetyl-CoA carboxylase carboxyltransferase subunit beta	25246.91095	-1601792477	0.24657501	-7.46208482	8.526-14	3.266-13	12.4673876
ABUW_RS05920	ABUW_1212	NZ_CP008706.1	1252061	1252504	-	WP_000464149.1		DUF2726 domain-containing protein	300.722539	-1603458327	0.305462721	-5.249276637	1535-07	3.666-07	6.436279739
ABUW_RS03440	ABUW_0699	NZ_CP008706.1	702919	703494	-	WP_000125649.1		Sdp family protein	3866.899451	-1607365998	0.100912454	-12.27817487	1196-34	1526-33	32.8188605
ABUW_RS1670	ABUW_2378	NZ_CP008706.1	2365305	2366399	+	WP_000694032.1		aspartate(glutamate) isomerase family protein	57.58993143	-1607489505	0.371636009	-4.332424802	1476-05	2.996-05	4.524279129
ABUW_RS1000	ABUW_2282	NZ_CP008706.1	2247058	2247495	-	WP_000023429.1		ParB/RepB/SpdJ family partition protein	2035.025231	-1612417452	0.14842567	-10.8644757	1726-27	1486-26	25.8310006
ABUW_RS17610	ABUW_3617	NZ_CP008706.1	3675184	367617	+	WP_000213742.1	argH	arginine:succinate lyase	9382.286941	-1613510276	0.19001428	-11.86392163	1826-32	2.086-31	30.6814435
ABUW_RS0685	ABUW_3231	NZ_CP008706.1	3260081	3260767	-	WP_000434304.1	tpe	ribulose-phosphate 3-epimerase	3100.924791	-161428421	0.201210233	-8.022873302	1036-16	4.466-16	14.3514978
ABUW_RS08216	ABUW_3825	NZ_CP008706.1	382531	383565	+	WP_001166920.1	nuvB	UDP-N-acetylglutamate dehydrogenase	9265.344704	-1615106626	0.100021272	-11.45394997	2.716-41	6.481-40	33.6337812
ABUW_RS17516	ABUW_3598	NZ_CP008706.1	3659338	3660528	-	WP_001021661.1	luf	elongation factor Tu	189728.8966	-1623694106	0.220187739	-7.374104966	1656-13	6.206-13	12.2073437
ABUW_RS03850	ABUW_0786	NZ_CP008706.1	768298	768828	+	WP_000041399.1		hypothetical protein	384.7616429	-1624938696	0.260237087	-6.24401704	4.266-10	1.255-09	8.039092889
ABUW_RS16965	ABUW_2255	NZ_CP008706.1	2241676	2241417	-	WP_001183027.1		PI2 domain-containing protein	363.9904423	-1625944106	0.17910063	-9.07727176	1.116-19	6.86-19	16.20934077
ABUW_RS09600	ABUW_1974	NZ_CP008706.1	1975742	1976932	+	WP_001165950.1	adeA	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	18712.97669	-1626548529	0.31056167	-5.21203832	1865-07	4.446-07	6.325885919
ABUW_RS02565	ABUW_0522	NZ_CP008706.1	530749	532620	-	WP_000143524.1		homethyl-2-thiouridine(34)-methyltransferase MtrD/FAD-dependent 5-carboxymethylisomerase	6198.72618	-1628633435	0.128088277	-12.7891533	4.765-27	6.806-26	35.1677656
ABUW_RS1915	ABUW_2707	NZ_CP008706.1	2688875	2691496	-	WP_000377525.1		copper-transferrin-binding P-type ATPase	557.206891	-1628804973	0.237011049	-6.872265741	6.326-12	2.136-11	10.4718904
ABUW_RS18790	ABUW_3859	NZ_CP008706.1	3826609	3927175	-	WP_000307043.1		5'-nucleosidase	4411943964	-1628901074	0.12301164	-11.39177648	1806-40	2.399-39	38.53564819
ABUW_RS03070	ABUW_0624	NZ_CP008706.1	625258	626544	-	WP_000813093.1	foiC	bifunctional tetrahydrofolate synthase/dihydrofolate synthase	716.911081	-1631211469	0.187269834	-8.71487098	3.0336-18	1.516-17	16.8212286
ABUW_RS18705	ABUW_3235	NZ_CP008706.1	3263630	3264421	-	WP_000055117.1		class I SAM-dependent methyltransferase	784.9692544	-1635999302	0.23710973	-6.888125631	5.656-12	1.916-11	10.8718251
ABUW_RS19770	ABUW_2256	NZ_CP008706.1	2241429	2242409	-	WP_001075416.1		DNA polymerase II subunit delta	603.0433584	-1636758985	0.137169808	-12.23563829	2.016-34	2.546-33	32.95506721
ABUW_RS18620	ABUW_3825	NZ_CP008706.1	3889759	3892012	-	WP_000884147.1		oligosaccharide repeat unit polymerase	300.520246	-1642740638	0.21884981	-7.75262931	8.886-16	3.666-14	14.4564183
ABUW_RS05050	ABUW_0295	NZ_CP008706.1	140318	142105	-	WP_000303578.1	lepA	elongation factor G	9644.403319	-1643948768	0.190629364	-8.623716103	6.486-18	3.176-17	16.4993534
ABUW_RS02925	ABUW_0595	NZ_CP008706.1	593061	594168	+	WP_000599626.1	wscB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	1070.862239	-1645738364	0.18622972	-8.83710893	9.826-19	5.066-19	17.2931787
ABUW_RS15585	ABUW_2590	NZ_CP008706.1	2582189	2582705	+	WP_001186263.1		NAD(P)+-dependent oxidoreductase	167.262395	-1645800875	0.24224681	-6.759331225	1095-11	3.606-11	10.44336932
ABUW_RS04865	ABUW_0990	NZ_CP008706.1	1002393	1003793	-	WP_000067970.1		class I-dependent biophosphatase	26327.275644	-164622219	0.176450887	-9.65964418	4.546-22	2.926-21	20.5338406
ABUW_RS18055	ABUW_0326	NZ_CP008706.1	348612	349517	+	WP_000201869.1	tnuB	RNA pseudouridine(55) synthase TnuB	865.4788919	-1649529951	0.20610497	-10.06992346	1186-16	5.066-16	14.29554638
ABUW_RS05060	ABUW_0311	NZ_CP008706.1	1430597	1434331	-	WP_001021439.1		DUF484 domain-containing protein	140.244316	-1649687303	0.167102634	-10.48960705	8.7336-28	6.786-25	24.9880416
ABUW_RS06060	ABUW_0121	NZ_CP008706.1	150405	151610	+	WP_000419830.1		RNA domain-containing protein	492.8491628	-1649708445	0.341617021	-4.830529265	1366-06	3.036-06	5.95877583
ABUW_RS04420	ABUW_0901	NZ_CP008706.1	892021	898515	-	WP_000466167.1		hypothetical protein	657.935525	-1650973788	0.268446766	-6.50097187	7.746-10	2.236-09	8.652301952
ABUW_RS19145	ABUW_2709	NZ_CP008706.1	2691763	2692722	-	WP_000423280.1		LyxR family transcriptional regulator	327.7681079	-1651623292	0.259348951	-6.367958245	1502-10	5.756-10	9.240571644
ABUW_RS02265	ABUW_0461	NZ_CP008706.1	472920	473804	-	WP_0000914774.1		energy transducer TonB	6811204612	-1653338366	0.18762802	-9.719705869	1166-22	7.696-22	21.11390805
ABUW_RS16375	ABUW_3166	NZ_CP008706.1	319396	3192894	-	WP_000421864.1	nuvM	NADH-quinone oxidoreductase subunit M	36966.21065	-1654343638	0.259932805	-6.592786374	4.326-11	1356-10	9.869252074
srNA5	no	no	no	no	no	no	no		22.65063245	-1655379479	0.447783987	-3.696825988	0.000218312	0.00039396	3.4053196
ABUW_RS19355	ABUW_2751	NZ_CP008706.1	2741866	2742432	-	WP_000491583.1	mbB	ribonuclease HI	925.057271	-1653814919	0.20344576	-8.19701459	2.886-16	1.126-16	14.88842075
ABUW_RS07245	ABUW_1486	NZ_CP008706.1	147340	1473778	-	WP_000590096.1		YnfP family transcriptional regulator	44.50392304	-1665699803	0.1204730631	-13.82632566	0.166777558	0.202821244	0.648866557
ABUW_RS04295	ABUW_0875	NZ_CP008706.1	857894	859000	+	WP_0010418573.1	sucC	ATP-forming succinate-CoA ligase subunit beta	53007.1766	-1667828816	0.245904408	-6.782431366	1186-11	10.4718275	
ABUW_RS09405	ABUW_0311	NZ_CP008706.1	939051	9390628	-	WP_001032686.1		MF5 transporter	204.7777776	-1669763504	0.220716173	-7.565023323	3.876-14	1.506-14	12.8257731
ABUW_RS04970	ABUW_010	NZ_CP008706.1	102711	102611	-	WP_000167224.1	queE	7-carboxy-7-deaza-guanine synthase QueE	5381.1205999	-1672999475	0.20544746	-8.0934439	3.076-16	1.7716-16	11.78219718
ABUW_RS02220	ABUW_0452	NZ_CP008706.1	465228	465725	+	WP_0001018385.1		YcaB family protein	368.1320797	-1675867777	0.169422275	-10.51210064	7.606-26	5.846-25	24.2263765
ABUW_RS08880	ABUW_0204	NZ_CP008706.1	142291	142875	-	WP_000925669.1		aminoacylserine/threonine/alanine synthase component II	1340.84241	-1676873354	0.103333888	-5.16919765	3.646-12	8.996-11	50.0463163
ABUW_RS1930	ABUW_0367	NZ_CP008706.1	365064	350739	+			RNA-lyase	506.185311	-167691886	0.444453225	-3.772928299	0.000161001	0.000239311	3.531574377
ABUW_RS1800	ABUW_0367	NZ_CP008706.1	365064	350739	-	WP_000808509.1	glyQ	glycine-IRNA ligase subunit alpha	4614.471838	-1678218765	0.244665478	-6.859229925	6.926-12	2.336-11	10.6329480
ABUW_RS16275	ABUW_2610	NZ_CP008706.1	2603666	2603883	-	WP_0001638420.1		formylglutamate symporter	626.6208053	-1678293931	0.22446026	-7.477020361	7.606-14	2.916-13	12.53585268
ABUW_RS07200	ABUW_1477	NZ_CP008706.1	1465281	1465516	-	WP_000393747.1	glsR	Sodium/glutamate symporter	4470.134707	-1678823110	0.234814921	-7.14955989	8.716-13	3.126-12	11.05605564
ABUW_RS18145	ABUW_2917	NZ_CP008706.1	2927564	2928202	-	WP_000102721.1	nfsA	Fd-5 biophosphate protein NfsA	4343.830476	-167924267	0.19684905	-5.830703936	1456-17	6.976-17	6.686555
ABUW_RS18435	ABUW_3786	NZ_CP008706.1	3848203	3849702	-	WP_0002015436.1		amino acid permease	6927.73174	-1679600711	0.280648437	-5.984735663	2.976-09	6.076-09	8.21892197
ABUW_RS18015	ABUW_0038	NZ_CP008706.1	146497	146847	-	WP_000555783.1		hypothetical protein	48.04445358	-1679928031	0.31005742	-4.780593574	1756-06	3.846-06	5.416714346
ABUW_RS15060	ABUW_2691	NZ_CP008706.1	269490	2688017	+	WP_0001001965.1		LyxR family translocator	286.8007187	-1680068872	0.342255393	-4.908814978	9.166-07	2.066-06	5.685627872
ABUW_RS04300	ABUW_0676	NZ_CP008706.1	657895	659965	+	WP_000119637.1	sucD	succinate-CoA ligase subunit alpha	491529.37226	-1681255867	0.220730167	-7.395944576	1406-13	5.266-13	12.27720479
ABUW_RS02940	ABUW_0598	NZ_CP008706.1	595379	597167	-	WP_000986465.1	aspS	aspartate-IRNA lyase	26296.28745	-1682427551	0.193403262	-8.699056103	3.356-18	1.666-17	16.77929
ABUW_RS16045	ABUW_3099	NZ_CP008706.1	312433	3124											

ABUW_R06645	ABUW_1862	NZ_CP008706.1	1375420	1377678	+	WP_001985433.1		dicarboxylate/amino acid cation symporter	4 023 145006	-1.786440255	0.220031613	-8.180 9592	4.70E-16	2.08E-16	14.68 020285
ABUW_R05380	ABUW_180	NZ_CP008706.1	116011	116649	+	WP_001279312.1		RNA family pseudouridine synthase	1859 852472	-1.787394441	0.289513742	-6.17378 019	6.67E-10	1.93E-09	8.74795 161
ABUW_R02740	ABUW_2628	NZ_CP008706.1	262382	2623453	+	WP_001833905.1		exo-alpha-sialidase	591 555 9667	-1.78278668	0.28727002	-6.225079386	4.8E-10	1.40E-09	8.853 98008
ABUW_R05085	ABUW_3358	NZ_CP008706.1	346085	346880	+	WP_000729408.1	ptdJ	pyridoxal 5'-phosphate synthase	2201 1274449	-1.78868883	0.150205384	-11.90948543	1.06E-32	1.23E-31	30.9 070355
ABUW_R01585	ABUW_3164	NZ_CP008706.1	3199661	3199696	+	WP_001807343.1	upp	uracil hydrophobyltransferase	5288 398926	-1.789 98525	0.999529508	-8.966036971	3.05E-9	1.64E-18	17.78432838
ABUW_R033400	ABUW_0691	NZ_CP008706.1	698433	698508	+			RNA-Vai	1556 04195	-1.791403071	0.336267992	-5.849 05871	1.94E-09	1.35E-08	7.870632802
ABUW_R0975	no	NZ_CP008706.1	332 074	332 825	-	WP_012297364.1	hIC	translation inhibitor factor F-3	9 05 63424	-1.79227421	0.88774446	-6.49426395	2.22E-21	1.35E-20	9.86579424
sRNA7	no	no	no	no	no	no	no		1508 47 858	-1.79700382	0.419048288	-4.352042783	1.55E-05	2.75E-05	4.560878 67
ABUW_R007880	ABUW_164	NZ_CP008706.1	1607409	1607918	-	WP_000009660.1		peptidyl-prolyl cis-trans isomerase	9065 265	-1.799263143	0.220430342	-8.92052 051	3.28E-16	1.47E-15	14.83350359
ABUW_R00690	ABUW_0351	NZ_CP008706.1	1563763	1565520	+	WP_001820919.1	tadA	Pip plus assembly complex ATPase component TadA	494 7244398	-1.8019564	0.18133655	-9.933960708	2.96E-23	2.0 E-22	21.69706278
ABUW_R02140	ABUW_0435	NZ_CP008706.1	448800	449057	+	WP_001828210.1		succinate dehydrogenase assembly factor 2	262 465 899	-1.802814122	0.21651921	-8.52 880449	1.57E-17	7.5 E-17	16.1247463
ABUW_R01570	ABUW_0319	NZ_CP008706.1	343566	343991	+	WP_000788336.1		prelin-type N-terminal cleavage/methylation domain-containing protein	305 54267 5	-1.80378832	0.185 133756	-10.923 9754	8.93E-28	7.77E-27	26.1095535
ABUW_R01675	ABUW_3452	NZ_CP008706.1	349829	3499993	+	WP_001828078.1		hydrophobic protein	7514 5891	-1.807 9304 8	0.13025 853	-13.87398448	9.1E-44	1.68E-42	41.7758533
ABUW_R01465	ABUW_2910	NZ_CP008706.1	2922149	2922773	-	WP_00114 8992.1		carbonic anhydrase	14 023 8559	-1.808317594	0.1703886 18	-10.6390 033	2.60E-26	2.1E-25	24.67604392
ABUW_R0070	ABUW_3710	NZ_CP008706.1	3772479	3772554	-			RNA- Ala	3600 446472	-1.809142771	0.274365882	-6.593050771	4.28E-11	1.34E-10	9.872 90054
ABUW_R02230	ABUW_0458	NZ_CP008706.1	470499	47 874	-	WP_000543071.1		xanthine phosphoribosyltransferase	2287 203375	-1.81075033	0.204248578	-8.878252926	6.79E-19	3.57E-18	17.44708897
ABUW_R08840	ABUW_3869	NZ_CP008706.1	3838248	3838323	-			RNA- Ala	3588 094969	-1.81584975	0.270688936	-6.699635388	2.09E-11	6.72E-11	10.258223
ABUW_R01585	ABUW_2239	NZ_CP008706.1	2229526	2229624	-	WP_000392931.1	pyrF	oxidative 5'-phosphate decarboxylase	2312 45 924	-1.821245574	0.147 79635	-12.37435 91	3.60E-35	4.75E-34	33.32 02 16
ABUW_R05610	ABUW_3256	NZ_CP008706.1	3287705	3287790	-			RNA- Ala	3602 73212	-1.82193 167	0.271445231	-6.709755887	1.99E-11	6.30E-11	10.29074445
ABUW_R015300	ABUW_3 87	NZ_CP008706.1	1 982896	3 947185	-	WP_00107197.1	nuL	NADH-quinone oxidoreductase subunit L	34396 29339	-1.84021934	0.257055546	-7.688034978	8.14E-9	2.83E-12	11.5364621
ABUW_R017505	ABUW_3596	NZ_CP008706.1	3658868	3659 026	-	WP_000063880.1	secE	preproton translocase subunit SecE	8589 430001	-1.840537 867	0.253983383	-7.2468634	4.27E-10	1.56E-12	11.80684793
ABUW_R017700	ABUW_3634	NZ_CP008706.1	3693846	3694661	+	WP_000011618.1		DnaC family protein	2029 563286	-1.844003029	0.262596351	-12.084 97054	1.28E-33	1.57E-32	11.80458991
ABUW_R016925	ABUW_3480	NZ_CP008706.1	3530566	3530641	+			RNA- Lys	1074 2558 2	-1.846877928	0.453788555	-10.69926506	4.70E-05	9.04E-05	4.04383777
ABUW_R015810	ABUW_3100	NZ_CP008706.1	3129955	3129990	-	WP_000290730.1	rpmF	SOS ribosomal protein L32	70590 58997	-1.84705091	0.1819337 19	-10.857 8865	2.30E-24	1.63E-23	22.788 041
ABUW_R00035	ABUW_0007	NZ_CP008706.1	7678	9609	-	WP_000 00882.1		ATP-binding cassette domain-containing protein	1538 690281	-1.848485089	0.80692884	-10.2355 0703	1.37E-24	9.98E-24	23.0009226
ABUW_R01235	ABUW_3746	NZ_CP008706.1	3801040	3802737	-	WP_000623 84.1		NAD-dependent nucleic enzyme	8849 815 92	-1.84951845	0.227346044	-8.152 0967	4.1E-16	1.83E-15	14.73765676
ABUW_R01360	ABUW_2958	NZ_CP008706.1	2970802	2971 521	-	WP_000856365.1	pgsA	poly-beta-1,6-N-acetyl-D-glucosamine biosynthesis protein PgsA	802 9848679	-1.851275 969	0.93035406	-9.59267 107	8.88E-22	5.44E-21	20.2640268
ABUW_R02605	ABUW_0530	NZ_CP008706.1	538095	539060	-	WP_001 865897.1	secF	protein translocase subunit SecF	12 6133325	-1.853819379	0.207635491	-8.928209556	4.33E-19	2.30E-18	13.83745 93
ABUW_R015010	ABUW_0024	NZ_CP008706.1	27363	28667	-	WP_000084730.1	nmb	16S rRNA [cytosine(87)-CDS]-methyltransferase RnmB	1775 498883	-1.855692477	0.155430671	-11.93903661	7.41E-33	8.73E-32	31.059 0971
ABUW_R015400	ABUW_3271	NZ_CP008706.1	31963	31985	-	WP_001 070986.1	nuoH	NADH-quinone oxidoreductase subunit NuoH	23369 85271	-1.857653233	0.281995956	-6.58858 102	4.44E-11	1.39E-10	9.85762493
sRNA4	no	no	no	no	no	no	no		26 4677612	-1.8600448 8	0.537 93651	-3.463638895	0.000539291	0.000919235	3.038467575
ABUW_R015400	ABUW_3098	NZ_CP008706.1	3 923116	3 924 02	+	WP_001 873422.1	gylT	SOS ribosomal protein L25	8014 32945	-1.862806911	0.240207793	-7.0566489 9	1.78E-12	6.24E-12	11.02448843
ABUW_R010390	ABUW_2342	NZ_CP008706.1	23257 11	2326802	-	WP_000506572.1	yhcH	redox-regulated ATPase YhcH	3 86 96062	-1.864892749	0.267645856	-6.967 76246	3.22E-12	1.1E-11	10.93324402
ABUW_R014065	ABUW_2899	NZ_CP008706.1	2904183	2905091	-	WP_000104008.1	cydD	sulfate adenylyltransferase subunit CydD	7526 103791	-1.865687681	0.21279471	-8.787548053	1.83E-18	9.25E-18	17.03337 47
ABUW_R01660	ABUW_0337	NZ_CP008706.1	358322	359551	+	WP_000790198.1		MSF transporter	4481333756	-1.866 14749	0.247103636	-4.425256266	9.63E-06	1.93E-05	4.70536469
ABUW_R0147 6	ABUW_3032	NZ_CP008706.1	30591 97	306 835	+	WP_000347036.1		PTP1B family type 4 plus ATPase	3955 7358021	-1.869955082	0.17856021	-10.5733 9874	3.96E-26	3.1E-25	24.50748742
ABUW_R0147 0	ABUW_3031	NZ_CP008706.1	30582	3059889	+	WP_000355491.1		type IV pilus twitching motility protein PIT	964 5924693	-1.870405737	0.254 021 968	-12.3602 73595	1.84E-13	6.73E-13	10.8330269
ABUW_R0138 6	ABUW_2842	NZ_CP008706.1	2855958	2857001	+	WP_001829231.1		hydrophobic protein	1774 662033	-1.87098792	0.200282278	-9.34409585	9.5 E-21	5.65E-20	19.24805456
ABUW_R000235	ABUW_0044	NZ_CP008706.1	55 94	55399	-	WP_001 827365.1		hydrophobic protein	398 387744	-1.88027234	0.16629 078	-12 04208 172	2.1E-33	2.56E-32	31.59714601
ABUW_R01935	no	NZ_CP008706.1	2530381	2531471	+	WP_000594664.1		IS4 family transposase IS4a1	521 1645012	-1.882296961	0.26029384	-8.71852492	2.96E-18	1.47E-17	16.8399978
ABUW_R01995	ABUW_3484	NZ_CP008706.1	3542358	3543563	-	WP_001824664.1		TG0R0362 family transposase	345 0466804	-1.88472 1425	0.16064 844	-11.35089593	7.34E-30	7.38E-29	26.1332944
ABUW_R01280	ABUW_2186	NZ_CP008706.1	2190953	2191 961	-	WP_00077 840.1		NAD(P)H-dependent oxidoreductase	294 940 725	-1.88737849	0.243704856	-7.748018025	9.48E-15	3.86E-14	13.053 9537
ABUW_R01760	ABUW_3244	NZ_CP008706.1	3272721	3272771	+	WP_00201 5787.1		chromatin-binding protein	301803641	-1.88782 912	0.21853 966	-8.638632272	5.69E-18	2.78E-17	15.5356673
ABUW_R01285	ABUW_2953	NZ_CP008706.1	279723	28 184	-	WP_000090002.1	edaA	energy-dependent translocated trotonic protein EdaA	27429 052 9	-1.889364804	0.19787 91	-10.50327777	8.34E-26	6.50E-25	24.96899 91
ABUW_R014245	ABUW_0865	NZ_CP008706.1	844176	845408	-	WP_000994655.1		flotaxene-related sulfatransferase	4834 555696	-1.889338267	0.230317887	-8.576 17904	9.79E-18	4.73E-17	18.23478274
ABUW_R014200	ABUW_2925	NZ_CP008706.1	2935728	2937359	-	WP_001 68764.1		inorganic phosphate transporter	84 12 527363	-1.8890938 5	0.170862742	-11.06205832	1.92E-28	1.76E-27	26.75476235
ABUW_R01430	ABUW_3381	NZ_CP008706.1	342637	342 068	-	WP_000993851.1	ndk	nucleoside-diphosphate kinase	13627 87967	-1.890552545	0.2119 4999	-8.95496376	3.42E-19	1.84E-18	17.73520535
ABUW_R000705	ABUW_0307	NZ_CP008706.1	306897	306547	+	WP_000213000.1	pyrE	uracil hydrophobyltransferase	141928369	-1.890744085	0.178296804	-10.60448202	2.84E-26	2.29E-25	24.64040321
ABUW_R007495	ABUW_1635	NZ_CP008706.1	162165	162210	-	WP_00081703.1	pma	SOS ribosomal protein L1 methyltransferase	2958 38 955	-1.89282031	0.149646506	-13.330309 5	1.49E-40	2.42E-39	38.63903564
ABUW_R014995	ABUW_1018	NZ_CP008706.1	102915	1030397	-	WP_00184811.1	cywW	sulfate ABC transporter permease subunit CywW	95 90656251	-1.894912 033	0.229 64436	-8.268787851	1.35E-16	6.22E-16	15.2064 021
ABUW_R009605	ABUW_1875	NZ_CP008706.1	1876929	1880039	+	WP_000987602.1	adeB	multidrug efflux RND transporter permease subunit AdeB	5514 20474	-1.89632 610	0.298272372	-6.474908719	9.49E-11	2.90E-10	9.537399965
ABUW_R014440	ABUW_2974	NZ_CP008706.1	2990622	299 992	+	WP_001 950229.1		hydrophobic protein	85 02492676	-1.897324693	0.2686 784	-17.067 87751	1.64E-12	5.78E-12	11.23739581
ABUW_R008495	ABUW_1144	NZ_CP008706.1	1142774	1143239	+	WP_001045523.1	fabZ	3-hydroxyacyl-ACP dehydratase FabZ	10027 39061	-1.897402888	0.154085399	-12 342 7061	5.37E-35	7.00E-34	33.16457851
ABUW_R01195	ABUW_3618	NZ_CP008706.1	3676627	3678896	+	WP_000098996.1		oxidative damage protection protein	797 0002336	-1.903342338	0.18089094	-16.42097 865	1.35E-60	4.33E-59	58.36314653
ABUW_R008890	ABUW_3627	NZ_CP008706.1	3623 87	3624456	+	WP_000778452.1	eno	phosphopyruvate hydratase	24287 5 993	-1.90466744	0.156248393	-12.90044 18	3.51E-34	4.43E-33	32.3543727
ABUW_R015140	ABUW_3727	NZ_CP008706.1	3785438	3786652	+	WP_000372838.1		MSF transporter	378 433434	-1.905894424	0.163564698	-11.6502 9751	2.24E-31	2.4 E-30	29.6791341
ABUW_R016360	ABUW_3367	NZ_CP008706.1	3407929	3408495	-	WP_000099430.1	om	oligonucleotidase	2344 009604	-1.91970 842	0.13258273	-14.43403909	3.1E-47	6.63E-46	45.17926382
ABUW_R003100	ABUW_0638	NZ_CP008706.1	638450	638704	-	WP_001 828986.1									

ABUW_RS02635	ABUW_0536	NZ_CP008706.1	54597	545634	-	WP_001077536.1	queA	IRNA pteQ(p34) S-adenosylmethionine:ribosyltransferase-isomerase QueA	9256.065852	-2.0100659	0.166878543	-0.21445062	17'E-24	1.226-23	22.9183888
ABUW_RS03710	ABUW_1459	NZ_CP008706.1	1450338	145041	+			IRNA: Ttp	6075.739896	-2.0181905	0.314082963	-6.410424	1446-10	4.346-10	9.362326485
ABUW_RS17290	ABUW_3553	NZ_CP008706.1	3619290	3619204	-	WP_000750101.1		DMT family transporter	723.2407981	-2.022240896	0.162045835	-0.30024495	2.136-40	3.666-39	8.43656765
ABUW_RS1860	ABUW_2851	NZ_CP008706.1	2863397	2864238	-	WP_000896578.1		cation transporter	480.262505	-2.0232723	0.2221825	-9.0440316	8.676-20	4.866-19	8.15330196
ABUW_RS1475	ABUW_2359	NZ_CP008706.1	2342758	2343825	+	WP_000956445.1		type I farnesylase	7550.84452	-2.026692786	0.269248283	-7.527226419	5.186-14	2.006-10	12.6992661
ABUW_RS1635	ABUW_3097	NZ_CP008706.1	312066	312066	+	WP_001031287.1		ribosa-3-phosphate pyrophosphokinase	31431.0057	-2.02682561	0.230302341	-8.850716477	13.66-18	6.966-18	17.657425
ABUW_RS19005	ABUW_3993	NZ_CP008706.1	3999443	3971503	-	WP_001185090.1	yiiC	membrane protein insertase YiiC	33583.20947	-2.043328007	0.219550905	-9.418389943	4.586-21	2.756-20	19.5599339
ABUW_RS05835	ABUW_1165	NZ_CP008706.1	1228070	122818	-	WP_0011817843.1	h0E	GTP cyclohydrolase I h0E	9009.4445	-2.040733645	0.208854969	-9.799784309	1.016-22	7.505-22	21.0486497
ABUW_RS08875	ABUW_1781	NZ_CP008706.1	1775988	1779229	-	WP_000105830.1	gnD	Gn4 family monothiolase protein	5237.880884	-2.047154103	0.193356428	-11.47777025	1.716-30	1.772-29	28.76271212
ABUW_RS08265	ABUW_1697	NZ_CP008706.1	1694854	1695273	-	WP_000354611.1	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein	7855.670085	-2.04770472	0.2451062	-9.545936345	13.65-21	8.416-21	20.07507624
ABUW_RS16500	ABUW_3274	NZ_CP008706.1	3303957	3307778	-	WP_000710403.1		acetyl-CoA carboxylase carboxyltransferase subunit alpha	33166.61407	-2.050076131	0.184529209	-11.10976488	1.016-28	1.045-27	26.98231939
ABUW_RS1720	ABUW_2823	NZ_CP008706.1	2828665	2830023	+	WP_001086427.1	argG	argininosuccinate synthase	8253.635988	-2.050933326	0.237461606	-8.622380726	6.566-18	3.206-17	16.49503618
ABUW_RS02630	ABUW_0535	NZ_CP008706.1	543415	544443	+	WP_001021110.1		hypothetical protein	578.6805979	-2.051816718	0.216425087	-9.747734212	18.96-22	1.246-21	20.90806418
ABUW_RS07560	ABUW_1549	NZ_CP008706.1	1534055	1534933	-	WP_000919319.1	cylE1	prothrombin IIa farnesyltransferase	16347.49179	-2.054272945	0.212880782	-9.649875026	4.936-22	3.166-21	20.49956668
ABUW_RS00755	ABUW_082	NZ_CP008706.1	817724	88626	+	WP_000240700.1		UDP-3-O-acetyl-N-acetylglucosamine deacetylase	2634.371151	-2.055666609	0.127146165	-16.74732245	5.926-63	2.016-61	60.97778558
ABUW_RS18975	ABUW_3897	NZ_CP008706.1	3964832	3965339	+	WP_000214980.1	hpt	hypoxanthine phosphoribosyltransferase	2927.398254	-2.057601917	0.173192109	-11.88045995	1.506-32	1.736-31	30.7681806
ABUW_RS16020	ABUW_0304	NZ_CP008706.1	3120663	312167	+	WP_0001031287.1		IRNA: Gln	266.3045712	-2.063011221	0.306582043	-6.72960737	17.16-11	5.531-11	10.9560301
ABUW_RS10380	ABUW_2278	NZ_CP008706.1	2265495	2264175	+	WP_001116532.1		DUF 275 domain-containing protein	963.876156	-2.063249018	0.188482833	-10.94651066	6.905-28	6.075-27	26.21856199
ABUW_RS02385	ABUW_2897	NZ_CP008706.1	2905035	2905215	-	WP_000201265.1		hypothetical protein	1798.85203	-2.064675493	0.228449908	-8.998367505	2.295-19	1.2416-19	17.9053384
ABUW_RS02770	ABUW_3897	NZ_CP008706.1	393634	354586	-			ATP-binding protein	4696.10362	-2.069209231	0.214147175	-9.66265716	4.355-22	2.806-21	20.5523242
ABUW_RS15010	ABUW_3092	NZ_CP008706.1	3100759	3121592	+	WP_000621866.1	ispE	4-[pyridine S1'-diphospho]-2-C-methyl-D-erythritol kinase	7003.354157	-2.071077002	0.259759074	-8.220426832	1.9356-16	8.7716-16	15.05694743
ABUW_RS16900	ABUW_2242	NZ_CP008706.1	2232512	2232512	-	WP_000140309.1	rpaA	30S ribosomal protein S12	206336.9575	-2.073499636	0.19523919	-12.80539439	15.36-37	2.222-36	35.0430724
ABUW_RS18575	ABUW_2379	NZ_CP008706.1	2366107	2336998	-	WP_000192522.1	tauD	taurine dioxygenase	573.810798	-2.081428459	0.23465587	-8.870038771	7.116-19	3.8316-19	17.4890478
ABUW_RS09345	ABUW_1919	NZ_CP008706.1	1917828	1917839	+	WP_001046322.1		hypothetical protein	272.6759663	-2.086330641	0.332010856	-6.274417336	3.16-10	1.0316-09	8.98613334
ABUW_RS19170	ABUW_2621	NZ_CP008706.1	2626184	2626283	-			IRNA: Ser	904023687	-2.088940157	0.500420177	-4.196370683	2.966-05	5.8316-05	4.234552025
ABUW_RS17500	ABUW_3595	NZ_CP008706.1	3658145	3658678	-	WP_0008332994.1	nusG	transcription termination/antitermination protein NusG	90505.55763	-2.094845682	0.220782197	-9.504777613	2.006-21	1.246-20	19.90765373
ABUW_RS19155	ABUW_3738	NZ_CP008706.1	3794701	3795576	-	WP_000718586.1	atpB	IF1/ATP synthase subunit A	81619.58938	-2.100742259	0.273726147	-7.674615577	1.6061-14	6.616-14	11.796071
ABUW_RS18965	ABUW_0380	NZ_CP008706.1	414111	409941	+	WP_000433618.1		fosfolipid monophosphatase	4545.493775	-2.106721259	0.173028877	-12.1754723	4.2016-34	5.236-33	32.2820026
ABUW_RS00590	ABUW_0337	NZ_CP008706.1	4164917	1474461	+	WP_000109056.1		IRNA-[img]([img])A)-hydroxylase	9663.334553	-2.109126535	0.103095386	-16.17485058	7.596-49	2.306-57	56.63855302
ABUW_RS11070	ABUW_2256	NZ_CP008706.1	2283503	2284819	+	WP_000102545.1		methylamine dehydrogenase	10122.92054	-2.109133333	0.148326197	-14.21859142	6.9316-46	1.3816-44	10.55502687
ABUW_RS17240	ABUW_3543	NZ_CP008706.1	3603374	3603798	-	WP_000777730.1	rnpP	ribosome maturation factor RnpP	90506.9315	-2.109396943	0.244523577	-6.526779163	6.2016-18	3.046-17	16.517208
ABUW_RS01870	ABUW_0381	NZ_CP008706.1	407251	409198	+	WP_000041795.1		DNADEADEN box helicase	81960.62306	-2.110044468	0.102363657	-5.214158372	1.595-07	3.816-07	8.41623878
ABUW_RS14875	ABUW_3065	NZ_CP008706.1	3092709	3093938	+	WP_000832710.1		beta-ketocacyl-ACP synthase II	44223.65246	-2.11093408	0.185081348	-11.40543929	3.9316-30	4.006-29	28.9833816
ABUW_RS14865	ABUW_3063	NZ_CP008706.1	3090512	3090886	-	WP_000124374.1	rplL	30S ribosomal protein S12	390230.15657	-2.111720348	0.221807952	-9.572735345	1.0516-21	6.671-21	20.1821602
ABUW_RS19125	ABUW_3668	NZ_CP008706.1	366038	3662010	-	WP_001189538.1		benzocyclo[1,1']symportin BenI family transporter	328.650121	-2.120910312	0.242292736	-8.76197599	1.9216-18	9.7216-18	17.0244269
ABUW_RS03865	ABUW_0788	NZ_CP008706.1	769640	769858	-	WP_001027169.1		hypothetical protein	616.397191	-2.132755597	0.274730581	-7.763080438	8.2896-16	3.396-14	11.47107225
ABUW_RS00580	ABUW_1840	NZ_CP008706.1	1860639	1860719	-	WP_000616791.1	epmB	EF-P beta-lysyl-tRNA transfer protein EpmB	1740.716242	-2.136110104	0.19628564	-8.26442785	14.861-74	7.6316-73	72.11076365
ABUW_RS00460	ABUW_0093	NZ_CP008706.1	105317	105765	-	WP_000088418.1	nusB	transcription antitermination factor NusB	80003.19964	-2.145171043	0.188039502	-11.41097514	3.6916-30	3.766-29	28.4248157
ABUW_RS06410	ABUW_0434	NZ_CP008706.1	432666	126117	+	WP_000072151.1		DUF4481 domain-containing protein	364123794	-2.151918822	0.231876581	-9.288371621	1575-20	9.246-20	95.04244786
ABUW_RS14855	ABUW_3061	NZ_CP008706.1	3087565	3089703	-	WP_000110524.1	fusA	elongation factor G	48169.1235	-2.155425566	0.248956222	-8.657105722	4.846-18	2.396-17	16.6219002
ABUW_RS00360	ABUW_0683	NZ_CP008706.1	691552	692016	+	WP_000078916.1		hypothetical protein	7510380837	-2.156908054	0.190381995	-11.32934696	9.396-29	9.366-29	28.02862224
ABUW_RS00335	ABUW_1646	NZ_CP008706.1	1640874	1643144	-	WP_000527016.1		TonB-dependent sensor	20339187431	-2.161091587	0.374777004	-5.72509468	1.0316-08	2.746-08	7.561645578
ABUW_RS10550	ABUW_0315	NZ_CP008706.1	337394	338395	-	WP_000079197.1		PilH family protein	555946306	-2.164746537	0.267933096	-8.079429417	6.516-16	2.856-16	14.54520634
ABUW_RS02635	ABUW_0534	NZ_CP008706.1	543759	543338	-	WP_000141760.1		LeuX family protein	1187.512676	-2.188453075	0.192088807	-11.288719977	1.586-29	1.466-28	27.3363441
ABUW_RS08900	ABUW_1945	NZ_CP008706.1	1743256	1744044	+	WP_000064876.1	ispA	acyl-ACP--LipoN-N-acetylglucosamine O-acyltransferase	91165.63392	-2.174777483	0.182780195	-13.24688365	6.446-46	1.916-44	43.99127758
ABUW_RS04395	ABUW_0896	NZ_CP008706.1	893329	893865	-	WP_0001719363.1		DOMON-like domain-containing protein	886.3264542	-2.18408076	0.174357462	-12.52633947	5.3616-36	7.446-35	34.028595
ABUW_RS17310	ABUW_2207	NZ_CP008706.1	2162467	2162605	-	WP_001187383.1	fdx	ISC system 2Fe-2S type ferredoxin	9057157401	-2.18440281	0.186634392	-11.70418169	12.16-31	1.3416-30	29.87433653
ABUW_RS16025	ABUW_3095	NZ_CP008706.1	3121789	3121863	+	WP_0001031287.1		IRNA: Gln	916.1736355	-2.189752954	0.338196419	-12.464018887	1.0516-10	3.1616-10	9.497395019
ABUW_RS00400	ABUW_0897	NZ_CP008706.1	893880	894203	-	WP_000729551.1	yhbY	ribosome assembly RNA-binding protein YhbY	43398.065065	-2.198133491	0.150505986	-16.27720194	14.316-59	4.446-58	17.35252818
ABUW_RS02340	ABUW_0476	NZ_CP008706.1	487891	487906	-			IRNA: Aua	2861124124	-2.200289732	0.286920001	-7.668411952	17416-14	6.9316-14	13.159516
ABUW_RS06415	ABUW_1516	NZ_CP008706.1	1526106	1526411	+	WP_000106804.1		hypothetical protein	71919651073	-2.214826624	0.260610059	-4.898622925	1.9216-17	9.1416-17	16.03920447
ABUW_RS05935	ABUW_0163	NZ_CP008706.1	1620202	152977	-			IRNA: Asn	114.8801338	-2.220943357	0.443214188	-5.016993368	5.416-07	1.2166-06	5.903747457
ABUW_RS18200	ABUW_3739	NZ_CP008706.1	3795681	3796079	-	WP_0001084237.1		ATP synthase subunit I	7626.162559	-2.222212292	0.323254144	-6.890064499	5.5816-12	1.8816-11	10.72375565
ABUW_RS08070	ABUW_1655	NZ_CP008706.1	1648022	1650119	+	WP_0001189921.1		TonB-dependent sensor	3516875437	-2.223755657	0.548066762	-10.57453366	4.9616-05	9.516-05	40.2654377
ABUW_RS10240	ABUW_0533	NZ_CP008706.1	546667	546742	-			IRNA: Phe	53.84833723	-2.223872073	0.558376353	-3.982747588	8.816-05	0.0001904	3.889275844
ABUW_RS07070	ABUW_1511	NZ_CP008706.1	1443081	1444127	-	WP_0002029410.1		GaB/YiaY domain-containing protein	20557.99746	-2.226683466	0.193487659	-12.1510189	5.6716-34	7.006-33	32.15477618
ABUW_RS04810	ABUW_0891	NZ_CP008706.1	893691	893761	-	WP_0007071894.1	psuM	phosphoribosylformylglycinamide cyclo-ligase	97016.62391	-2.229768084	0.186342841	-11.96109536	5.3616-33	6.356-32	31.9703881

ABUW_R5165	ABUW_3111	NZ_CP008706.1	312765	-	WP_001275712.1		DUF177 domain-containing protein	61220.7249	-2.366664205	0.218269703	-0.84284336	2.1E-27	1.83E-26	25.73680719
ABUW_R51745	ABUW_2828	NZ_CP008706.1	283455	233559+	WP_000364482.1		TonB-dependent receptor	1231342145	-2.372344670	0.419470927	-5.655564006	1.55E-08	4.05E-08	7.39271486
ABUW_R51805	ABUW_3093	NZ_CP008706.1	312591	317655+			rRNA-Gln	527.5722379	-2.38071413	0.337168025	-7.050289014	1.79E-12	6.26E-12	11.03274911
ABUW_R51890	ABUW_3737	NZ_CP008706.1	373731	379416	-	WP_000424060.1	atpB	45828.50365	-2.387194908	0.271378877	-8.796211906	1.42E-18	7.23E-18	17.14108573
ABUW_R523220	ABUW_0654	NZ_CP008706.1	659510	665058	-	WP_000707856.1	uracil-xanthine permease	1750.287403	-2.372787809	0.310288103	-7.629815961	2.35E-14	9.23E-14	13.03471691
ABUW_R524165	ABUW_0849	NZ_CP008706.1	829992	830249	+	WP_000291632.1	rpmA	30326.02303	-2.382185918	0.210023325	-11.33011022	4.68E-30	4.74E-29	29.3240808
ABUW_R518700	ABUW_2841	NZ_CP008706.1	391011	391627	-	WP_001177232.1	gph	4069.859881	-2.394210594	0.853367799	-5.41002206	1.34E-53	3.41E-52	51.68710365
ABUW_R517890	ABUW_3633	NZ_CP008706.1	3632372	3692635	-	WP_001019121.1	ferric iron transport protein A	2492.348434	-2.395077871	0.250473921	-9.362188807	1.16E-21	7.20E-21	20.16258197
ABUW_R518020	ABUW_3906	NZ_CP008706.1	3971862	3972096	-	WP_000818293.1	rpmH	22591.97003	-2.400127188	0.20206551	-11.877196563	1.54E-32	1.78E-31	30.74909598
ABUW_R514755	ABUW_3042	NZ_CP008706.1	3068759	3069211	-	WP_000868162.1	dut	803.3596108	-2.408762486	0.177849061	-13.543585834	8.61E-42	1.50E-40	39.82319589
ABUW_R510525	ABUW_2166	NZ_CP008706.1	2147811	214810	+	WP_000091760.1	hypothetical protein	94.97048432	-2.418581988	0.53104558	-4.54083504	5.60E-06	1.9E-05	4.928082661
ABUW_R500790	ABUW_0159	NZ_CP008706.1	176219	178375	-	WP_000194085.1	TonB-dependent siderophore receptor	1568.219191	-2.426024484	0.378690894	-6.406344926	1.49E-10	4.49E-10	9.347033444
ABUW_R515145	ABUW_3119	NZ_CP008706.1	3138825	3139982	-	WP_000054321.1	8-amino-7-oxononanoate synthase	1340.319106	-2.427607505	0.164869529	-14.72414584	4.49E-49	10.1E-47	46.95970543
ABUW_R519335	ABUW_2665	NZ_CP008706.1	2659934	2660566	-	WP_001160766.1	hypothetical protein	570.171018	-2.432022264	0.218792277	-11.208547598	3.70E-29	3.55E-28	17.44959597
sRNA30	no	no	no	no	no	no	no	55.3702823	-2.44121031	0.329605322	-7.405645459	1.30E-13	4.90E-13	12.30990609
ABUW_R503210	ABUW_0652	NZ_CP008706.1	657052	658512	-	WP_000004974.1	amino acid permease	4.190104265	-2.451338892	0.224099491	-9.93861874	7.53E-28	6.58E-27	26.18166166
ABUW_R516550	ABUW_3322	NZ_CP008706.1	3471050	3471870	-	WP_001118664.1	MeaA/TuqI/EstB protein chain family protein	4560.680571	-2.452860154	0.348487089	-7.038586926	1.94E-12	6.77E-12	11.18918688
ABUW_R518175	ABUW_3734	NZ_CP008706.1	379722	3793256	-	WP_001186635.1	FGF1 ATP synthase subunit alpha	102342.9981	-2.454415026	0.28215434	-8.69081065	3.35E-18	1.66E-17	16.776259
ABUW_R519610	ABUW_3904	NZ_CP008706.1	3971029	3971629	-	WP_000231652.1	membrane protein insertion efficiency factor YidD	5043.038825	-2.452461025	0.235912518	-9.43802695	1.06E-25	1.27E-24	23.89672799
ABUW_R517655	ABUW_3632	NZ_CP008706.1	3636522	3692375	-	WP_001177232.1	ferric iron transporter B	9.168161691	-2.464071492	0.291020563	-8.452471864	2.85E-17	1.35E-16	16.87012111
ABUW_R500830	ABUW_0167	NZ_CP008706.1	88619	87614	+	WP_096642024.1	peptide chain release factor 2	8124.173448	-2.464175787	0.140382286	-7.55332429	5.61E-69	2.31E-67	66.63707192
ABUW_R511685	ABUW_0322	NZ_CP008706.1	345003	345743	-	WP_000464595.1	rRNA (guanine(37)-N1-methyltransferase TmD	337.01.9309	-2.465150688	0.25389302	-5.709352723	2.75E-22	20.7484378E-21	27.03510651
ABUW_R518560	ABUW_3810	NZ_CP008706.1	387810	3876565	-	WP_001022772.1	transcriptional regulator LMR	1208.141217	-2.467311849	0.338136255	-7.282619907	3.04E-13	1.03E-12	11.95041346
ABUW_R502165	ABUW_0420	NZ_CP008706.1	442897	443253	+	WP_000100816.1	30S ribosomal protein S10	81939.95891	-2.469793933	0.27198002	-8.826991307	1.08E-18	5.55E-18	17.92502753
ABUW_R502420	ABUW_0493	NZ_CP008706.1	505180	505546	-	WP_000224786.1	gpi	43603.8864	-2.469999688	0.217185659	-11.3727569	5.72E-30	5.74E-29	28.24050522
ABUW_R501595	ABUW_0224	NZ_CP008706.1	246048	246362	+	WP_000654307.1	helic-tun-helic transcriptional regulator	103.877626	-2.473774334	0.336100395	-7.358214056	1.86E-13	6.59E-13	12.6714098
ABUW_R502110	ABUW_0429	NZ_CP008706.1	443273	443659	+	WP_001041616.1	30S ribosomal protein S11	59266.30441	-2.477049458	0.27184104	-8.897019524	5.74E-19	3.04E-18	17.575297
ABUW_R517280	ABUW_3551	NZ_CP008706.1	3608835	3609695	+	WP_001152277.1	peptidyl peptidase	643.232918	-2.483398999	0.182634644	-8.59763372	4.1E-42	7.34E-41	40.15424849
ABUW_R501145	ABUW_0234	NZ_CP008706.1	252970	254049	+	WP_001016712.1	DNA/RNA non-specific endonuclease	898.1026902	-2.494821767	0.17014858	-14.66233893	1.0E-48	2.48E-47	46.60527576
ABUW_R508270	ABUW_0698	NZ_CP008706.1	2952371	2955746	-	WP_000594021.1	type III 3-dehydroquinate dehydratase	2697.083034	-2.502914003	0.2682987	-20.5691568	5.19E-94	5.19E-92	91.292527654
ABUW_R507795	ABUW_0596	NZ_CP008706.1	592397	594106	-	WP_002013461.1	MF5 transporter	495.3069794	-2.505730609	0.216770848	-11.6192471	3.54E-31	3.80E-30	29.42063615
ABUW_R517940	ABUW_3684	NZ_CP008706.1	3724375	3724271	+	WP_000418116.1	cation transporter	321.866652	-2.516272791	0.326489224	-7.707062305	1.29E-14	5.19E-14	8.28431576
ABUW_R503225	ABUW_0655	NZ_CP008706.1	661167	662982	+	WP_001018092.1	translational GTPase TypA	37234.40902	-2.518834298	0.233516259	-0.78840927	3.99E-27	3.39E-26	25.47043754
ABUW_R517730	ABUW_3641	NZ_CP008706.1	3701009	3702430	-	WP_000481054E.1	sigma-54-dependent P1a family transcriptional regulator	2381180.296	-2.53422464	0.23833938	-11.12123656	9.89E-29	9.22E-28	27.03510651
ABUW_R516335	ABUW_R516335	NZ_CP008706.1	3447176	3448310	-	WP_001198432.1	trigger factor	29049.47583	-2.540197606	0.15656607	-5.34607904	3.76E-53	9.42E-52	51.02615125
ABUW_R518016	ABUW_3505	NZ_CP008706.1	3971640	3971832	-	WP_001042377.1	rnpA	41525.29991	-2.541833062	0.188477806	-13.48618523	1.89E-41	3.24E-40	39.49007240
ABUW_R519555	ABUW_3285	NZ_CP008706.1	3318233	3318427	-	WP_001019635.1	50S ribosomal protein L35	10405.93484	-2.550770815	0.241332256	-5.598258459	3.03E-26	2.43E-25	24.61422207
ABUW_R501560	ABUW_0323	NZ_CP008706.1	345951	346319	+	WP_0001001562.1	30S ribosomal protein L19	31388.52231	-2.558525417	0.227137489	-11.25248364	2.25E-29	2.19E-28	27.66025992
ABUW_R516095	ABUW_3359	NZ_CP008706.1	331066	332352	-	WP_000174181.1	ACP 3-malonyltransferase	14528.87998	-2.566265319	0.204866337	-12.52712804	5.30E-36	7.40E-35	34.9102424
ABUW_R517380	ABUW_3571	NZ_CP008706.1	3628500	3629519	-	WP_0001091662.1	hypothetical protein	2130.826286	-2.578675287	0.265407194	-9.700073686	3.01E-22	1.95E-21	20.7096242
ABUW_R500995	ABUW_R500995	NZ_CP008706.1	219500	220582	+	WP_000680210.1	DUF475 domain-containing protein	5334.950811	-2.584046959	0.164284499	-8.3032487	2.30E-40	3.66E-39	38.43567676
ABUW_R507800	ABUW_0997	NZ_CP008706.1	1954365	1954793	+	WP_001022338.1	membrane protein	618.4302409	-2.584643275	0.22964038	-11.2560486	2.16E-29	2.16E-28	17.67669597
ABUW_R514380	ABUW_2862	NZ_CP008706.1	2917235	2917565	+	WP_001185261.1	YaeK family protein	6.14.5604144	-2.586710331	0.24223391	-0.67858472	1.28E-26	1.05E-25	24.97770233
ABUW_R517495	ABUW_3584	NZ_CP008706.1	3657088	3668036	-	WP_001174882.1	30S ribosomal protein L11	87835.05866	-2.602043469	0.2368505	-11.46956241	1.98E-30	1.94E-29	28.71822035
ABUW_R518180	ABUW_3180	NZ_CP008706.1	3199984	3191454	+	WP_001019412.1	adenosylmethionine-8-amino-7-oxononanoate transaminase	3.8921018881	-2.607844293	0.184687699	-8.96709952	7.99E-57	1.97E-55	54.70574326
ABUW_R501640	ABUW_0310	NZ_CP008706.1	336368	336819	+	WP_001014060.1	GcpH/FimT family pseudopilin	91.1256043	-2.619173562	0.238458798	-0.97872497	4.84E-28	4.31E-27	26.36536284
ABUW_R514435	ABUW_2973	NZ_CP008706.1	2988890	2990530	-	WP_000714073.1	mcp	10328.92757	-2.631412509	0.27196388	-5.49731841	4.52E-21	2.72E-20	9.5645841
ABUW_R504805	ABUW_0980	NZ_CP008706.1	92065	926294	-	WP_0001975532.1	phosphoribosylglycylamide formyltransferase	92062.52714	-2.633721287	0.198303815	-13.30141472	2.27E-40	3.63E-39	38.43929249
ABUW_R502116	ABUW_0430	NZ_CP008706.1	443672	444238	+	WP_001015204.1	30S ribosomal protein S4	14827.8671	-2.63795211	0.272438105	-9.682757506	3.67E-22	2.30E-21	20.63737279
ABUW_R5181970	ABUW_3733	NZ_CP008706.1	3790775	3791644	-	WP_001024971.1	FGF1 ATP synthase subunit gamma	56467.57216	-2.638765026	0.269139139	-9.75628532	1.18E-22	7.82E-21	21.0065179
ABUW_R501905	ABUW_0346	NZ_CP008706.1	367358	368635	+	WP_000360761.1	hypothetical protein	4246.64162	-2.647256406	0.1444377	-21.173282091	1.98E-100	2.96E-98	97.52853791
ABUW_R517445	ABUW_3584	NZ_CP008706.1	3642842	3644266	+	WP_000948934.1	TRAP transporter large permease subunit	3010.051945	-2.649180518	0.229234886	-11.55662021	6.83E-31	7.27E-30	29.13877721
ABUW_R519155	ABUW_3107	NZ_CP008706.1	3137434	3138078	-	WP_0001001597.1	ATP-dependent dehydrobiotin synthetase BioD	998.9619666	-2.654843951	0.149776429	-7.72537893	2.67E-10	1.46E-08	67.94104463
ABUW_R519550	ABUW_3284	NZ_CP008706.1	3317862	3318221	+	WP_001018488.1	gltI	33645.3677	-2.656161325	0.256878488	-10.34007654	4.64E-25	3.46E-24	23.48102605
ABUW_R514180	ABUW_2916	NZ_CP008706.1	2925130	2927394	+	WP_000044186.1	TonB-dependent siderophore receptor	9611.762005	-2.660735047	0.551023387	-4.828170111	1.37E-06	3.05E-06	51.5193144
ABUW_R5181865	ABUW_3736	NZ_CP008706.1	3793862	3794332	-	WP_001024691.1	FGF1 ATP synthase subunit B	36085.43341	-2.662852556	0.293359546	-9.07709592	1.0E-19	6.21E-19	9.20642788
ABUW_R5181820	ABUW_3733	NZ_CP008706.1	3791483	3782919	+	WP_001191625.1	DNA-processing protein DpsK	605.6564717	-2.667245972	0.16349018	-18.19725009	1.93E-58	5.68E-57	56.24934627
ABUW_R503335	ABUW_0682	NZ_CP008706.1	687335	691555	+	WP_000658892.1	Hpt domain-containing protein	688.1129179	-2.670909863	0.203526034	-12.12350207	2.41E-39	3.68E-38	37.43357288
ABUW_R502525	ABUW_0514	NZ_CP008706.1	524436	525955	+	WP_000717937.1	hypothetical protein	9323.446871	-2.672806344	0.				

ABUW_RS02070	ABUW_0421	N2_CP008706.1	439262	439795	+	WP_00009932.1	pfIF		50S ribosomal protein L6	77599.17305	-2.92151063	0.26041524	-112.8689864	3.37E-29	3.24E-28	27.48964377
ABUW_RS16350	ABUW_3365	N2_CP008706.1	3406102	3406905	-	WP_002027450.1			enoyl-ACP reductase	24203.58424	-2.923533901	0.21810309	-13.80200441	2.48E-43	4.48E-42	41.34859739
ABUW_RS19180	ABUW_3731	N2_CP008706.1	3788910	3789332	-	WP_000224542.1			FOF1ATP synthase subunit epsilon	31715.21031	-2.930381785	0.245619327	-11.93058306	8.20E-33	9.58E-32	310.9182307
ABUW_RS05525	ABUW_1029	N2_CP008706.1	1150658	1151029	-	WP_000846423.1			hypothetical protein	175.7476276	-2.930901295	0.279645898	-10.48075911	1.06E-25	8.16E-25	24.08844803
ABUW_RS07545	ABUW_1446	N2_CP008706.1	1532793	1533239	-	WP_000382591.1	pfII		50S ribosomal protein L9	135263.3301	-2.93129426	0.248174366	-11.8191751	3.39E-32	3.83E-31	30.41667547
ABUW_RS01425	ABUW_0290	N2_CP008706.1	309823	310881	+	WP_002014066.1			plus assembly protein PIM	4481.295578	-2.933381826	0.224562755	-10.06283733	5.38E-39	8.09E-38	37.01919257
ABUW_RS19725	ABUW_0405	N2_CP008706.1	432160	432471	+	WP_000707092.1	pfSJ		30S ribosomal protein S10	89528.80339	-2.933467954	0.238630572	-2.29292595	9.89E-35	1.27E-33	32.8970405
ABUW_RS19785	ABUW_2422	N2_CP008706.1	2409332	2410063	-	WP_001190359.1			amino acid ABC transporter ATP-binding protein	163.9656982	-2.949474433	0.37589522	-7.846533483	4.28E-15	1.78E-14	13.7504407
ABUW_RS02055	ABUW_0418	N2_CP008706.1	437990	438526	+	WP_000110187.1	pfIE		50S ribosomal protein L5	24190.0444	-2.963800488	0.263820699	-11.23414891	2.77E-29	2.68E-28	27.5716866
ABUW_RS05565	ABUW_1107	N2_CP008706.1	1160910	1161134	+	WP_001200845.1	rpmE		50S ribosomal protein L31	6336.271843	-2.967415414	0.278835376	-10.64217694	1.90E-26	1.55E-25	43.24058629
ABUW_RS02065	ABUW_0420	N2_CP008706.1	438853	439248	+	WP_000062816.1	rpsH		30S ribosomal protein S8	14152.66771	-2.980145494	0.253848397	-11.73990078	7.96E-32	8.86E-31	30.05270867
ABUW_RS15635	ABUW_3221	N2_CP008706.1	3250917	3250993	-			RNA- Pro	1954.140052	-3.006306285	0.334450084	-8.98897311	2.50E-19	1.35E-18	17.8686321	
sRNA57	no	no	no	no	no	no	no	no		18.02129697	-3.008239519	1.00079717	-3.005843348	0.00264854	0.004197434	2.379371165
ABUW_RS19170	ABUW_2276	N2_CP008706.1	2261557	2261665	+	WP_000651164.1			helic- turn- helix transcriptional regulator	492.0673339	-3.015036533	0.339520444	-8.880279767	6.67E-19	3.51E-18	17.45495508
ABUW_RS17895	ABUW_3634	N2_CP008706.1	3692779	3693699	+	WP_000608735.1	xeiD		site- specific tyrosine recombinase XeiD	1343.210569	-3.025552074	0.142331051	-21.25710219	2.83E-100	4.08E-98	97.38958694
ABUW_RS02060	ABUW_0419	N2_CP008706.1	438536	438841	+	WP_001074624.1	rpsN		30S ribosomal protein S14	45389.76961	-3.053810567	0.24572767	-12.42762188	1.85E-35	2.51E-34	33.60025122
ABUW_RS19775	ABUW_3550	N2_CP008706.1	3607609	3608835	+	WP_000279218.1			type II secretion system F family protein	1140.98519	-3.06648029	0.21286175	-14.40597145	4.75E-47	9.86E-46	45.02627934
ABUW_RS12940	ABUW_2666	N2_CP008706.1	2660607	2660795	-	WP_000032786.1			DUF2158 domain- containing protein	134.8355848	-3.086444428	0.277725887	-11.15275956	1.08E-28	1.01E-27	26.99738944
ABUW_RS03340	ABUW_0679	N2_CP008706.1	683804	684186	+	WP_000101096.1			response regulator	1823.299273	-3.102230578	0.989726493	-5.10553665	6.17E-55	1.66E-53	52.78061110
ABUW_RS06035	ABUW_1235	N2_CP008706.1	1278330	1279082	-	WP_001982116.1	rpsB		30S ribosomal protein S2	102238.9676	-3.10576426	0.220000471	-14.10780003	2.98E-45	5.75E-44	43.24060031
ABUW_RS17835	ABUW_3663	N2_CP008706.1	3722859	3723371	-	WP_000021528.1			signal peptidase I	237.5434144	-3.114310514	0.344167661	-9.048817958	1.45E-19	7.97E-19	18.08877932
ABUW_RS01995	ABUW_0406	N2_CP008706.1	432529	433167	+	WP_001982642.1	pfIC		50S ribosomal protein L3	151789.6693	-3.118663799	0.310761543	-9.933224337	1.86E-23	2.02E-22	21.65851672
ABUW_RS03350	ABUW_0681	N2_CP008706.1	684180	684888	+	WP_000505931.1			methyl- accepting chemotaxis protein	8701.720525	-3.140931355	0.213151281	-13.57080171	5.98E-42	1.05E-40	39.97981981
ABUW_RS06040	ABUW_1236	N2_CP008706.1	1279220	1280095	+	WP_000105378.1			elongation factor Ts	41843.25274	-3.14108041	0.219157073	-14.4310271	3.29E-47	6.86E-46	45.16356681
ABUW_RS03335	ABUW_0678	N2_CP008706.1	683397	683780	+	WP_000389061.1	pfIG		twitching motility response regulator PIG	5691.783327	-3.170418732	0.255999991	-12.38448683	3.17E-35	4.22E-34	43.24058629
ABUW_RS01440	ABUW_0293	N2_CP008706.1	312270	312797	+	WP_000695059.1			plus assembly protein PIP	402.4531548	-3.181489549	0.23585085	-13.53197277	1.01E-41	1.15E-40	39.57599667
ABUW_RS02000	ABUW_0407	N2_CP008706.1	433179	433781	+	WP_001050255.1	pfID		50S ribosomal protein L4	190424.3185	-3.230878058	0.332478207	-9.771563395	1.54E-21	1.65E-20	70.78203337
ABUW_RS08765	ABUW_1800	N2_CP008706.1	1792099	1795008	+	WP_000831236.1			TonB- dependent siderophore receptor	1957.479374	-3.233236617	0.269526015	-11.99600944	3.73E-33	4.46E-32	31.35019058
ABUW_RS02010	ABUW_0409	N2_CP008706.1	431410	434934	+	WP_001122317.1	pfIB		50S ribosomal protein L2	171297.5468	-3.240285902	0.318102768	-10.25073853	1.17E-24	8.57E-24	23.06691568
ABUW_RS18565	ABUW_3814	N2_CP008706.1	3876585	3878252	-	WP_011857993.1	ldpP		L- lactate permease	5075.973923	-3.28111153	0.350021045	-9.376340031	6.83E-21	4.07E-20	19.39031215
ABUW_RS11115	ABUW_2285	N2_CP008706.1	2270136	2271626	+	WP_000187951.1	putP		sodium/proline symporter PutP	22222.76953	-3.29536486	0.302947927	-10.87769164	1.47E-27	1.27E-26	25.89503067
ABUW_RS02005	ABUW_0408	N2_CP008706.1	433778	434098	+	WP_001058538.1	pfIW		50S ribosomal protein L23	57055.10086	-3.295407948	0.295629811	-11.14707593	7.40E-29	6.95E-28	27.1580386
ABUW_RS03345	ABUW_0680	N2_CP008706.1	684227	684763	+	WP_000729762.1			putine- binding chemotaxis protein CheW	2158.743622	-3.312150446	0.263559103	-12.56702579	3.21E-36	4.50E-35	34.34677834
ABUW_RS16790	ABUW_3453	N2_CP008706.1	3500053	3501915	+	WP_000967566.1			hypothetical protein	1224.585304	-3.353008053	0.215349746	-15.5700811	1.9E-54	3.10E-53	52.68019426
ABUW_RS02015	ABUW_0410	N2_CP008706.1	434948	435223	+	WP_001108119.1	rpsS		30S ribosomal protein S19	97612.51417	-3.358864579	0.337824306	-9.942637403	2.72E-23	1.85E-22	21.73328827
ABUW_RS17485	ABUW_3592	N2_CP008706.1	3656083	3656589	-	WP_001186210.1	pfIU		50S ribosomal protein L10	88989.34102	-3.416538563	0.228450167	-14.95529028	1.44E-50	3.39E-49	48.46987967
ABUW_RS01845	ABUW_3591	N2_CP008706.1	3656669	3656040	-	WP_001202980.1	rplU		50S ribosomal protein L7/L12	125896.0159	-3.421560783	0.20822018	-16.43241677	1.02E-30	3.16E-29	58.4421041
ABUW_RS02025	ABUW_0412	N2_CP008706.1	435566	436318	+	WP_000529922.1	rpsC		30S ribosomal protein S3	129966.0493	-3.516792089	0.321089197	-10.94315237	7.17E-28	6.29E-27	26.20151482
ABUW_RS00710	ABUW_0143	N2_CP008706.1	165658	165877	-	WP_001698816.1			TonB- dependent siderophore receptor	669.1208509	-3.559167308	0.387528426	-9.184274158	4.14E-20	2.37E-19	18.05207911
ABUW_RS02030	ABUW_0413	N2_CP008706.1	436322	436735	+	WP_000941215.1	pfIP		50S ribosomal protein L18	174795.373	-3.567893498	0.315329032	-11.31410292	1.12E-29	1.10E-28	27.95876543
ABUW_RS01435	ABUW_0292	N2_CP008706.1	311519	312259	+	WP_000076101.1			type 4a plus biogenesis protein P10	134.943211	-3.589185678	0.272705099	-13.10344211	1.48E-39	2.25E-38	37.64739439
ABUW_RS02020	ABUW_0411	N2_CP008706.1	435235	435564	+	WP_001982638.1	pfIV		50S ribosomal protein L22	52252.33271	-3.603304364	0.31818538	-11.32451409	9.92E-30	9.84E-29	28.00684505
ABUW_RS02040	ABUW_0415	N2_CP008706.1	436929	437186	+	WP_001029145.1	rpsQ		30S ribosomal protein S19	35740.46642	-3.603471849	0.310242395	-11.61502701	3.46E-31	3.78E-30	29.43012883
ABUW_RS02035	ABUW_0414	N2_CP008706.1	436735	437632	+	WP_000849928.1	rpmC		50S ribosomal protein L29	45189.28456	-3.606900216	0.31510762	-11.44427293	2.15E-30	2.51E-29	28.58806628
ABUW_RS01430	ABUW_0291	N2_CP008706.1	310881	311522	+	WP_000201229.1			PIW domain- containing protein	1612.438045	-3.688978899	0.26411409	-13.95729573	2.84E-44	5.32E-43	42.27391188
ABUW_RS10540	ABUW_2169	N2_CP008706.1	2150091	2150978	+	WP_000011678.1			sulfate effector TauC/SatE family protein	1667.46087	-3.823949591	0.379992265	-10.06323007	6.03E-24	5.55E-23	22.25565307
ABUW_RS11280	ABUW_2319	N2_CP008706.1	2304179	2304616	-	WP_001161759.1			PACE efflux transporter	486.7408237	-3.862776958	0.537975621	-7.180208182	6.96E-13	2.51E-12	11.59982432
ABUW_RS01290	ABUW_0263	N2_CP008706.1	281563	282156	+	WP_000772134.1			hypothetical protein	4441.725076	-4.002182964	0.257190423	-5.56105255	1.34E-54	3.52E-53	52.45381974
ABUW_RS11790	ABUW_2423	N2_CP008706.1	2410066	2410731	+	WP_000418072.1			amino acid ABC transporter permease	108.884913	-4.061697402	0.484479987	-8.214078449	2.14E-16	9.69E-16	15.01598724
ABUW_RS05000	ABUW_1019	N2_CP008706.1	1030394	1031227	-	WP_000083117.1	cysT		sulfate ABC transporter permease subunit CysT	118.0387869	-4.08782975	0.448930127	-9.165714916	8.57E-20	4.82E-19	18.3734042
ABUW_RS14450	ABUW_2976	N2_CP008706.1	2992193	2993527	+	WP_001071333.1			amino acid permease	704.2848933	-4.180009409	0.243526992	-17.03305814	4.67E-25	1.73E-23	62.7629424
ABUW_RS11585	ABUW_2381	N2_CP008706.1	2367863	2368657	+	WP_000119471.1			ATP- binding cassette domain- containing protein	719.963052	-4.2332199428	0.456054604	-9.28232541	1.66E-20	9.75E-20	19.01069709
ABUW_RS100635	ABUW_0128	N2_CP008706.1	143273	143998	+	WP_0011916274.1			ion channel protein Tax	2811.272538	-4.283234105	0.239802172	-17.91532021	8.95E-72	4.15E-70	69.38225908
ABUW_RS08145	ABUW_1069	N2_CP008706.1	1766667	1767173	+	WP_000782978.1			pega domain- containing protein	206.5046345	-4.18804546	0.322205452	-13.70803927	9.09E-43	1.03E-41	40.78657924
ABUW_RS09025	ABUW_0187	N2_CP008706.1	209373	210254	-	WP_000733010.1	omp33-36		peromp33-36	43762.53578	-4.444636498	0.332334379	-13.37398951	8.58E-41	1.43E-39	38.84507029
ABUW_RS08010	ABUW_1641	N2_CP008706.1	1637480	1637818	+	WP_001243508.1			hypothetical protein	2614524357	-4.541486359	0.352108924	-12.89680309	4.69E-38	6.90E-37	36.10123245
ABUW_RS11590	ABUW_2382	N2_CP008706.1	2368667	2369707	-	WP_00006										

ABUW_RS07500	ABUW_536	NZ_CP008706.1	1523327	1523557	-	WP_000859008.1		hypothetical protein	5416.89278	8.237385396	0.408299165	20.17487742	1635.90	1.09618	87.9625735
ABUW_RS08050	ABUW_551	NZ_CP008706.1	9452792	945262	+	WP_00123841.1		hypothetical protein	984.5032291	8.184348814	0.50807266	6.03761048	6.986158	1.265156	55.8996245
ABUW_RS1020	ABUW_2703	NZ_CP008706.1	2687015	2687371	+	WP_00088862.1		four-helix bundle copper-binding protein	7279.866477	8.036665315	0.45666317	17.59868556	2.526169	6.826168	67.862163
ABUW_RS02650	ABUW_053	NZ_CP008706.1	58624	58782	-	WP_000490267.1		DUF4328 domain-containing protein	5808.425003	7.855934823	0.35276182	22.26942667	7.255110	1.921107	106.950782
ABUW_RS1860	ABUW_2437	NZ_CP008706.1	2426277	2427186	-	WP_001450960.1		ion-containing redox enzyme family protein	6730.655542	7.799319007	0.44400034	18.8207416	5.116179	2.026177	76.0946463
ABUW_RS02335	ABUW_2515	NZ_CP008706.1	2607870	2506022	+	WP_00127954.1		hypothetical protein	1186087951	7.795587605	0.7487851	10.43887601	1655.25	8.22625	24.085108
ABUW_RS1230	ABUW_2514	NZ_CP008706.1	2507184	2507484	-	WP_000338617.1		hypothetical protein	200.4946675	7.76014264	0.66541584	11.62033465	1.096131	1.265130	29.89962945
ABUW_RS1510	ABUW_3122	NZ_CP008706.1	3142445	3143296	+	WP_001664773.1	otdB	trehalase-phosphatase	1639.033208	7.750712726	0.578080537	13.4076894	5.455141	5.066140	39.29584948
ABUW_RS1040	ABUW_2686	NZ_CP008706.1	2673924	2676382	-	WP_00167319.1		hypothetical protein	1593.96074	7.732645482	0.379460169	20.37801623	2.625192	1.825190	89.73992861
ABUW_RS20200	ABUW_2143	NZ_CP008706.1	2129710	2129874	+	WP_000686293.1		hypothetical protein	2812.637964	7.644332541	0.33684103	22.69417843	5.116114	9.376110	111028204
newcandRNA1		no	no	no	no	no	no	no							
sRNA104		no	no	no	no	no	no	no							
ABUW_RS1225	ABUW_2510	NZ_CP008706.1	2506724	2506933	-	WP_000072126.1		cold-shock protein	427.5802554	7.384827036	0.38627312	9.11814881	1.785181	8.266180	79.083195
ABUW_RS0870	ABUW_1787	NZ_CP008706.1	1783246	1793605	+	WP_000195571.1		hypothetical protein	808.9824084	7.360393042	0.749196095	9.824387892	8.845123	3.945122	21.40450378
ABUW_RS08590	ABUW_1763	NZ_CP008706.1	1760845	1761088	-	WP_000102025.1		universal stress protein	4077.391926	7.14218403	0.355870806	20.0808356	1.086189	6.945188	87.1684053
ABUW_RS1010	ABUW_2679	NZ_CP008706.1	2670707	2671000	-	WP_000644336.1		DUF4142 domain-containing protein	1077.486021	7.042274119	0.362345651	9.4352384	3.896184	1.986182	81.70333481
ABUW_RS1855	ABUW_2436	NZ_CP008706.1	2424078	2428222	-	WP_001858565.1	katE	catalase HP8	1255.376016	7.040945533	0.60184902	11.69884748	1.296131	8.206131	30.0861961
ABUW_RS1960	ABUW_2458	NZ_CP008706.1	2446555	2450437	+	WP_001017562.1		indolyglyoxylate ferredoxin oxidoreductase family protein	40275.84516	7.007876664	0.385059393	18.9946646	5.216174	1.745172	71.75945075
ABUW_RS02155	ABUW_1657	NZ_CP008706.1	1657771	1651908	+	WP_000191254.1			10779.54957	7.002643368	0.302202662	23.12701416	8.725119	1.675116	116.777335
ABUW_RS1510	ABUW_1657	NZ_CP008706.1	1657771	1651908	+	WP_000191254.1			53.538163	6.956280444	0.60109462	11.57425959	5.566131	3.445130	29.46341156
ABUW_RS1510	ABUW_1657	NZ_CP008706.1	1657771	1651908	+	WP_000191254.1			9244.359405	6.936735991	0.41879469	6.75786409	4.905193	1.056161	60.37445914
ABUW_RS1850	ABUW_2435	NZ_CP008706.1	2423944	2424022	+	WP_000423235.1		glucose-1-dehydrogenase	1873.767352	6.935500498	0.456916434	15.979244	4.855192	6.845191	50.894349
sRNA175		no	no	no	no	no	no	no							
sRNA18		no	no	no	no	no	no	no							
ABUW_RS1115	ABUW_2702	NZ_CP008706.1	2686026	2686535	+	WP_000890495.1		hypothetical protein	975.7778727	6.86440916	0.29132451	23.57010087	7.795193	1.775102	19.7520267
ABUW_RS1335	ABUW_3158	NZ_CP008706.1	3155300	3155527	-	WP_000543705.1		hypothetical protein	190.102781	6.849249981	0.42521091	16.8074718	2.250158	4.955157	56.389519
ABUW_RS1885	ABUW_2442	NZ_CP008706.1	2428085	2430233	-	WP_001108759.1		hypothetical protein	252.1945201	6.737222282	0.342625064	9.6634192	4.435186	2.446184	83.6161917
ABUW_RS1010	ABUW_2061	NZ_CP008706.1	2047554	2043121	-	WP_001108786.1		hypothetical protein	253.3190753	6.690952587	0.507002656	13.8076001	9.016140	7.996139	38.07943322
ABUW_RS1330	ABUW_3167	NZ_CP008706.1	3163396	3165072	-	WP_001001666.1		hypothetical protein	4239.277092	6.633359911	0.305522408	21.1753322	1.606104	1.745102	101.7994508
ABUW_RS0295	ABUW_2099	NZ_CP008706.1	2081690	2082762	+	WP_000095311.1		mechanosensitive ion channel	1019.722788	6.536566249	0.301919455	21.68796807	2.675104	2.835102	101.5482106
ABUW_RS1330	ABUW_2099	NZ_CP008706.1	2081690	2082762	+	WP_000095311.1		thiolase family protein	6678.388232	6.510516493	0.34474819	18.80354804	1.296179	5.306178	77.2571240
ABUW_RS0295	ABUW_2922	NZ_CP008706.1	2931938	2932162	+	WP_000854552.1		hypothetical protein	944.8374549	6.493306774	0.372419170	17.43573489	4.432168	1.955166	65.93554201
ABUW_RS1675	ABUW_2400	NZ_CP008706.1	2387183	2387462	-	WP_000448952.1		malonate decarboxylase subunit delta	85.82535069	6.488494187	0.476218293	10.55396061	4.905142	4.845141	40.31516454
ABUW_RS10475	ABUW_2196	NZ_CP008706.1	2198394	2199194	-	WP_000564561.1		hypothetical protein	2039.365429	6.333716493	0.358002029	17.6631869	7.965170	2.205168	67.65717320
ABUW_RS1070	ABUW_2317	NZ_CP008706.1	2301991	2302455	+	WP_001046928.1		hypothetical protein	710.2993559	6.227101178	0.360193877	17.29041077	5.566167	1.405165	64.8538706
ABUW_RS1670	ABUW_2399	NZ_CP008706.1	2386319	2387170	+	WP_001029850.1		biotin-independent malonate decarboxylase subunit beta	152.6957987	6.20165152	0.387645449	15.99752499	1.335157	2.345156	55.6307814
ABUW_RS09210	ABUW_1891	NZ_CP008706.1	1892175	1892867	+	WP_000442008.1		type I glutamine amidotransferase domain-containing protein	1710.050375	6.1106171	0.408950353	14.84108433	1.785150	2.346149	48.3037814
ABUW_RS20240		no	no	no	no	no	no	no							
ABUW_RS1665	ABUW_2398	NZ_CP008706.1	2385495	2386322	-	WP_001017588.1	mdcE	biotin-independent malonate decarboxylase subunit gamma	198.0471592	6.001431834	0.457850892	13.878304	2.975139	2.535138	37.9688748
ABUW_RS0895	ABUW_0181	NZ_CP008706.1	189427	200194	-	WP_001026735.1		hypothetical protein	319.6520009	5.890536682	0.266196197	22.0293844	16.561108	2.216106	55.6556077
ABUW_RS1665	ABUW_2901	NZ_CP008706.1	2900841	2900988	-	WP_000449056.1		SRPBCC domain-containing protein	8551.7197251	5.863356954	0.305929191	19.9573599	7.616182	3.395180	79.468003
ABUW_RS09435	ABUW_1937	NZ_CP008706.1	1937397	1938368	+	WP_001016331.1		SDR family oxidoreductase	833.2803379	5.859242796	0.22644495	11.87333883	1.975147	6.725145	144.1726307
ABUW_RS1665	ABUW_2438	NZ_CP008706.1	2428002	2428481	+	WP_000448209.1		CoA family protein	165.3707082	5.824878256	0.776540401	7.500939496	6.345114	1.845113	92.73516218
ABUW_RS1620	ABUW_3147	NZ_CP008706.1	3173306	3173806	-	WP_000206192.1		hypothetical protein	6879.766036	5.819565193	0.38216821	15.20303052	3.385192	4.775151	50.3214862
ABUW_RS03310	ABUW_0673	NZ_CP008706.1	676159	676357	+	WP_000829502.1		YegP family protein	186.384488	5.83866306	0.296024768	19.6060159	1.376185	7.385184	83.1941364
sRNA86		no	no	no	no	no	no	no							
ABUW_RS17460	ABUW_3587	NZ_CP008706.1	3584993	3584549	-	WP_001034851.1		hypothetical protein	327.713904	5.789633964	0.273190516	21.9576431	1.045199	9.795198	97.0992731
ABUW_RS07155	ABUW_1458	NZ_CP008706.1	1457939	1458733	+	WP_000536984.1		PGS-L family deacylase	938.7108039	5.787850525	0.301770034	19.7968776	5.476182	2.666180	79.57511636
ABUW_RS07155	ABUW_1458	NZ_CP008706.1	1457939	1458733	+	WP_000536984.1		PGS-L family deacylase	1655.013356	5.78296922	0.439493778	13.8762932	1.545139	1.335138	37.8761836
ABUW_RS07155	ABUW_1459	NZ_CP008706.1	1458708	1459307	+	WP_000581927.1		class I SAM-dependent methyltransferase	1017.161545	5.730065384	0.430914054	13.29872008	2.355140	2.116139	38.6757714
sRNA37		no	no	no	no	no	no	no							
ABUW_RS10200	ABUW_2720	NZ_CP008706.1	2707433	2707148	+	WP_000024050.1		KTCS domain-containing protein	33.85163499	5.719191979	0.328001018	17.40905543	7.045168	1.835166	65.7374891
ABUW_RS08045	ABUW_1649	NZ_CP008706.1	1645128	1645379	+	WP_000197474.1		hypothetical protein	964.834324	5.693195526	0.382454416	14.88572029	4.085100	5.245149	48.2806687
ABUW_RS07960	ABUW_1631	NZ_CP008706.1	1628562	1629092	+	WP_000750672.1		spore coat protein U domain-containing protein	1723.808466	5.653888529	0.323657748	17.46872603	2.485168	6.625167	66.17914201
ABUW_RS1725	ABUW_2621	NZ_CP008706.1	2618949	2619007	+	WP_001167331.1		hypothetical protein	7973.259285	5.62239948	0.41802018	14.5006710	3.085141	2.895140	39.5391921
sRNA77		no	no	no	no	no	no	no							
ABUW_RS1860	ABUW_2401	NZ_CP008706.1	2387465	2388349	-	WP_000968303.1		thiophosphoryl-coA synthase	484.1499428	5.6227383	0.370706374	14.84422362	7.585100	9.645149	48.1952297
ABUW_RS07620	ABUW_1561	NZ_CP008706.1	1549584	1550417	-	WP_000020711.1		hypothetical protein	100.7270866	5.457427859	0.365761918	14.92075003	2.425150	3.915149	48.50031932
ABUW_RS17395	ABUW_3574	NZ_CP008706.1	3532952	3533783	-	WP_001919102.1		hypothetical protein	311.4948929	5.456477998	0.209125459	26.05200076	4.465100	3.025147	146.519931
ABUW_RS18415	ABUW_3782	NZ_CP008706.1	3843938	3843828	-	WP_001917291.1	rmuB	3-hydroxybutyryl-CoA dehydrogenase	788.0269994	5.434668841	0.221796402	24.45787575	4.916192	1.965199	62.924543
ABUW_RS10210		no	no	no	no	no	no	no							
ABUW_RS10210		no	no	no	no	no	no	no							
ABUW_RS0425	ABUW_1935	NZ_CP008706.1	1934964	1935109	-	WP_001018885.1		TeiRAcR family transcriptional regulator	414.5369476	5.359196785	0.485431625	11.55447734	1.126130	6.835130	29.855793
ABUW_RS03380	ABUW_0687	NZ_CP008706.1	695949	696052	-	WP_001984826.1		formylacyl-coenzyme A thiolase family protein	134.5420987	5.339107045	0.492542822	10.8804959	1.435127	7.825127	26.10679325

ABUW_RS14395	ABUW_2965	N2_CP008706.1	2978751	2978951	+	WP_000761677.1		hypothetical protein	9338.562044	4.54766706	0.616736401	7.385736904	1526.19	4.306.19	12.36653164
ABUW_RS14240	ABUW_3783	N2_CP008706.1	3843840	3845357	-	WP_001692394.1		CoA-acylating methylmalonate-semialdehyde dehydrogenase	15409.02284	4.546885327	0.395271465	1162079459	3.236.31	2.026.30	29.69464863
ABUW_RS13630	ABUW_1232	N2_CP008706.1	219183	219189	+	WP_000364558.1	lpa	lipoyl synthase	500.7776	4.54342912	0.337063184	13.47945855	2.076.41	1.956.40	39.70996939
ABUW_RS19090	ABUW_2098	N2_CP008706.1	208015	208124	+	WP_000416929.1		short-chain fatty acid transporter	1602.912259	4.536180731	0.356321204	12.73059442	4.006.37	3.105.36	35.50863831
sRNA33	no	no	no	no	no	no	no	no	84.75596552	4.527536029	0.319307574	14.59047862	3.236.48	3.876.47	64.14292803
ABUW_RS07630	ABUW_1663	N2_CP008706.1	651904	652207	-	WP_000783724.1		hypothetical protein	307.0784207	4.523768796	0.320499887	11.7842382	3.086.45	3.336.44	43.47555577
ABUW_RS19790	ABUW_3252	N2_CP008706.1	3281966	3282304	-	WP_001874611	raIA	ribosome-associated translation inhibitor RaIA	3509.359416	4.441418582	0.23808079	8.82319026	4.886.79	1.965.77	76.70996939
ABUW_RS07890	ABUW_1674	N2_CP008706.1	166421	166494	+	WP_000855336.1		AMP-binding protein	1264.802328	4.45229912	0.286070873	15.86306077	1.945.56	1.965.58	54.70774933
ABUW_RS19435	ABUW_2767	N2_CP008706.1	2758007	2759994	+	WP_000483430.1		NAD(P)FAD-dependent oxidoreductase	159.719524	4.450482663	0.262345606	16.96423566	1.516.64	3.506.63	62.45593196
ABUW_RS19720	ABUW_0885	N2_CP008706.1	167406	168148	+	WP_079398453.1		lyg-like domain-containing protein	50908.24393	4.449454058	0.204405387	21.76779253	4.696.105	5.396.103	102.268412
ABUW_RS19890	ABUW_3898	N2_CP008706.1	3965532	3965783	+	WP_000269732.1		GlulY/YeaQ/YmgE family stress response membrane protein	865.088656	4.429883848	0.347560456	12.74564976	3.306.37	2.566.36	35.59176003
ABUW_RS17105	ABUW_3516	N2_CP008706.1	3564335	3564664	+	WP_000207459.1		MerR family transcriptional regulator	924.2330037	4.39968141	0.324177231	13.57183968	5.896.42	5.706.41	40.24412514
sRNA30	no	no	no	no	no	no	no	no	8442.530602	4.398107774	0.25296539	17.38620358	1.056.67	2.696.66	65.57024772
ABUW_RS07965	ABUW_1632	N2_CP008706.1	1629165	1629869	+	WP_000739311.1		molecular chaperone	944.5380165	4.385086354	0.434440426	10.0960109	5.906.24	2.776.23	22.56752023
ABUW_RS07820	ABUW_1601	N2_CP008706.1	1597650	1597868	+	WP_000351255.1		hypothetical protein	132.387892	4.377237367	0.442694946	9.887705752	4.716.23	2.126.22	21.67366414
ABUW_RS02975	ABUW_1605	N2_CP008706.1	1604783	1605424	-	WP_000200064.1		hydrolase	833.8059455	4.371644774	0.20192656	217358888	9.396.105	1.056.102	90.19788107
sRNA30	no	no	no	no	no	no	no	no	119376122	4.350889526	0.85419416	5.093506377	3.516.07	6.896.07	6.167180778
sRNA10	no	no	no	no	no	no	no	no	3166.532064	4.324504108	0.25714677	16.82163775	1.706.63	3.786.62	61.4225982
ABUW_RS01820	ABUW_0371	N2_CP008706.1	394311	395411	+	WP_000119668.1		HPP family protein	462.1841785	4.30819596	0.18278601	23.56961627	7.905.53	1.775.20	18.7532067
ABUW_RS19265	ABUW_2316	N2_CP008706.1	2300949	2301978	+	WP_001637930.1		DMF family transporter	175.036632	4.307202057	0.327164074	11.6786497	1.546.39	1.165.38	37.03554201
ABUW_RS19445	ABUW_2333	N2_CP008706.1	2316780	2316673	-	WP_000830363.1		amino acid ABC transporter substrate-binding protein	5036.266782	4.260320315	0.164867068	25.82527755	4.616.147	2.325.144	143.634512
sRNA55	no	no	no	no	no	no	no	no	3.947129552	4.258831612	1.341808919	6.316500271	0.001495011	0.002190473	2.665451167
sRNA44	no	no	no	no	no	no	no	no	4.781878039	4.247657102	1.306688625	3.260703382	0.0018189	0.001844773	2.773458606
ABUW_RS19640	ABUW_2372	N2_CP008706.1	2358457	2358619	-	WP_000784879.1		DUF1427 family protein	85.86948507	4.243481008	0.434314135	9.770534238	1.516.22	2.11948467	
sRNA103	no	no	no	no	no	no	no	no	1014560683	4.234309307	0.405367287	10.44561077	1.536.25	7.876.25	34.1620464
ABUW_RS07970	ABUW_1633	N2_CP008706.1	1628979	1632338	+	WP_000783962.1		fbnA1/biogenesis outer membrane usher protein	2618.722312	4.233002273	0.350272233	12.0763861	14.14.33	6.656.33	22.10547269
ABUW_RS19290	ABUW_1349	N2_CP008706.1	1376284	1376472	-	WP_000735804.1		NF0382.5 family lipoprotein	102.945047	4.21916847	0.355552492	11.86651356	1.775.32	1.166.31	30.70555421
ABUW_RS01015	ABUW_0623	N2_CP008706.1	21716	217319	+	WP_001697630.1		methionine/alanine import family NES transporter small subunit	778.9216626	4.16545019	0.196455717	21.20389767	8.775.100	8.426.98	97.07468191
ABUW_RS19890	ABUW_2674	N2_CP008706.1	2667054	2667332	-	WP_000072985.1		hypothetical protein	324.1449194	4.165347805	0.45904018	9.0522561	14.06.19	5.336.19	18.27327279
ABUW_RS19350	ABUW_1200	N2_CP008706.1	1216823	1216842	+	WP_001103050.1		alpha-ketolactide dehydrogenase subunit beta	780.1459166	4.164958034	0.570819323	2.6946282	3.616.13	1.005.12	12
ABUW_RS19305	ABUW_2655	N2_CP008706.1	2676287	2676531	-	WP_001004676.1		hypothetical protein	76.1912652	4.12647002	0.486343263	8.476835566	2.316.17	8.006.17	60.0699101
ABUW_RS19690	ABUW_3433	N2_CP008706.1	3478521	3478799	+	WP_000207403.1		hypothetical protein	2065.486317	4.167189401	0.340334276	12.06786898	1.566.33	1.075.32	31.97081922
ABUW_RS06865	ABUW_0411	N2_CP008706.1	1282739	1283191	-	WP_000835608.1		DUF162 domain-containing protein	639.0061919	4.0902100725	0.260571393	15.69704442	1.586.55	2.586.54	53.08838029
ABUW_RS19250	ABUW_2730	N2_CP008706.1	2716760	2718175	+	WP_000026486.1		OmpA family protein	7519.248195	4.083363032	0.203384855	20.03234893	2.886.89	1.816.87	86.74232163
ABUW_RS1140	ABUW_2290	N2_CP008706.1	2278041	2278271	+	WP_000116719.1		hypothetical protein	696.4927119	4.080339058	0.248481783	16.4210793	1.356.60	2.666.59	7.98193366
ABUW_RS19605	ABUW_2584	N2_CP008706.1	2588077	2589240	+	WP_001002394.1		glutathione-dependent formaldehyde dehydrogenase	678.6762962	4.06530216	0.459784443	8.841756783	9.426.19	3.476.19	17.45967033
ABUW_RS08100	ABUW_1673	N2_CP008706.1	1665334	1665968	+	WP_004834484.1	acel	chlorhexidine efflux PACE transporter AceI	940.9392433	4.049128932	0.337855053	10.94808095	4.276.33	2.876.32	31.542181
ABUW_RS10310	ABUW_2122	N2_CP008706.1	210619	2107774	-	WP_000412172.1		TEGR5 D44 family phosphatase	345.7110745	4.032923284	0.335607084	10.0201002	2.796.33	1.896.32	31.72353842
ABUW_RS14335	ABUW_2953	N2_CP008706.1	2967330	2967635	-	WP_000118514.1		non-heme iron oxygenase ferredoxin subunit	45.0306163	4.036169331	0.432654952	9.338702504	1.075.20	4.306.20	9.36653164
ABUW_RS19765	ABUW_3508	N2_CP008706.1	3554710	3555054	+	WP_000643174.1		hypothetical protein	105.935238	4.01729777	0.435165703	9.231706607	2.666.20	1.046.19	9.88266166
ABUW_RS18805	ABUW_3874	N2_CP008706.1	3942424	3942750	+	WP_001274778.1		hypothetical protein	144.8107409	4.00675187	0.300603954	13.32900597	1.575.40	1.426.39	38.84771965
ABUW_RS09415	ABUW_1633	N2_CP008706.1	163994	1633071	+	WP_000162473.1		aldehyde dehydrogenase (NADP+)	264.469189	3.983696894	0.297325429	14.3207914	3.926.41	3.686.40	39.4342162
ABUW_RS19180	ABUW_2096	N2_CP008706.1	2079851	2079355	+	WP_001045567.1		CoA transferase subunit A	2383.11861	3.976916332	0.327046019	10.1061989	5.075.34	3.576.33	32.44731798
ABUW_RS19255	ABUW_2348	N2_CP008706.1	2379744	2383200	-	WP_001191880.1	acnA	acetyltransferase AcnA	5478.718644	3.971270326	0.264628372	10.00697673	6.616.51	8.886.50	49.0558703
ABUW_RS19595	ABUW_3799	N2_CP008706.1	3797904	3799104	+	WP_000972685.1	astA	arginine N-acetyltransferase	767.9744239	3.953718568	0.38773909	10.16681365	2.056.24	8.826.24	32.00788861
ABUW_RS05330	ABUW_1686	N2_CP008706.1	161100	161013	+	WP_000638740.1		DUF1962 domain-containing protein	252.0169256	3.919102359	0.198587387	19.73505176	1.086.86	6.121.85	84.21524588
ABUW_RS19405	ABUW_4082	N2_CP008707.1	11428	114980	-	WP_000776261.1		hypothetical protein	326.010942	3.891786037	0.315191446	10.09917642	13.12.18	7.466.28	27.0726107
sRNA84	no	no	no	no	no	no	no	no	6102.121865	3.865601497	0.245963017	11.6713227	12.15.55	1.995.54	53.70146892
ABUW_RS19905	no	N2_CP008706.1	280712	2807896	+	no	no	no	102.17.1006	3.863706716	0.245011936	15.7373541	8.396.56	14.05.64	68.85387196
ABUW_RS19000	ABUW_2658	N2_CP008706.1	2654223	2654966	-	WP_002039934.1		DUF1482 family protein	375.148108	3.81444071	0.21638197	17.466805023	2.566.68	6.796.67	66.1810023
sRNA39	no	no	no	no	no	no	no	no	1755571931	3.816014478	1.395444552	2.73318884	0.006272436	0.008604577	2.065270475
ABUW_RS14330	ABUW_2952	N2_CP008706.1	2967003	2967302	-	WP_000847096.1		hypothetical protein	5127333168	3.754429374	0.37600919	9.982552155	1.825.23	8.396.23	22.0762804
ABUW_RS02965	ABUW_0603	N2_CP008706.1	602648	603031	+	WP_000743009.1		RcnB family protein	10.3210222	3.74741237	0.470864633	7.95857179	1.746.15	5.506.15	42.5593731
ABUW_RS19165	ABUW_2500	N2_CP008706.1	2496075	2496677	+	WP_000420415.1		amino acid synthetase family protein	63.6305106	3.743198241	0.36942318	10.8248913	4.106.24	1.965.23	22.77043179
ABUW_RS14300	ABUW_2946	N2_CP008706.1	2961189	2961990	+	WP_000218626.1		cupin domain-containing protein	93.7346648	3.734089993	0.309858497	12.0460156	2.046.33	1.386.32	31.86010091
ABUW_RS19585	ABUW_1886	N2_CP008706.1	187347	1888177	+	WP_000542602.1		alpha/beta hydrolase	3697.17142	3.730433534	0.277191076	11.46191552	2.636.41	2.486.40	39.05541832
ABUW_RS04835	ABUW_0886	N2_CP008706.1	900926	900919	-	WP_000225917.1		DUF3156 domain-containing protein	712.1990786	3.72314574	0.231973623	16.10540894	2.346.58	4.306.57	56.36653164
ABUW_RS19440	ABUW_2768	N2_CP008706.1	2760039	2760893	+	WP_000834590.1		SDR family oxidoreductase	47.0978105	3.71216282	0.340654699	10.8971021	1.196.27	6.546.27	26.1844225
ABUW_RS05695	ABUW_1652	N2_CP008706.1	1656502	1656961	+	WP_000783900.1		NGV/YgWY/Gel family stress tolerance protein	5721.840856	3.702335677	0.300899329	12.30423372	8.596.35	6.265.34	33.20342567
ABUW_RS19165	ABUW_2091	N2_CP008706.1	2077190	2077176	-	WP_001865051.1		Aac family transcriptional regulator	383.080						

ABUW_RS2016	ABUW_0720	NZ_CP008706.1	725967	726140	+	WP_001030306.1	hypothetical protein	906.004198	3.25559314	0.230697835	14.118772	3.226-45	3.476-44	43.4569703
ABUW_RS2085	no	NZ_CP008706.1	940476	941003	+		sulfite exporter TsaI/SaE family protein	35.62498375	3.251457636	0.377304088	8.67605165	6.846-18	2.46-17	6.61798296
ABUW_RS0440	ABUW_0987	NZ_CP008706.1	900005	901025	-	WP_00105075.1	hypothetical protein	1042.79193	3.245477168	0.200583494	6.1826765	6.816-59	1.286-57	56.89279003
ABUW_RS6609	ABUW_3214	NZ_CP008706.1	3245266	3246486	-	WP_001984486.1	acyl-CoA dehydrogenase	403.7460432	3.239874482	0.318627979	10.39662578	2.576-25	1.271-24	23.96619628
ABUW_RS0716	ABUW_0440	NZ_CP008706.1	926290	927840	+	WP_001250509.1	circularly permuted type 2 ATP-grasp protein	880.90564	3.237339616	0.247148629	13.09875611	3.356-39	2.836-38	37.54821596
ABUW_RS6610	ABUW_5007	NZ_CP008706.1	3036	3330	+	WP_001983304.1	Bm1 antitoxin family protein	1774.667993	3.22716514	0.204519868	6.77944943	4.516-56	7.306-55	54.15667174
ABUW_RS07425	ABUW_0521	NZ_CP008706.1	806545	807790	+	WP_000957794.1	sorbitosone dehydrogenase family protein	7814887356	3.227099933	0.243196337	13.27149637	3.396-40	3.026-39	38.51999906
ABUW_RS1260	ABUW_2630	NZ_CP008706.1	2627268	2628200	-	WP_001053599.1	lauryl acyltransferase	121629346	3.2180067	0.385824347	8.33747454	7.596-17	2.576-16	16.50100688
ABUW_RS1030	ABUW_2330	NZ_CP008706.1	2310406	2314149	-	WP_001032006.1	amino acid ABC transporter ATP-binding protein	680.359521	3.210695567	0.234923164	13.67979068	1.346-42	1.336-41	40.8761836
ABUW_RS6605	ABUW_5006	NZ_CP008706.1	2762	3049	+	WP_000438826.1	Bm1 family toxin	3299.834776	3.197899406	0.206745462	5.46716107	5.736-54	8.776-53	62.05700041
ABUW_RS0320	ABUW_2865	NZ_CP008706.1	2873297	2875726	+	WP_001292274.1	lon endopeptidase La	55429.76605	3.180302372	0.22381416	14.20923362	8.036-46	8.826-45	44.05453141
ABUW_RS0355	ABUW_0742	NZ_CP008706.1	743342	744103	-	WP_000371040.1	hypothetical protein	81124272504	3.179495587	0.318808088	9.973048143	2.006-23	9.216-23	22.03374037
ABUW_RS08375	ABUW_1720	NZ_CP008706.1	178317	178685	-	WP_000105718.1	tusD sulfuryltransferase complex subunit TusD	3942.661732	3.170048197	0.324466369	9.77003612	11.16-22	6.656-22	21.9717935
ABUW_RS1345	ABUW_4069	NZ_CP008707.1	40921	41416	+	WP_000758689.1	molecular chaperone DnaJ	220.6958265	3.16506881	0.42401711	7.466146318	8.266-14	2.386-13	12.62342304
ABUW_RS07375	ABUW_1634	NZ_CP008706.1	932329	933348	+	WP_000055766.1	spore coat protein U domain-containing protein	1453.5572	3.162927651	0.286154226	11.05399971	2.106-28	1.965-27	26.92811799
ABUW_RS07430	ABUW_0522	NZ_CP008706.1	1057940	1058392	+	WP_001166574.1	GNA1 family N-acetyltransferase	306.4885997	3.15555528	0.318164141	10.0241865	1.346-23	6.246-23	22.20481541
ABUW_RS20519	ABUW_2297	NZ_CP008706.1	224943	228191	+	WP_000668850.1	hypothetical protein	3517313127	3.147803874	0.935819997	6.26042963	1.876-59	3.596-58	57.44490555
ABUW_RS0310	ABUW_0640	NZ_CP008706.1	643621	644739	+	WP_000205332.1	Cdk transferase	366.76373	3.147259923	0.20103143	16.5017269	3.316-55	5.346-54	63.27410674
ABUW_RS1826	ABUW_2430	NZ_CP008706.1	2419606	2419606	+	WP_000885227.1	LysC family translocator	165.6287038	3.14640099	0.27070719	11.63232222	3.146-31	1.965-30	39.70774393
ABUW_RS06905	ABUW_0661	NZ_CP008706.1	654662	655105	-	WP_001163442.1	universal stress protein	8100.889653	3.143192191	0.270369354	11.25091234	2.296-29	1.365-28	27.86646169
ABUW_RS1265	no	NZ_CP008706.1	2664972	2665616	+		transposase	93.4438502	3.14006083	0.3861075	8.12539262	4.206-16	1.376-16	14.86327943
ABUW_RS01615	ABUW_0328	NZ_CP008706.1	503523	503523	+	WP_001019905.1	hemerythrin domain-containing protein	1429.973452	3.137960987	0.265700996	11.81916128	3.466-32	2.246-31	31.6798296
ABUW_RS03785	ABUW_2016	NZ_CP008706.1	2007107	2007111	+	WP_000050492.1	DUF2523 domain-containing protein	19.52870962	3.12866169	0.553666033	5.65081385	1.606-08	3.446-08	7.463441657
ABUW_RS0380	ABUW_1626	NZ_CP008706.1	924491	924934	+	WP_000053789.1	MFS transporter	102.9871624	3.126504317	0.27846475	11.22748445	2.986-29	1.756-28	27.7696195
ABUW_RS1100	ABUW_3516	NZ_CP008706.1	3563367	3564323	+	WP_001167194.1	DnaJ domain-containing protein	988.614969	3.121049487	0.269708675	11.57180036	5.736-31	3.546-30	29.45096764
ABUW_RS01860	ABUW_0237	NZ_CP008706.1	255242	255931	+	WP_001045986.1	aqpZ aquaporin Z	10712.6277	3.110937569	0.287145041	10.40409365	2.206-27	1.961-26	25.04462304
ABUW_RS0260	ABUW_1602	NZ_CP008706.1	902188	903149	+	WP_000849751.1	sorbitosone dehydrogenase family protein	1069.888758	3.10778806	0.26232018	11.82439753	2.926-32	1.896-31	30.7235382
ABUW_RS08540	ABUW_1753	NZ_CP008706.1	1749233	1749526	+	WP_000896660.1	hypothetical protein	493.58747	3.100333378	0.312631475	9.91694566	3.526-23	1.696-22	21.79860288
ABUW_RS1425	ABUW_2951	NZ_CP008706.1	296519	2966986	+	WP_000919783.1	aromatic ring-hydroxylating oxygenase subunit alpha	78.46636974	3.089468709	0.401820777	6.68674324	1.496-14	4.466-14	13.50605146
ABUW_RS0545	ABUW_1210	NZ_CP008707.1	7310	73459	+	WP_000644930.1	hypothetical protein	47.65014111	3.088277672	0.316290077	7.95036067	1.96-22	5.232-22	21.29419631
ABUW_RS0345	ABUW_2109	NZ_CP008706.1	214286	214621	-	WP_001289728.1	2-oxo acid dehydrogenase subunit E2	734.8421235	3.07672879	0.426356445	7.20357807	5.876-13	1.606-12	17.5568002
sRNA99	no	no	no	no	no	no	no	20022.9812	0.069736058	0.336912444	9.11103022	8.856-20	3.136-19	8.50445666
ABUW_RS08380	ABUW_1721	NZ_CP008706.1	178751	178758	+	WP_000604789.1	SCR family NAD(P)-dependent oxidoreductase	2742.637338	3.064658829	0.23256011	13.17792191	1.166-39	1.036-38	37.98716278
sRNA91	no	no	no	no	no	no	no	255.279932	3.06215803	0.204817395	11.94824086	1.606-50	2.116-49	48.67577154
ABUW_RS20160	no	NZ_CP008706.1	143794	143846	-	WP_001985370.1	hypothetical protein	3.773757164	3.06102049	0.177783189	2.690499323	0.007104518	0.009727571	2.01999591
ABUW_RS12616	ABUW_2596	NZ_CP008706.1	2598981	2599541	-	WP_001131098.1	TerR/AcrR family transcriptional regulator	211.7833828	3.061144241	0.891534851	3.43356655	0.000596696	0.000489666	3.048318762
ABUW_RS1690	ABUW_4121	NZ_CP008707.1	82170	82821	-	WP_000572025.1	hypothetical protein	276.143323	3.051521024	0.258000783	11.62679879	2.846-32	1.846-31	30.73516216
ABUW_RS08585	ABUW_1762	NZ_CP008706.1	1759348	1760790	+	WP_001032848.1	PQQ-dependent sugar dehydrogenase	2276.90416	3.048953623	0.18535104	16.45447497	7.796-61	1.556-59	88.8096863
ABUW_RS1330	ABUW_1206	NZ_CP008706.1	210972	2110030	+	WP_000642316.1	2,3-butanediol dehydrogenase	837.2140566	3.04454309	0.23835541	11.72420603	2.286-37	1.796-36	35.74714697
ABUW_RS1265	ABUW_2737	NZ_CP008706.1	2724819	2727398	+	WP_001020050.1	cspB ATP-dependent chaperone CspB	14167.99093	3.040286452	0.206655509	4.71185778	5.416-49	6.656-48	47.1771935
ABUW_RS0580	ABUW_2177	NZ_CP008706.1	2167690	2169637	+	WP_001051784.1	HAD family hydrolase	101.1276091	0.323599202	0.14822388	20.38810253	17.16-62	1.236-60	89.91004489
ABUW_RS1400	ABUW_2984	NZ_CP008706.1	3000533	3001024	+	WP_001991918.1	transferrin-binding protein-like solute binding protein	714.899866	3.020100861	0.444092662	6.800609952	1.046-11	2.656-11	10.5767514
ABUW_RS20430	ABUW_0750	NZ_CP008706.1	747874	748951	+	WP_0000047869.1	hypothetical protein	67.0145086	3.01328853	0.291932166	10.32178446	5.616-25	2.736-24	23.56387335
ABUW_RS03885	ABUW_4091	NZ_CP008706.1	55668	56337	+	WP_000581089.1	hypothetical protein	594.2973545	3.012201766	0.319644972	9.803897984	7.706-32	3.276-31	20.48542525
ABUW_RS04860	ABUW_0991	NZ_CP008706.1	903976	904184	+	WP_000208542.1	NF038165 family protein	538.143144	3.006033592	0.244099798	12.31779194	7.546-35	5.506-34	33.59603731
ABUW_RS1850	ABUW_2395	NZ_CP008706.1	2383496	2383897	+	WP_000587903.1	malE malonate transporter subunit MalE	158.182647	2.986528888	0.264953843	11.271876	1.816-29	1.076-28	27.9761622
ABUW_RS1316	ABUW_1223	NZ_CP008706.1	1207784	1210479	+	WP_000465449.1	MBL-like metallo-hydrolase	127.523542	2.982176179	0.348104337	8.567172922	1.066-17	3.896-17	6.43297363
ABUW_RS2460	ABUW_1424	NZ_CP008706.1	1414627	1414997	+	WP_000072947.1	hypothetical protein	1014138001	2.978585254	0.637124935	4.675041099	2.946-06	5.406-06	5.26760624
ABUW_RS1405	ABUW_3780	NZ_CP008706.1	3840068	3841195	+	WP_001801766.1	acyl-CoA dehydrogenase family protein	643.959498	2.977718902	0.3301026	9.020039539	1.886-19	7.136-19	8.16691467
ABUW_RS0650	ABUW_2191	NZ_CP008706.1	2174621	2176723	+	WP_001985715.1	hypothetical protein	532.521793	2.973822107	0.284526462	10.4585239	1.446-25	7.196-25	24.14327111
ABUW_RS0690	ABUW_1784	NZ_CP008706.1	178988	1792362	+	WP_001200584.1	DUF2750 domain-containing protein	602.0149776	2.973789432	0.237332717	12.53004419	5.116-36	3.866-35	34.4141027
ABUW_RS0445	ABUW_1103	NZ_CP008706.1	1181668	1183389	+	WP_000469453.1	alpha-keto acid decarboxylase family protein	4938.377473	2.967595868	0.422180321	7.030073461	2.066-12	5.486-12	11.26121444
sRNA73	no	no	no	no	no	no	no	40.42810639	2.965898059	0.66167208	4.484022587	7.326-06	1.306-05	4.886056648
ABUW_RS07895	ABUW_1618	NZ_CP008706.1	161128	161143	-	WP_000774022.1	eutC ethanolanine ammonia-lyase subunit EutC	125.951649	2.964290141	0.267036514	11.0071052	1.246-28	7.107-28	27.14871405
ABUW_RS08075	ABUW_1656	NZ_CP008706.1	1650485	1651597	+	WP_001987572.1	OnpW family protein	178.8564883	2.960588195	0.245335472	12.06652527	1.596-33	1.086-32	31.9665724
ABUW_RS14295	ABUW_2943	NZ_CP008706.1	2963308	2961102	+	WP_000988619.1	alpha/beta hydrolase	49.58310409	2.959356849	0.34100825	8.576562306	9.856-18	4.516-17	46.8021809
ABUW_RS1430	ABUW_2950	NZ_CP008706.1	2963932	2960928	+	WP_000243770.1	SCR family oxidoreductase	43.97958787	2.946266821	0.373838837	7.881114876	3.246-16	1.016-14	13.95967863
ABUW_RS1465	ABUW_3388	NZ_CP008706.1	3428111	3429424	+	WP_001684480.1	alpha/beta hydrolase	1850.71289	2.944927314	0.196175364	15.0170781	6.166-51	8.296-50	49.08145447
ABUW_RS1790	no	NZ_CP008706.1	940746	941073	-	WP_000469453.1	helicase-helicase transcriptional regulator	45.49551811	2.93833516	0.34718102	8.4634322097	2.606-17	8.966-17	6.04769199
ABUW_RS1445	ABUW_3384	NZ_CP008706.1	3422058	3423356	+	WP_001991918.1	glycosyltransferase family 1 protein	198.9548678	2.925844329	0.229235377	12.76248859	2.666-37	2.086-36	35.68

ABUW_RS07520	ABUW_541	N2_CP008706.1	627863	928459	+	WP_000243522.1		alpha-E domain-containing protein	258.043436	2.725282002	0.278455613	9.787323565	1286-22	5.656-22	21247959.65
ABUW_RS07520	ABUW_5206	N2_CP008706.1	23701	232327	-	WP_000046156.1		hydrolase	42.0.509722	2.724663261	0.28494605	0.47092625	1096-35	8.096-35	34.0292048
ABUW_RS07520	ABUW_2724	N2_CP008706.1	270557	273001	+	WP_001937898.1		hydrolytic protein	7937.004811	2.722442787	0.384778627	7.075348247	1496-12	3.996-12	113990271
ABUW_RS04745	ABUW_5912	N2_CP008706.1	970991	908608	+	WP_000688053.1	gfpD	glycine-3-phosphate dehydrogenase	9006.051678	2.72103711	0.20840315	0.305692229	5.806-39	4.836-38	37.3.905287
ABUW_RS1945	ABUW_2455	N2_CP008706.1	244260	244458	+	WP_000461920.1		acetylphosphorylmethylcrotonyl-CoA carboxylase subunit alpha	9373.508829	2.78708479	0.292474386	9.288705632	1566-20	6.206-20	9.2076031
ABUW_RS02355	ABUW_5479	N2_CP008706.1	49708	482058	+	WP_000455817.1		GFA family protein	833.945629	2.71650008	0.378878472	7.90076195	8.67E-13	2.356-12	1162893.24
ABUW_RS02495	ABUW_5011	N2_CP008706.1	6979	7161	-	WP_00182484.1		hydropetalin	219.651666	2.718706379	0.246549981	11.04817527	3.24E-28	1826-27	26.73992861
ABUW_RS07275	ABUW_4992	N2_CP008706.1	479364	480383	+	WP_002019760.1	csuE	Csu fibrillar tip adhesin CsuE	294.431251	2.714473309	1.09615877	2.446318014	NA	NA	#VALUE!
ABUW_RS08910	ABUW_1831	N2_CP008706.1	627256	627527	+	WP_000566027.1		3-oxoacid-CoA-transferase subunit A	93.05852272	2.719424083	0.327625001	8.270949676	133E-16	4.45E-16	9.35.903599
ABUW_RS07410	ABUW_1516	N2_CP008706.1	103894	104040	-	WP_000894317.1		GNA1 family N-acetyltransferase	25.3651604	2.708818555	0.60389868	4.484875563	7.30E-06	1.30E-05	4.88056648
ABUW_RS02175	ABUW_0443	N2_CP008706.1	455176	457230	-	WP_000266455.1		M3 family metalloprotease	6798.480322	2.704100921	0.29463495	9.277768803	173E-20	6.84E-20	9.1.94349
ABUW_RS14285	ABUW_2943	N2_CP008706.1	295891	295942	-	WP_000735778.1		aspartate dehydrogenase	62.5041874	2.654001117	0.31448922	7.889888784	3.02E-15	9.41E-15	14.0241038
ABUW_RS12310	ABUW_2532	N2_CP008706.1	2523715	2524215	-	WP_001177936.1	paaj	phenylacetate-CoA oxygenase subunit Paaj	2571070063	2.68427771	0.534725332	5.019918729	5.17E-07	1.00E-06	6
ABUW_RS12545	ABUW_3140	N2_CP008706.1	316474	3166807	-	WP_000209896.1		hydropetalin	11.9.458006	2.67766821	0.22166636	0.206337527	160E-33	1.12E-32	3.190078198
ABUW_RS19065	ABUW_4007	N2_CP008707.1	4890	5262	+	WP_000910917.1		hydropetalin	422.042738	2.671765914	0.340471623	7.84724992	4.25E-16	1.3E-14	13.8827287
ABUW_RS12915	no	N2_CP008706.1	2656702	26571888	-			flourenetin type II domain-containing protein	552.3316222	2.668590006	0.14912438	7.89519492	129E-71	3.78E-70	69.4225082
ABUW_RS06995	ABUW_1436	N2_CP008706.1	1427346	1429004	+	WP_000647631.1	terL	phage terminase large subunit	2615972255	2.668485071	0.265725993	0.104210725	9.95E-24	4.66E-23	62.1331408
ABUW_RS16165	ABUW_3217	N2_CP008706.1	3249351	3250348	+	WP_000629034.1	add	adenosine deaminase	916.2527694	2.668138063	0.41325253	6.430718656	120E-10	2.87E-10	9.54218193
ABUW_RS12560	ABUW_3141	N2_CP008706.1	397036	398385	-	WP_001048745.1		hydropetalin	921.666093	2.669492685	0.58432698	7.97925794	2.77E-43	5.99E-42	6.122257319
ABUW_RS14940	ABUW_2167	N2_CP008706.1	2139265	2139890	-	WP_00065213.1		GFA family protein	72.482608	2.659802462	0.389424557	6.830084967	8.49E-12	2.17E-11	8.62534027
ABUW_RS09735	ABUW_2004	N2_CP008706.1	2000651	2000935	+	WP_000050492.1		DUF2523 domain-containing protein	18.51642684	2.655258812	0.489046241	5.42946386	5.65E-08	1.17E-07	6.93181418
ABUW_RS10095	ABUW_2698	N2_CP008706.1	2683223	2684485	+	WP_001028335.1		exodeoxyribonuclease VIIarge subunit	319.4859929	2.65124852	0.200295769	3.23854497	5.40E-40	4.79E-39	8.3.905287
ABUW_RS03030	ABUW_1855	N2_CP008706.1	1851667	1852916	-	WP_00176622.1		MFS transporter	51.7541872	2.649331682	0.356370889	7.434198655	105E-13	3.01E-13	12.5214335
ABUW_RS10335	ABUW_1927	N2_CP008706.1	210260	210245	-	WP_000238448.1		acetoin reductase	222.5993893	2.64800976	0.379141697	6.984225618	2.86E-12	7.33E-12	11.5232002
ABUW_RS07600	ABUW_1857	N2_CP008706.1	184338	1846276	+	WP_000913011.1	pgaA	poly-beta-1,6 N-acetyl-D-glucosamine exporter porin PgaA	181.4309274	2.641106337	0.27198391	9.736228681	2.1E-22	9.22E-22	21.0326008
ABUW_RS04545	ABUW_1754	N2_CP008706.1	1749878	1750114	+	WP_000373225.1		GNA1 family N-acetyltransferase	304.760239	2.639340087	0.242715972	0.8716454	158E-27	8.96E-27	6.06008084
ABUW_RS17135	ABUW_2331	N2_CP008706.1	2314163	2314840	+	WP_000347804.1		amino acid ABC transporter permease	1107.851938	2.630490467	0.245242556	0.74466712	6.28E-27	3.33E-26	25.47755577
ABUW_RS12615	ABUW_2533	N2_CP008706.1	2524232	2524987	+	WP_001016799.1	paac	phenylacetate-CoA oxygenase subunit Paac	2688.519042	2.631668567	0.580518556	5.533065452	5.81E-06	1.04E-05	4.88266661
ABUW_RS18470	ABUW_3064	N2_CP008706.1	3091987	3092412	-	WP_00180012.1		EscC family protein	9.058.11949	2.61048997	0.232664448	11.22135735	3.12E-29	1.83E-28	27.73745491
ABUW_RS05475	ABUW_1178	N2_CP008706.1	1160333	1161495	+	WP_000897187.1	sohB	hydroxyphenylacetate-CoA oxygenase subunit SohB	9116.465687	2.59556739	0.250439356	0.36405552	3.1E-25	1.78E-24	23.74598
ABUW_RS10195	ABUW_2081	N2_CP008706.1	2061943	2063058	+	WP_000204398.1	anIA	anthranilate 12-oxoxygenase large subunit	63.53341166	2.594973449	0.51319863	8.282186203	121E-16	4.06E-16	15.39147307
ABUW_RS17910	ABUW_0363	N2_CP008706.1	385327	385521	+	WP_000375468.1		hydropetalin	790.3552333	2.59404343	0.196922402	0.17291691	1.26E-39	1.09E-38	37.9625735
ABUW_RS08935	ABUW_2028	N2_CP008706.1	2018604	2018888	-	WP_000050492.1		DUF2523 domain-containing protein	19.73905256	2.59187406	0.49588312	5.227012785	172E-07	3.47E-07	6.499670525
ABUW_RS04930	ABUW_1805	N2_CP008706.1	1819736	1820053	+	WP_000916029.1		NF3.1	843.1942883	2.590547119	0.16343367	16.85075539	139E-56	2.37E-55	54.62265105
ABUW_RS07855	ABUW_1808	N2_CP008706.1	1803081	1804025	+	WP_000570779.1	msaA	tRNA (adenosine(37)-N6)-dimethyltransferase MsaA	250.287125	2.588072173	0.21615467	1197.261595	4.94E-33	3.18E-32	314807201
ABUW_RS07685	ABUW_1873	N2_CP008706.1	186164	1862200	+	WP_000602467.1		acyl-CoA dehydrogenase family protein	91.7.664098	2.58493338	0.32892205	7.588802356	3.88E-16	1.20E-14	13.92081875
ABUW_RS10000	ABUW_2059	N2_CP008706.1	2040335	2041498	+	WP_000404098.1		catalase family protein	658.888624	2.584440788	0.23549139	0.17465118	5.06E-28	2.81E-27	26.52520368
ABUW_RS05955	ABUW_1965	N2_CP008706.1	1962776	1968199	+	WP_000860158.1		alpha/beta hydrolase	121.1768011	2.579627266	0.23422189	10.1360925	3.29E-28	1.84E-27	26.7518218
ABUW_RS18995	no	N2_CP008706.1	2653044	2654148	-			hydropetalin	34.27594609	2.579121107	0.382692708	6.669457523	5.05E-11	1.23E-10	9.93004889
ABUW_RS02330	no	N2_CP008706.1	3878099	3878033	+			hydropetalin	5.51458729	2.577540526	0.93838126	2.74679444	0.008018084	0.008264954	
ABUW_RS18550	ABUW_3405	N2_CP008706.1	3452403	3454100	+	WP_000918841.1	leuA	2-isopropylmalate synthase	11671.898979	2.575082268	0.21638471	11.95573366	6.00E-33	4.05E-32	1.319254408
ABUW_RS18485	no	no	no	no	no	no	no	no	103.6167108	2.575039148	0.343459408	7.48738094	6.51E-14	1.89E-13	12.7235382
ABUW_RS02820	ABUW_0388	N2_CP008706.1	1037638	1038093	+	WP_001106767.1		hydropetalin	784.5427279	2.572935178	0.383321981	6.17203588	150E-11	4.80E-11	9.3.975876
ABUW_RS07970	ABUW_1877	N2_CP008706.1	1870332	1871991	+	WP_000588779.1		serine hydrolase	857.965759	2.572642029	0.58589104	6.51106098	2.82E-54	4.55E-53	52.34582246
ABUW_RS03275	no	N2_CP008706.1	2879203	2879303	+			outer membrane assembly protein BamE	101843105	2.571961372	0.349352337	7.358421981	1.86E-10	5.29E-10	0.2779407
ABUW_RS14310	ABUW_2948	N2_CP008706.1	2962980	2964191	+	WP_00041872.1		FAD-dependent oxidoreductase	98.40976079	2.565929616	0.321419664	7.889817549	133E-15	4.30E-15	14.36651184
ABUW_RS05145	ABUW_1648	N2_CP008706.1	1666888	1667475	+	WP_00085844.1		lipocalin family protein	104.444737	2.564023084	0.28474079	11.68257819	150E-31	9.91E-31	30.03929235
ABUW_RS13575	ABUW_2795	N2_CP008706.1	2793499	2793937	+	WP_000671321.1		hydropetalin	37.1232524	2.563732981	0.59205972	4.33051939	1.49E-05	2.58E-05	4.588380294
ABUW_RS06975	ABUW_1432	N2_CP008706.1	1423885	1424109	+	WP_000850407.1		hydropetalin	318.601445	2.563666946	0.22799329	11.24449213	2.47E-29	1.45E-28	27.738632
ABUW_RS02825	ABUW_1166	N2_CP008706.1	185359	186106	+	WP_000731729.1		putative porin	57522.16981	2.563534482	0.23742494	10.79700781	3.53E-27	1.90E-26	25.123264
ABUW_RS07900	ABUW_1819	N2_CP008706.1	181954	1819339	+	WP_000102142.1		ethanolamine-ammonia-lyase subunit EutB	514.872382	2.563339872	0.320870858	7.988869408	136E-15	4.33E-15	14.3635121
ABUW_RS07530	ABUW_1843	N2_CP008706.1	1829528	1829992	+	WP_000225477.1		proteaseome-type protease	10.88.14819	2.56046406	0.98008703	12.9754714	5.87E-38	4.73E-37	36.3251866
ABUW_RS05265	ABUW_1803	N2_CP008706.1	1803058	1803033	-	WP_000706933.1		hydropetalin	118.6996469	2.557194828	0.474128018	5.393342584	6.92E-08	1.43E-07	6.844693963
ABUW_RS05220	ABUW_1863	N2_CP008706.1	1872881	1874525	-	WP_000750598.1		hydropetalin	9709.858461	2.551637038	0.249958304	0.5441062	5.41E-26	2.76E-25	24.5880249
ABUW_RS19190	ABUW_2456	N2_CP008706.1	2444555	2445057	+	WP_001088910.1		hydroxyphenylglyoxyl-CoA lyase	9590.797706	2.549641032	0.287580623	8.865630401	7.50E-19	2.81E-18	17.55129368
ABUW_RS19476	no	no	no	no	no	no	no	no	118.9199062	2.5465097565	0.29833231	8.536110493	139E-17	4.83E-17	9.3.905287
ABUW_RS01505	ABUW_0306	N2_CP008706.1	133012	1330676	+	WP_000678123.1	bif	bacterioferritin	5782.339281	2.545840852	0.429106067	5.932473943	2.88E-09	6.69E-09	8.174573882
ABUW_RS05000	ABUW_0332	N2_CP008706.1	1425232	1431761	+	WP_000782587.1		alpha/beta fold hydrolase	284.0018271	2.540261969	0.214816229	11.62527961	2.89E-32	1.87E-31	30.72818639
ABUW_RS02075	ABUW_0207	N2_CP008706.1	223004	223476	+	WP_000719861.1		pin family protein	458.4837998	2.532526459</					

ABUW_RS19495	ABUW_4103	NZ_CP008707.1	63264	63524	+	WP_000876194.1		hypothetical protein	26.90464355	2.399509092	0.468055233	5.126551947	2.955-07	5.82E-07	6.235077016
ABUW_RS03430	ABUW_1731	NZ_CP008706.1	1272825	1272478	-	WP_0002543879.1	adeN	multidrug efflux transcriptional repressor AdeN	1486.450167	2.397198427	0.231642618	0.35627243	3.92E-25	1.92E-24	237.1666877
ABUW_RS05820	ABUW_1749	NZ_CP008706.1	174743	1747583	-	WP_000040963.1		RNA-binding protein	1577.098827	2.396577624	0.226241119	0.59302408	3.21E-26	1.66E-25	24.77989191
ABUW_RS10670	ABUW_2195	NZ_CP008706.1	218189	218242	-	WP_000093541.1		alkane 1-monooxygenase	236.1810285	2.396465415	0.257070814	0.932249949	1.16E-20	4.56E-20	9.3430315
ABUW_RS09865	ABUW_2032	NZ_CP008706.1	201919	2019136	-	WP_000274156.1		hypothetical protein	177.0031058	2.394644433	0.357556582	0.69707282	2.13E-11	5.30E-11	10.2757241
ABUW_RS04360	ABUW_0889	NZ_CP008706.1	885766	886095	-	WP_0001866339.1		MDMT family protein	192.5077069	2.39192875	0.254493658	9.38838255	5.54E-21	2.24E-20	9.6497598
ABUW_RS17635	ABUW_3622	NZ_CP008706.1	3680364	3680945	-	WP_000998520.1		TerR/AcrR family transcriptional regulator	73.4523951	2.396499656	0.310597375	7.683595438	1.05E-14	4.83E-14	13.2341901
ABUW_RS05085	ABUW_030	NZ_CP008706.1	1622207	1631475	-	WP_0001052957.1		MgtC/SagB family protein	216.1010863	2.385247819	0.242725936	9.82691896	8.62E-23	3.85E-22	21.14453927
ABUW_RS16220	ABUW_4039	NZ_CP008707.1	23096	23562	+	WP_000710385.1		hypothetical protein	497.882776	2.38167934	0.248886402	9.569342969	1.08E-21	4.53E-21	20.3439018
ABUW_RS02890	ABUW_0548	NZ_CP008706.1	553035	553226	-	WP_00043481.1		hypothetical protein	83.58032267	2.38102139	0.305817095	7.785749333	6.93E-15	2.13E-14	13.6726204
ABUW_RS07985	ABUW_1636	NZ_CP008706.1	1634269	1633030	-	WP_000155428.1		SDR family NAD(P)-dependent oxidoreductase	290.9334479	2.378639478	0.315416582	7.541263259	4.65E-14	1.36E-13	12.86646109
ABUW_RS1910	ABUW_2701	NZ_CP008706.1	2685172	2685765	-	WP_000253373.1		lysE family transporter	259.1475051	2.3777094576	0.287370408	8.271833649	1.13E-16	4.42E-16	15.35457773
ABUW_RS1285	ABUW_2527	NZ_CP008706.1	2518295	2519503	-	WP_000390385.1	pcrF	3-oxoadipyl-CoA thiolase	2489.600262	2.374140121	0.225333187	10.53613164	5.89E-26	2.99E-25	24.52432811
ABUW_RS03870	ABUW_0789	NZ_CP008706.1	769954	770304	-	WP_000064570.1		hypothetical protein	55.08734955	2.373190165	0.346740339	6.84428629	7.69E-12	1.97E-11	10.7055377
ABUW_RS07880	ABUW_1635	NZ_CP008706.1	1633575	1634261	-	WP_000127988.1		glutathione S-transferase family protein	468.2070354	2.370378096	0.26936052	8.798859824	1.38E-18	5.06E-18	17.29584948
ABUW_RS00325	ABUW_0066	NZ_CP008706.1	70383	71438	-	WP_00035193.1	hpdD	4-hydroxyphenylpyruvate dioxygenase	9314.533216	2.367778547	0.325526563	7.27388192	3.50E-13	9.7E-13	10.9278077
ABUW_RS11470	ABUW_2308	NZ_CP008706.1	2340367	2342074	-	WP_000819555.1		dicarboxylate/amino acid cation symporter	2310.197657	2.367249157	0.305609643	6.47479956	9.49E-11	2.29E-10	9.64094519
ABUW_RS05385	ABUW_1927	NZ_CP008706.1	1925935	1926667	-	WP_000366426.1		lysR family transcriptional regulator	98.41022967	2.367077994	0.207974236	11.38162244	5.1E-30	3.12E-29	28.0054541
ABUW_RS11915	ABUW_2083	NZ_CP008706.1	2065558	2064692	-	WP_000198561.1	antC	infrabactam 12-oxoguanine electron transfer component AntC	91.49394566	2.3634412	0.258076932	9.54019254	5.49E-30	2.1E-19	9.67571754
ABUW_RS10660	ABUW_1793	NZ_CP008706.1	2178563	2179446	-	WP_000318961.1		acyl-CoA dehydrogenase family protein	300.2371946	2.352426017	0.185103996	0.213602747	1.30E-36	9.99E-36	35.00308946
ABUW_RS00040	ABUW_0008	NZ_CP008706.1	9886	10870	-	WP_000746542.1		RND transporter	82.8526391	2.348128111	0.248252685	4.950564885	3.37E-21	1.38E-20	19.8901091
ABUW_RS12295	ABUW_2529	NZ_CP008706.1	252157	252148	-	WP_000386291.1		2-(1,2-epoxy)-1,2-dihydroxyphenylacetyl-CoA isomerase	1400.627779	2.340915208	0.416240142	5.6223953507	1.87E-08	4.00E-08	73.59740009
ABUW_RS19180	ABUW_2716	NZ_CP008706.1	2691992	2701164	-	WP_000442142.1		OspD family outer membrane porin	95.04380489	2.339867621	0.230935681	10.1328966	4.01E-24	1.90E-23	22.7214644
ABUW_RS19560	ABUW_4116	NZ_CP008707.1	71986	78528	+	WP_071085191		transglycolysase SLT domain-containing protein	232.0989959	2.335058325	0.20968992	11.13710812	8.40E-29	4.84E-28	27.31914644
ABUW_RS02095	ABUW_0382	NZ_CP008706.1	409290	409475	-	WP_000471161.1		hypothetical protein	52.110632	2.331070763	0.430298038	5.416440565	6.08E-08	1.26E-07	6.899621455
ABUW_RS12050	ABUW_2310	NZ_CP008706.1	2299188	2299207	-	WP_000738477.1		fmbA family protein	100.110686	2.309716776	0.348320262	6.613164688	3.33E-11	8.23E-11	10.04060191
ABUW_RS00515	ABUW_0104	NZ_CP008706.1	11610	11609	-	WP_00069878.1		alpha/beta fold hydrolase	928.8808829	2.2994721	0.17383311	11.228088608	6.04E-40	5.33E-39	38.27327279
ABUW_RS11925	ABUW_2329	NZ_CP008706.1	2310335	2310355	-	WP_000514545.1		hypothetical protein	36.12516401	2.297759751	0.47656313	5.51556372	3.76E-08	7.90E-08	16.72372909
ABUW_RS09970	ABUW_1431	NZ_CP008706.1	1423557	1423880	-	WP_000673007.1		hypothetical protein	216.941054	2.292416397	0.231051192	9.921685197	3.35E-23	1.63E-22	21.81938587
ABUW_RS03650	ABUW_0741	NZ_CP008706.1	742953	743345	-	WP_000566558.1		hypothetical protein	63.87815603	2.289795676	0.318003558	7.348325292	2.01E-13	5.64E-13	12.2487209
sRNA9	no	no	no	no	no	no	no	no	428458.4734	2.27759307	0.288217699	7.902335096	2.74E-15	8.55E-15	14.0663389
ABUW_RS19930	no	NZ_CP008706.1	3041499	3041858	-	WP_000185911.1	ssaK	transfer-messenger RNA	42.843617413	2.277149142	0.288227768	7.901708259	2.75E-15	8.59E-15	14.0660684
ABUW_RS17410	ABUW_3577	NZ_CP008706.1	3635128	3635888	-	WP_000105251.1		hypothetical protein	251.3820288	2.277342193	0.226547917	10.0305733	1.07E-23	5.00E-23	22.30103
ABUW_RS08570	ABUW_1759	NZ_CP008706.1	1755437	1756116	-	WP_000162604.1		S6 family peptidase	892.6907832	2.272612489	0.191445585	11.87019066	1.68E-32	1.10E-31	30.59860731
ABUW_RS18520	no	NZ_CP008706.1	388116	388334	-	WP_000350168.1		hypothetical protein	69.261191	2.262712217	0.398356008	5.60612575	1.35E-08	2.91E-08	7.51361071
ABUW_RS03550	ABUW_0721	NZ_CP008706.1	72619	727555	-	WP_000147585.1		wax ester/hydrolytic and synthase family O-acyltransferase	3949.426466	2.262045039	0.171082732	13.20648789	8.05E-40	7.06E-39	38.115953
ABUW_RS08245	ABUW_1693	NZ_CP008706.1	1690447	1691910	-	WP_000371356.1		iron-containing exonuclease family protein	593.608021	2.261951639	0.203813704	11.09813321	1.28E-28	7.30E-28	27.1066774
ABUW_RS07010	ABUW_1439	NZ_CP008706.1	1432011	1432448	-	WP_000187162.1		hypothetical protein	16.89901304	2.2518808624	0.444206804	5.08503833	3.68E-07	7.20E-07	6.14267504
ABUW_RS1025	ABUW_2683	NZ_CP008706.1	2671874	2674088	-	WP_000648020.1		MFS transporter	64.17278191	2.255979578	0.401733396	5.61610733	1.96E-08	4.20E-08	7.37671071
ABUW_RS1009	ABUW_2484	NZ_CP008706.1	2479806	2481008	-	WP_000166806.1		ATP-binding cassette domain-containing protein	27.9755687	2.25465687	0.413234043	5.456193737	4.87E-08	1.02E-07	6.99199828
ABUW_RS01745	ABUW_0356	NZ_CP008706.1	37977	379938	-	WP_000783289.1		hypothetical protein	41.9712757	2.252852629	0.23783862	9.474259681	2.73E-21	1.12E-20	19.9507198
sRNA27	no	no	no	no	no	no	no	no	240.0879551	2.244197702	0.268784298	8.349214279	6.87E-17	2.34E-16	16.03078414
ABUW_RS14525	ABUW_2991	NZ_CP008706.1	3019183	3019109	-	WP_000462311.1		OspD family outer membrane porin	58.04278998	2.240559628	0.3074441	12.781675996	3.15E-13	8.77E-13	10.05700041
ABUW_RS19985	ABUW_3291	NZ_CP008706.1	3324185	3325793	-	WP_000253062.1		acyl-CoA synthetase	358.5162186	2.2391951	0.311053147	7.062341212	1.64E-12	4.38E-12	11.35855589
ABUW_RS18600	no	NZ_CP008706.1	2051479	2051653	-	WP_000198221.1	pqgA	pyrimidoquinone quinoxaline precursor peptide PqgA	870.2859167	2.231917376	0.302617972	7.379071821	1.81E-13	4.55E-13	12.3418866
ABUW_RS17410	ABUW_3849	NZ_CP008706.1	3919133	3919179	-	WP_000877608.1		YrkR family oxidoreductase	2577.502109	2.223297455	0.234562838	4.978472693	2.58E-21	1.06E-20	19.97460413
ABUW_RS06600	ABUW_053	NZ_CP008706.1	166609	1666731	-	WP_000121451.1		response regulator transcription factor	739.2944548	2.217239519	0.178876526	12.39516325	2.77E-35	2.04E-34	33.6938983
ABUW_RS11645	ABUW_2373	NZ_CP008706.1	2368676	2369550	-	WP_000156119.1		amidohydrolase	403.068006	2.211021838	0.212163945	10.0177602	1.37E-23	6.34E-23	22.9179174
ABUW_RS03950	ABUW_0807	NZ_CP008706.1	784297	784659	-	WP_000835156.1		hypothetical protein	42.63824352	2.210102324	0.339352334	6.52181977	6.97E-11	1.69E-10	9.77211295
ABUW_RS1330	ABUW_2536	NZ_CP008706.1	2526527	2528629	+	WP_000929252.1	paaz	phenylacetic acid degradation bifunctional protein PaaZ	4627.007006	2.211987204	0.40164317	5.50323371	3.71E-08	7.83E-08	17.06232328
ABUW_RS12250	ABUW_2520	NZ_CP008706.1	2509867	2510469	-	WP_000131266.1		TerR/AcrR family transcriptional regulator	67.65542083	2.211293431	0.269100465	8.211762033	2.08E-16	6.90E-16	16.11091
ABUW_RS16280	ABUW_3351	NZ_CP008706.1	3387175	3388038	-	WP_000373641.1		hypothetical protein	980.7425242	2.207144142	0.426256704	5.178203941	2.24E-07	4.44E-07	6.3526703
ABUW_RS01890	ABUW_0343	NZ_CP008706.1	365274	365337	-	WP_000744750.1		hypothetical protein	729.9584919	2.207174593	0.207400191	10.6491795	1.90E-26	9.88E-26	25.05524306
ABUW_RS00690	ABUW_0109	NZ_CP008706.1	157533	154190	-	WP_000171912.1		DUF147 domain-containing protein	4566.10137	2.206851799	0.20266194	10.88934288	1.30E-27	7.18E-27	26.148104
ABUW_RS1910	ABUW_2086	NZ_CP008706.1	2067158	2067168	-	WP_000179558.1		flavin reductase family protein	15.36322968	2.202804938	0.474198069	4.645326674	3.40E-06	6.22E-06	2.50260296
ABUW_RS05160	ABUW_1547	NZ_CP008706.1	1557473	1557594	+	WP_000041884.1	uvrB	endonuclease ABC subunit UvrB	3746.381079	2.20259103	0.246979502	8.91810337	4.74E-19	1.77E-19	17.78427001
ABUW_RS13200	ABUW_3335	NZ_CP008706.1	3368532	3368792	-	WP_000790979.1		hypothetical protein	144.3185675	2.201971291	0.340604568	2.913074005	NA	NA	#1ALL1
ABUW_RS06285	ABUW_0289	NZ_CP008706.1	108085	108089	-	WP_000307808.1		hypothetical protein	8.170007101	2.197619948	0.38106666	5.758888513	8.47E-09	1.86E-08	7.730487295
ABUW_RS10690	ABUW_2072	NZ_CP008706.													

ABUW_RS0195	ABUW_0324	N2_CP008706.1	346371	347312	-	WP_085916568.1		triacylglycerol lipase	406.5285186	2.088027391	0.262582881	7.95187936	184E-16	5.79E-16	14.2373244
ABUW_RS1730	ABUW_2411	N2_CP008706.1	239744	2398304	+	WP_01085223.1	yghU	glutathione-dependent oxidoreductase	1321.96473	2.081783727	0.253319313	8.28314163	2.06E-16	8.84E-16	15.849439
ABUW_RS04365	ABUW_0890	N2_CP008706.1	886151	886588	-	WP_00066782.1		universal stress protein	708.074839	2.080890449	0.22381546	9.2585311	1.44E-20	5.81E-20	9.23582387
iRNA64	no	no	no	no	no	no	no		13.42638533	2.078004242	0.39080318	5.316488135	1.06E-07	2.16E-07	6.665546429
ABUW_RS1270	ABUW_2940	N2_CP008706.1	2954180	2955376	-	WP_000753778.1		hypothetical protein	6184667862	2.077578292	0.26576443	7.81173029	5.40E-16	1.66E-14	13.7789191
ABUW_RS01910	ABUW_2082	N2_CP008706.1	20631081	20631652	+	WP_000076817.1	anbB	antibianate 12--oxogluconase small subunit	18.70916606	2.076571811	0.455176794	4.556133259	5.21E-05	9.37E-06	5.028260429
ABUW_RS07195	ABUW_1464	N2_CP008706.1	1463227	1464795	+	WP_000191572.1		CoA-acylating methylmalonate-semialdehyde dehydrogenase	524.0297573	2.072197961	0.276588403	7.493184545	6.72E-14	1.99E-13	12.7099539
ABUW_RS06990	ABUW_1435	N2_CP008706.1	1427029	1427343	+	WP_010204863.1		hypothetical protein	45.9331899	2.065557364	0.277928933	7.431962238	1.07E-13	3.06E-13	12.5427857
ABUW_RS09970	ABUW_2053	N2_CP008706.1	2031437	2032171	+	WP_000174086.1		molecular chaperone	628.755828	2.063451023	0.606280076	3.40346187	0.00065377	0.00095162	3.002123401
ABUW_RS16285	ABUW_3352	N2_CP008706.1	3388369	3388941	+	WP_000043984.1		TeR/Acr family transcriptional regulator	492.5632601	2.06191988	0.329704078	6.253844357	4.00E-10	9.35E-10	9.029188389
ABUW_RS1930	ABUW_2324	N2_CP008706.1	23071851	2308714	-	WP_011047339.1		hypothetical protein	279.4984583	2.061884929	0.277046599	7.442375898	8.89E-14	2.84E-13	12.5466816
ABUW_RS09252	ABUW_1958	N2_CP008706.1	1959771	1962767	+	WP_001926336.1		DEAD/DEAH-box helicase family protein	1172.424893	2.061471035	0.192810281	10.69165286	1.1E-26	5.83E-26	25.23433145
ABUW_RS03690	ABUW_0751	N2_CP008706.1	748948	748941	+	WP_000061204.1		GntR family transcriptional regulator	96.8314177	2.055981786	0.208727774	9.943582927	2.64E-23	1.21E-22	21.91721463
ABUW_RS08195	ABUW_1832	N2_CP008706.1	1827946	1828599	+	WP_000121960.1		CoA transferase subunit B	94.29694725	2.0537572315	0.343384099	5.98091851	2.22E-09	5.00E-09	8.301029996
ABUW_RS05375	ABUW_1699	N2_CP008706.1	1115174	1116781	+	WP_000449851.1		isochromatase	460.2164859	2.051100896	0.22870325	8.98524478	3.01E-19	1.01E-18	17.94692156
ABUW_RS05450	ABUW_1194	N2_CP008706.1	1133530	1134049	+	WP_000383013.1		amino acid permease	196.508443	2.050558014	0.282445144	7.260022204	3.87E-13	1.07E-12	11.97061622
ABUW_RS19380	ABUW_4076	N2_CP008707.1	46117	461932	+	WP_000093856.1		conjugative relaxase	866.618744	2.049743237	0.21810482	9.752300597	1.80E-22	7.89E-22	21.012923
ABUW_RS07285	ABUW_1454	N2_CP008706.1	146195	146192	+	WP_000997611.1		hypothetical protein	94.5089825	2.047717807	0.338643129	6.046536982	1.48E-09	3.36E-09	8.473660723
ABUW_RS01910	ABUW_1875	N2_CP008706.1	1875004	1875204	-	WP_010181618.1	catA	catechol 12-oxogluconase	1161.65310	2.044847804	0.247403048	8.247337804	1.62E-16	5.40E-16	12.57606024
ABUW_RS17950	ABUW_2507	N2_CP008706.1	2554228	2554566	-	WP_000443038.1		RNA-binding protein	181.17973	2.044800538	0.207156108	9.870916023	5.57E-23	2.51E-22	21.60033028
ABUW_RS19161	ABUW_2449	N2_CP008706.1	2435735	2436406	-	WP_010125902.1		class I SAM-dependent methyltransferase	576.580408	2.043922486	0.297546705	8.689249279	6.45E-12	1.66E-11	17.7789191
ABUW_RS05145	ABUW_0257	N2_CP008706.1	939389	9394740	-	WP_000993522.1		PD-(D)E(X) nuclease-like domain-containing protein	49.3803484	2.040179527	0.286709341	6.29890337	8.49E-12	2.17E-11	10.63540227
ABUW_RS03200	ABUW_0270	N2_CP008706.1	299199	299912	+	WP_000200304.1		replication origin	49.9121567	2.03733956	0.331291509	6.19688484	7.76E-10	1.79E-09	8.747146669
ABUW_RS05825	ABUW_1750	N2_CP008706.1	1747667	1748253	-	WP_000184547.1		HAD family hydrolase	77.1310558	2.032275868	0.187901932	10.8561885	2.90E-27	1.57E-26	24.00440035
ABUW_RS14275	ABUW_2941	N2_CP008706.1	2955532	2957172	-	WP_000140226.1		thiamine pyrophosphate-binding protein	92.9680367	2.028668625	0.285285269	7.11017788	1.05E-12	3.18E-12	11.00723361
ABUW_RS18140	ABUW_3322	N2_CP008706.1	3357517	3357882	-	WP_000083613.1		hypothetical protein	526.5169002	2.028317785	0.403942198	5.021006988	5.01E-07	9.97E-07	16.00104442
ABUW_RS08060	ABUW_1653	N2_CP008706.1	1646907	1647290	+	WP_000425555.1		hypothetical protein	97.81685171	2.028452602	0.307079927	6.509194752	4.14E-11	1.02E-10	9.991999996
ABUW_RS02780	ABUW_0566	N2_CP008706.1	565087	565055	-	WP_010107612.1		phage major tail tube protein	1067.57995	2.0256191	0.300329098	6.732510293	1.55E-11	3.86E-11	14.4100504
ABUW_RS08080	ABUW_1865	N2_CP008706.1	1860751	1861707	+	WP_00083767.1		flavin reductase family protein	216.7643261	2.021363422	0.388975332	5.90467971	2.16E-07	4.16E-07	7.378823718
ABUW_RS12265	ABUW_2523	N2_CP008706.1	2514933	2515276	+	WP_000117104.1		PasA family thioesterase	68.1666517	2.019952316	0.41141856	4.909796937	9.12E-07	1.74E-06	5.759450752
ABUW_RS19355	ABUW_4071	N2_CP008707.1	41932	42324	+	WP_000997531.1		hypothetical protein	90.850162	2.019357611	0.343504973	5.794799862	6.84E-09	1.50E-08	7.823090741
ABUW_RS02820	ABUW_0398	N2_CP008706.1	402269	402760	-	WP_010172311.1		hypothetical protein	34.2834814	2.017371497	0.422665363	4.772989787	1.82E-06	3.36E-06	5.4718933
ABUW_RS09180	ABUW_1885	N2_CP008706.1	188610	1887196	-	WP_010122305.1		hypothetical protein	117.7267189	2.012372479	0.206201875	9.759234644	1.68E-22	7.38E-22	21.0184184
ABUW_RS09025	ABUW_1854	N2_CP008706.1	1850184	1851450	-	WP_000421436.1		Osp family outer membrane protein	88.1490572	2.012165177	0.3128917702	6.42788817	1.29E-10	3.10E-10	9.588183306
ABUW_RS04950	ABUW_0935	N2_CP008706.1	944654	945046	-	WP_000406450.1		hypothetical protein	7.933914076	2.008851605	0.89510456	2.240499425	0.024826005	0.03192941	1.495862605
ABUW_RS10105	ABUW_2469	N2_CP008706.1	2461860	2462421	+	WP_000181037.1		SDR family oxidoreductase	317.210262	2.008934539	0.402026007	4.98140614	6.16E-07	1.96E-06	5.924453039
ABUW_RS05335	ABUW_1752	N2_CP008706.1	1748882	1749118	+	WP_000525043.1		hypothetical protein	214.241962	2.00559394	0.331476228	6.004091027	1.44E-09	3.29E-09	6.488248074
ABUW_RS02165	no	N2_CP008706.1	1731621	1731637	+	WP_000201566.1		hypothetical protein	612.050589	2.004705079	0.372921462	5.371667632	7.63E-08	1.57E-07	6.804100348
ABUW_RS02925	ABUW_1909	N2_CP008706.1	191252	1913052	-	WP_000276394.1		hypothetical protein	96.2182281	2.004579397	0.224651995	8.923066752	4.54E-19	1.70E-18	17.05019585
ABUW_RS09165	ABUW_2052	N2_CP008706.1	2030815	2031048	+	WP_00073819.1		type I fibronectin protein	6554.754857	2.00183154	0.590387587	3.380707324	0.000697105	0.001641423	2.882372835
ABUW_RS19345	ABUW_2432	N2_CP008706.1	2420572	2420808	+	WP_000755915.1		hypothetical protein	53.1239958	2.0014194	0.299247453	6.688174354	2.26E-11	6.53E-11	10.24949161
ABUW_RS09635	ABUW_1981	N2_CP008706.1	1966688	1967177	+	WP_000773262.1		hypothetical protein	924.288302	2.00169783	0.20805185	9.18274413	6.69E-22	2.85E-21	20.54459514
ABUW_RS19875	no	N2_CP008706.1	2550238	2551052	+			site-specific integrase	95.8289823	2.00199564	0.381145609	5.200223261	1.52E-07	3.06E-07	5.41276784
ABUW_RS09630	ABUW_1980	N2_CP008706.1	1985528	1986901	+	WP_010159828.1		FAD-binding oxidoreductase	1320.13176	2.000640202	0.21928612	9.433191876	3.98E-21	1.62E-20	9.79044498
ABUW_RS19161	ABUW_2508	N2_CP008706.1	2478	25889	+	WP_000932953.1	znuD2	TenB-dependent receptor ZnuD2	10663.74017	1.99949993	0.18801928	11.86213034	2.48E-32	1.8E-31	30.793191412
ABUW_RS09995	ABUW_2058	N2_CP008706.1	2038281	2040152	-	WP_000632243.1		hypothetical protein	2583.471181	1.999429682	0.21019687	8.691764553	5.91E-12	1.43E-11	10.84466336
ABUW_RS03205	ABUW_1060	N2_CP008706.1	106431	107051	+	WP_010166306.1		hypothetical protein	933.053233	1.998957528	0.231919002	8.633218379	5.96E-18	2.12E-17	46.73661414
ABUW_RS06765	ABUW_1989	N2_CP008706.1	1992257	1992481	+	WP_010172101.1		hypothetical protein	419.8554679	1.99647437	0.320628987	6.226743227	4.76E-10	1.11E-09	8.954677121
ABUW_RS01490	ABUW_1877	N2_CP008706.1	1876399	1877505	-	WP_010186612.1		muconate cycloisomerase	92.5848332	1.996166184	0.258084682	7.734539006	1.04E-14	3.15E-14	30.9168945
ABUW_RS19135	ABUW_2087	N2_CP008706.1	2071017	2068955	-	WP_010152581.1		hypothetical protein	53.9691036	1.994761983	0.315439295	6.323758694	2.55E-10	6.01E-10	9.22125508
ABUW_RS09475	ABUW_1948	N2_CP008706.1	1947325	1948785	+	WP_000036370.1	iaaH	indoleacetamide hydrolase	67.566367	1.990565953	0.267005642	4.738430449	1.02E-13	2.92E-13	5.2346715
ABUW_RS03755	ABUW_0765	N2_CP008706.1	765258	765634	+			iRNA-Ang	3.72310664	1.988323257	0.8871169107	2.237309648	0.025266109	0.032440198	1.488919737
ABUW_RS14750	ABUW_3039	N2_CP008706.1	3065135	3066097	-	WP_000890283.1		GNA1 family N-acetyltransferase	903.1858184	1.985386727	0.261219354	7.600457981	2.95E-14	8.73E-14	10.58898576
ABUW_RS02925	ABUW_1900	N2_CP008706.1	1901527	1901556	+	WP_000079402.1		NADH family oxidoreductase/NADH oxidase family protein	231.4216651	1.98520815	0.198099908	10.02142711	1.23E-23	5.78E-23	22.243338801
ABUW_RS12260	ABUW_2528	N2_CP008706.1	2519156	2521054	-	WP_000105074.1		3-hydroxyacyl-CoA dehydrogenase	91.1510009	1.983879476	0.242643876	1.816905384	2.93E-16	9.67E-16	10.91497353
ABUW_RS04600	ABUW_1524	N2_CP008706.1	1538770	1538826	+	WP_000138204.1		hypothetical protein	24.05319584	1.981953678	0.55175196	3.37269313	0.000333329	0.000542723	3.264321773
ABUW_RS02795	ABUW_0569	N2_CP008706.1	568907	569912	-	WP_010150805.1		phage tail protein I	95.32600410	1.981927844	0.300493525	6.553461911	5.62E-11	1.37E-10	9.863279433
ABUW_RS19110	ABUW_4018	N2_CP008707.1	1898	19177	+	WP_000389915.1		DUF2786 domain-containing protein	615.0217821	1.981854218	0.246831146	7.975298356	1.52E-16	4.81E-16	14.31785492
ABUW															

ABUW_RS0445	ABUW_2769	NZ_CP008706.1	2760966	2767859	+	WP_000816587.1		alpha/beta hydrolase	45.75772442	18663997	0.297639327	6.270675725	3.596E-0	8.40E-0	9.075720714
ABUW_RS07670	ABUW_670	NZ_CP008706.1	657863	658837	+	WP_000054101.1		aliphatic sulfonate ABC transporter substrate-binding protein	77.2724825	1863977737	0.3368173	5.883449964	4.02E-09	8.93E-09	6.049148541
ABUW_RS0880	ABUW_2654	NZ_CP008706.1	265366	2652094	+	WP_000471735.1		hydrophobic protein	834.681045	1861038962	0.358515498	5.92347263	2.08E-07	4.46E-07	6.382999569
ABUW_RS0500	ABUW_3395	NZ_CP008706.1	3438237	3439439	+	WP_000236000.1		acetate kinase	893.10292	1859634059	0.27292745	6.810025682	9.56E-02	2.44E-11	8.0526107
ABUW_RS05330	ABUW_1751	NZ_CP008706.1	1748425	1747874	+	WP_000798370.1		hydrophobic protein	139.7445399	1856214364	0.37189707	4.996579457	5.84E-07	1.18E-06	5.946921957
ABUW_RS0675	ABUW_2237	NZ_CP008706.1	2226261	2228768	+	WP_085020587.1		NAD(P)FAD-dependent oxidoreductase	276.9668729	1855402265	0.240269626	7.722877381	1.16E-14	3.46E-14	81.4602938
ABUW_RS1180	ABUW_2298	NZ_CP008706.1	2285450	2285635	+	WP_00093258.1		hydrophobic protein	225.7903063	1851905338	0.287982235	6.430727796	1.27E-0	3.05E-0	9.516700161
ABUW_RS07745	ABUW_686	NZ_CP008706.1	675910	677337	-	WP_000165610.1		glutamine synthetase	142.2008056	1849670671	0.198488963	9.320186955	1.16E-20	4.64E-20	19.33340222
ABUW_RS0577	ABUW_0577	NZ_CP008706.1	573523	573873	-	WP_001149336.1		membrane protein	29.28178339	1849456102	0.354426646	5.21893341	1.81E-07	3.63E-07	6.440093375
ABUW_RS09985	ABUW_2056	NZ_CP008706.1	2035907	2036884	+	WP_00079470.1		DUF4882 family protein	429.0684263	1847420501	0.301035951	6.06529672	8.43E-0	1.94E-09	8.71219627
ABUW_RS07915	ABUW_622	NZ_CP008706.1	616669	617859	+	WP_000494374.1		transcriptional regulator	784.188775	1844345908	0.148299645	12.43661718	1.60E-35	1.22E-34	33.91064017
ABUW_RS0150	ABUW_2575	NZ_CP008706.1	2568076	2569074	-	WP_001180395.1	tsaG	type VI secretion system basoplate subunit TsaG	369.6562697	1843038369	0.262424006	7.023239926	2.17E-02	5.73E-02	11.24184538
ABUW_RS08325	ABUW_1710	NZ_CP008706.1	1710282	171836	+	WP_001187654.1		membrane protein	238.2220708	184216347	0.92869324	9.551544438	1.28E-21	5.37E-21	20.27002571
ABUW_RS0970	ABUW_3489	NZ_CP008706.1	3338557	3339855	+	WP_00096920.1		ABC transporter	676.54707	183908110	0.94601976	4.950475	3.37E-21	1.38E-20	9.84002091
ABUW_RS04935	ABUW_606	NZ_CP008706.1	620050	6200850	-	WP_000175548.1		enoyl-CoA hydratase/isomerase family protein	74.2674083	1836451765	0.227969352	8.056695859	7.90E-16	2.54E-15	6.59556628
ABUW_RS0570	ABUW_418	NZ_CP008707.1	79719	81011	+	WP_000662932.1		Y-family DNA polymerase	356.4776989	1835197839	0.233731281	7.851742525	4.10E-15	1.27E-14	8.09698628
ABUW_RS01265	no	NZ_CP008706.1	2628331	2629679	+			EAL domain-containing protein	58.196964	1832325308	0.251077140	7.298014665	2.92E-03	8.18E-03	12.08990495
ABUW_RS04690	ABUW_3027	NZ_CP008706.1	3052319	3052792	-	WP_000162327.1		OsmC family protein	108.712135	1831798703	0.263625736	6.940535665	3.90E-02	1.02E-11	10.99195963
ABUW_RS05625	ABUW_1949	NZ_CP008706.1	1973699	1977549	+	WP_001088745.1		aromatic ring-hydroxylating deoxygenase subunit alpha	103.5590402	1830691183	0.214040723	7.594945662	3.08E-14	9.18E-14	10.04958661
ABUW_RS05905	no	NZ_CP008706.1	655977	657107	+			hydrophobic protein	8184231451	1826797942	0.265372718	6.899440216	5.52E-02	1.43E-11	10.54460396
ABUW_RS07340	ABUW_1460	NZ_CP008706.1	1454899	1456296	+	WP_001058165.1		amino acid permease	1015931751	1822806581	0.271424762	6.735072249	1.64E-11	4.1E-11	10.38810818
ABUW_RS04715	ABUW_3186	NZ_CP008706.1	3219372	3219296	+	WP_000470123.1		hydrophobic protein	5716706206	182206051	0.243088617	7.495512228	6.60E-14	1.92E-03	12.71669877
ABUW_RS07605	ABUW_658	NZ_CP008706.1	546276	548105	+	WP_001061002.1	pgaB	poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgaB	133.021942	1820763308	0.244119574	7.458630153	8.74E-14	2.52E-03	12.58954946
ABUW_RS0780	ABUW_2219	NZ_CP008706.1	2202653	2203387	+	WP_001821376.1		phosphoglycerate mutase family protein	680.9439331	18198823204	0.939399827	11.08644965	1.30E-28	7.42E-28	27.12959069
ABUW_RS0240	no	NZ_CP008707.1	25247	25726	+			hydrophobic protein	363.2716329	1816225703	0.251071264	7.233905123	4.69E-03	1.29E-02	11.88891929
ABUW_RS07650	ABUW_566	NZ_CP008706.1	554084	554923	+	WP_000735895.1		type I glutamine amidotransferase domain-containing protein	153.5022634	181311649	0.220701935	8.220643608	2.02E-16	6.72E-16	15.7263073
ABUW_RS0830	ABUW_2228	NZ_CP008706.1	2210683	2218797	+	WP_000731404.1		TonB-dependent receptor	624.6149448	181144321	0.142308683	12.7479242	3.20E-37	2.49E-36	35.60380605
ABUW_RS08015	ABUW_0231	NZ_CP008706.1	2728325	2747039	+	WP_000189408.1		MFS transporter	185.959426	1810650254	0.19423181	10.8227079	5.08E-24	2.39E-23	22.626021
ABUW_RS0195	ABUW_4026	NZ_CP008707.1	6564	61797	+	WP_000241707.1		hydrophobic protein	130.890858	1810673275	0.19267364	5.743294363	9.29E-09	2.03E-08	7.69250362
ABUW_RS04895	ABUW_0998	NZ_CP008706.1	9300326	9306650	-	WP_000276836.1		amidohydrolase	120.464832	180506102	0.236820797	7.628389655	2.38E-14	7.06E-14	13.16193
ABUW_RS04195	ABUW_0655	NZ_CP008706.1	635532	635912	+	WP_001001258.1		helicase-like transcriptional regulator	613020546	180583561	0.327879064	5.97636737	3.64E-08	7.64E-08	17.1690641
ABUW_RS05210	ABUW_061	NZ_CP008706.1	670554	671790	+	WP_000718056.1	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	119151854	1805708106	0.218007897	8.77346694	1.24E-16	4.8E-16	15.38090667
ABUW_RS07955	ABUW_630	NZ_CP008706.1	625405	6288011	+	WP_001017234.1	pepN	aminopeptidase N	8967.428778	1804730896	0.194058229	9.299945197	1.41E-20	5.60E-20	19.2811897
ABUW_RS08685	ABUW_1408	NZ_CP008706.1	1407335	1407739	+	WP_001061461.1		hydrophobic protein	45.5745087	180277599	0.346088318	5.205429128	1.94E-07	3.88E-07	6.411168274
ABUW_RS03995	ABUW_929	NZ_CP008706.1	927411	927189	+	WP_000933880.1		DMT family transporter	49.60445824	180112157	0.30152821	5.973330232	2.32E-09	5.23E-09	8.281498311
ABUW_RS0440	ABUW_2561	NZ_CP008706.1	2550793	2551275	+	WP_000646734.1		nucleoside deaminase	125.7430051	1794631451	0.271621928	6.44116426	1.19E-0	2.85E-0	9.54515154
ABUW_RS05470	ABUW_118	NZ_CP008706.1	1139284	1140186	+	WP_001091873.1		phosphate ABC transporter ATP-binding protein	142.485707	1794492216	0.144468972	12.421084	2.00E-35	1.48E-34	33.82973828
ABUW_RS04490	ABUW_0915	NZ_CP008706.1	911793	912551	+	WP_000924315.1		metallophosphatase	640.5849149	1793887877	0.181809107	9.865775739	5.88E-23	2.63E-22	21.80044025
ABUW_RS01970	ABUW_2094	NZ_CP008706.1	2076785	2077297	+	WP_001021659.1		hydrophobic protein	51.0182548	1791044358	0.363088973	4.934840473	8.02E-07	1.54E-06	9.547427279
ABUW_RS0510	ABUW_2782	NZ_CP008706.1	2777259	2778509	+	WP_000041602.1		CysD family protein	132.4745852	1788211477	0.34931105	5.19266383	3.07E-07	6.04E-07	6.28963601
ABUW_RS06945	ABUW_1426	NZ_CP008706.1	145623	1417011	+	WP_001053000.1		carboxylate-binding protein	123.6963864	1785145899	0.253480992	7.042534369	1.89E-02	5.02E-02	12.9929628
ABUW_RS0280	ABUW_2736	NZ_CP008706.1	2724724	2724762	+	WP_000941811.1		CNA family protein	58.6548475	1783454543	0.298071194	5.984629192	2.17E-09	4.89E-09	8.310691141
ABUW_RS0495	ABUW_1360	NZ_CP008706.1	1240911	1242017	+	WP_000734917.1		porin	319.0809585	1780211492	0.19711495	9.940360303	2.55E-23	1.16E-22	21.9354201
ABUW_RS01460	ABUW_2912	NZ_CP008706.1	2921993	2923126	+	WP_000201670.1		arabinose	3031489192	1780132053	0.319914662	12.72392002	4.14E-37	3.40E-36	35.46831298
ABUW_RS0240	ABUW_3343	NZ_CP008706.1	3376984	3377493	+	WP_00087862.1		hydrophobic protein	447.0977719	1779968317	0.369958464	4.811004195	1.05E-06	2.82E-06	5.549758992
ABUW_RS02155	ABUW_0434	NZ_CP008706.1	447440	448612	-	WP_001180546.1		acyl-CoA dehydrogenase family protein	306.5580056	1777607822	0.22492246	7.92054787	2.53E-05	7.91E-05	11.0182352
ABUW_RS04395	ABUW_0936	NZ_CP008706.1	945094	945366	-	WP_000362057.1		hydrophobic protein	68.58633297	1777829121	0.45419623	3.190943383	9.16E-05	0.000190999	3.826641797
ABUW_RS09790	ABUW_2016	NZ_CP008706.1	200714	2008885	+	WP_000996660.1		hydrophobic protein	264.6145911	17716793702	0.195475032	9.089618694	9.94E-20	3.80E-19	5.40022
ABUW_RS01845	ABUW_3850	NZ_CP008706.1	3918097	3918507	+	WP_000732887.1		RcnB family protein	9003.688375	1771060207	0.221743803	7.98786789	1.37E-15	4.36E-15	14.30051511
ABUW_RS08840	ABUW_617	NZ_CP008706.1	612757	6136174	+	WP_001147215.1		alpha/beta hydrolase	273.2753721	177010033	0.197368369	8.98662617	3.00E-09	1.15E-08	17.54962156
ABUW_RS04045	ABUW_0726	NZ_CP008706.1	1723523	1724800	+	WP_010052961.1		D-amino acid dehydrogenase	5169.893625	1770057057	0.25618419	6.909294532	4.87E-02	1.27E-11	10.8699682
ABUW_RS08835	ABUW_816	NZ_CP008706.1	811855	812710	+	WP_000939305.1		3-deoxy-D-phosphoglycolate synthase	900.652454	176931473	0.169948296	10.41900012	2.21E-25	1.06E-24	23.9625735
ABUW_RS0195	ABUW_3730	NZ_CP008706.1	3788252	3788851	+	WP_000757144.1		hydrophobic protein	793.8904303	1768503464	0.231464144	7.64050721	2.16E-14	6.45E-14	13.9044029
ABUW_RS0835	ABUW_2229	NZ_CP008706.1	2218907	2219623	+	WP_000525882.1		energy transducer TonB	67.88272103	1766557784	0.260597124	6.77881099	1.2E-11	3.06E-11	10.51427857
ABUW_RS0500	ABUW_2800	NZ_CP008706.1	2798101	2799366	-	WP_001058619.1		aspartate aminotransferase family protein	98.9554841	1763871052	0.301037166	5.854033387	4.80E-09	1.06E-08	7.974064135
ABUW_RS0915	ABUW_9596	NZ_CP008706.1	9582446	9588990	+	WP_000817287.1		hydrophobic protein	106.775428	1763793665	0.245624642	7.17916843	7.01E-03	1.91E-02	11.71896663
ABUW_RS01795	no	NZ_CP008706.1	960536	9605833	+			GNA1 family N-acetyltransferase	28.19202114	1763369961	0.467168192	3.769921616	0.000193561	0.000258934	3.56681992
ABUW_RS05420	ABUW_1108	NZ_CP008706.1	1125192	1125893	-	WP_001029423.1		SMPL domain-containing protein	1059.21077	1763162737	0.238526889	7.39183096	1.45E-07	4.12E-07	12.38510278
ABUW_RS04635	ABUW_0945	NZ_CP008706.1	953163	953943	+	WP_000187442.1	tdhD	formate dehydrogenase accessory sulfotransferase FdhD	96.06323002	1762884485	0.333336234	5.287750832	1.24E-07</		

ABUW_RS0945	ABUW_2667	N2_CP008706.1	2660875	2661987	-	WP_001273994.1	minor capsid protein	76.16448541	1.682306797	0.373054036	4.509552602	6.50E-06	1.16E-05	4.935542011
ABUW_RS0939	ABUW_1907	N2_CP008706.1	1706959	1970588	+	WP_00132653.1	NTP transferase domain-containing protein	1213399053	1.678260507	0.263409476	6.3748743	1.83E-10	4.34E-10	9.36259207
ABUW_RS1905	ABUW_2700	N2_CP008706.1	2684897	2685121	+	WP_000825869.1	hypothetical protein	704.976748	1.678097499	0.223635321	7.508194557	5.89E-14	1.75E-13	12.57690905
ABUW_RS0925	ABUW_1062	N2_CP008706.1	1971998	1972703	+	WP_000744219.1	hypothetical protein	573.6837546	1.677730597	0.195385376	5.866776707	8.94E-18	3.14E-17	6.50307035
ABUW_RS0355	ABUW_1003	N2_CP008706.1	1912524	1916558	+	WP_0002247952.1	hypothetical protein	26.6847225	1.676432222	0.342606368	4.893172975	9.92E-07	1.89E-06	5.723538196
ABUW_RS0910	ABUW_1051	N2_CP008706.1	1903555	1916989	+	WP_001183836.1	hypothetical protein	369.3034937	1.67591415	0.205666039	8.148715857	3.68E-16	1.21E-15	9.41271463
ABUW_RS0705	ABUW_1438	N2_CP008706.1	1430917	1431906	-	WP_001630121.1	acetyltransferase	49.82046937	1.675719899	0.472222524	3.54856366	0.000387338	0.00059193	3.226833269
ABUW_RS1745	ABUW_1088	N2_CP008706.1	1845387	1845484	+	WP_000999189.1	DUF4442 domain-containing protein	405.3375644	1.671961081	0.178993383	9.340910012	9.55E-21	3.84E-20	19.4566878
ABUW_RS0895	ABUW_1636	N2_CP008706.1	1632006	1633361	+	WP_000168123.1	MFS transporter	101.953398	1.670176701	0.316529699	5.273436844	1.34E-07	2.71E-07	6.567030709
ABUW_RS0960	ABUW_1861	N2_CP008706.1	1857196	1858473	+	WP_001084464.1	aromatic ring-hydroxylating dioxygenase subunit alpha	1047.429429	1.669856476	0.44311471	3.768479456	0.000164245	0.000259915	3.585168656
ABUW_RS0928	ABUW_1907	N2_CP008706.1	1906691	1908103	+	WP_001032870.1	POO-dependent sugar dehydrogenase	1705.062847	1.667290252	0.170007064	9.807182219	1.05E-22	4.66E-22	2.133161408
ABUW_RS0905	ABUW_1868	N2_CP008706.1	1865485	1866702	+	WP_085920624.1	hypothetical protein	19.08203253	1.666164227	0.49880811	3.340170679	0.000837269	0.001244781	2.904907049
ABUW_RS0918	ABUW_1866	N2_CP008706.1	1857273	1860029	+	WP_000675129.1	ngtA magnesium-translocating P ₁ -type ATPase	349.4118914	1.666055654	0.216447924	7.916712244	2.44E-15	7.63E-15	14.11747546
ABUW_RS1915	ABUW_1407	N2_CP008707.1	67345	67845	+	WP_001058570.1	ltpB signal peptidase I	84.35772292	1.664746769	0.270845078	6.146490746	7.82E-10	1.83E-09	8.73754891
ABUW_RS1925	ABUW_1785	N2_CP008706.1	2779566	2781917	+	WP_001180029.1	lannase/fenylolxesterase family alpha/beta hydrolase	148.1930492	1.662924701	0.339306205	4.909955764	9.54E-07	1.82E-06	5.739286192
ABUW_RS2030	ABUW_1241	N2_CP008706.1	3226904	3270431	+	WP_052692485.1	flE putative poly-sulfonate family FIE	638.6714502	1.662399737	0.157473842	10.92480482	1.16E-33	7.98E-33	32.09799711
ABUW_RS1980	ABUW_1234	N2_CP008706.1	2227120	2232385	-	WP_000162961.1	malate synthase G	9215.426337	1.660505963	0.177904235	9.333706786	1.02E-20	4.10E-20	9.38721614
ABUW_RS1610	ABUW_1263	N2_CP008706.1	1265055	1266179	-	WP_001071892.1	RsaA family protein	233.478402	1.658318549	0.224177243	7.397342943	1.39E-13	3.96E-13	10.42030481
ABUW_RS1490	ABUW_1162	N2_CP008707.1	62409	63221	+	WP_000714143.1	Dsb-C family protein	199.5015978	1.65747465	0.21979761	7.125353123	9.01E-15	2.75E-14	15.96067371
ABUW_RS2036	ABUW_1733	N2_CP008706.1	1739588	1739988	-	WP_001291625.1	ApaA family phage regulatory protein	91.4862411	1.654492005	0.276740482	5.978465395	2.25E-39	5.07E-39	8.294992041
ABUW_RS0148	ABUW_1002	N2_CP008706.1	132841	132923	+	WP_001046387.1	TPM domain-containing protein	2347.529646	1.654192963	0.161955105	10.88800311	1.34E-27	7.36E-27	26.133219
ABUW_RS0685	ABUW_1991	N2_CP008706.1	1993752	1994033	+	WP_000907899.1	DUF2523 domain-containing protein	131.5451287	1.651956687	0.21094842	7.766792417	8.05E-15	2.46E-14	11.60006489
ABUW_RS1065	ABUW_1303	N2_CP008706.1	1327340	1327999	+	WP_000096537.1	rdB 3,4-dihydroxy-2-butanone-4-phosphate synthase	642.1642465	1.651814899	0.212477814	7.773430395	7.64E-15	2.34E-14	13.0307814
ABUW_RS1935	no	N2_CP008707.1	11681	11958	+	WP_001019892.1	hypothetical protein	295.7223194	1.65093035	0.25213553	3.726819252	2.30E-13	6.44E-13	12.191113
ABUW_RS1040	ABUW_1762	N2_CP008706.1	2752596	2753915	+	WP_000026189.1	metal-dependent hydrolase	85.3805411	1.650201915	0.234158023	7.12959308	1.01E-12	2.72E-12	11.0563141
ABUW_RS0945	ABUW_1858	N2_CP008706.1	1855092	1856240	+	WP_085420623.1	acyl-CoA dehydrogenase family protein	206.1615711	1.650149055	0.630777638	2.616126437	0.008933962	0.010048203	1.199077274
ABUW_RS0720	ABUW_1481	N2_CP008706.1	1469822	1470816	+	WP_0001762703.1	SOR family oxidoreductase	155.7202769	1.649496368	0.174041462	9.477605771	2.60E-21	1.07E-20	19.97061622
ABUW_RS1540	ABUW_1234	N2_CP008706.1	2336883	2337728	+	WP_000535318.1	AraC family transcriptional regulator	652.444155	1.649218404	0.235740425	6.999098134	2.64E-12	1.148E-12	6.94612103
ABUW_RS0385	ABUW_1074	N2_CP008706.1	1773810	1774268	+	WP_000274931.1	helic-tum-helic domain-containing protein	2209.486695	1.649058547	0.206062555	8.002798429	1.22E-15	3.88E-15	4.41186827
ABUW_RS1970	ABUW_1534	N2_CP008707.1	143471	143481	+	WP_000182272.1	hypothetical protein	66.73348833	1.648625866	0.406727728	4.003389411	5.05E-05	8.38E-05	1.07675981
ABUW_RS0955	ABUW_1428	N2_CP008706.1	141858	1419556	+	WP_000350987.1	hypothetical protein	214.9163632	1.64458947	0.882333394	1.863309226	0.062334593	0.071661543	1.18662549
ABUW_RS0975	ABUW_1204	N2_CP008706.1	2032229	2034787	+	WP_001014963.1	fenH/biogenesis outer membrane usher protein	9242.003872	1.642792254	0.418702348	3.918220973	8.89E-05	0.000146011	0.335614425
ABUW_RS1970	ABUW_1417	N2_CP008706.1	2402975	2404858	+	WP_000218781.1	cysteine desulfurase	170.9243785	1.627020062	0.192619595	10.0053193	1.44E-23	6.69E-23	22.17457388
ABUW_RS1455	ABUW_1495	N2_CP008707.1	148287	148913	+	WP_000568625.1	lycE transglutaminase domain-containing protein	136.7218453	1.626932111	0.334076996	4.869995837	1.52E-06	2.12E-06	5.673664104
ABUW_RS0260	ABUW_1074	N2_CP008706.1	117906	1179433	+	WP_000742888.1	phage tail protein	100.889403	1.626729504	0.184912031	7.87300417	1.40E-18	5.12E-18	9.270073001
ABUW_RS0245	ABUW_1288	N2_CP008706.1	1281405	1281830	-	WP_001000626.1	hypothetical protein	14.01582369	1.626606863	0.616424819	2.610044291	0.007803794	0.0162182	1.973801063
ABUW_RS0295	ABUW_1291	N2_CP008706.1	1290258	1290978	+	WP_000021266.1	DUF2280 domain-containing protein	60.9980582	1.625425968	0.379192199	4.287444993	1.81E-05	3.11E-05	4.507239611
ABUW_RS1945	ABUW_1089	N2_CP008706.1	2069797	2070147	+	WP_000918647.1	denitratase hydrolase family protein	38.94643016	1.625279901	0.369898102	4.330585451	1.11E-05	1.95E-05	9.70956389
ABUW_RS1820	ABUW_1385	N2_CP008706.1	1393369	1394181	+	WP_000064180.1	NAD(P) ⁺ -dependent oxidoreductase	7815200885	1.62406192	0.256652019	6.324262585	2.59E-10	6.09E-10	4.21661063
ABUW_RS1475	ABUW_1200	N2_CP008706.1	2929148	2930324	+	WP_000875361.1	arylsulfatase	234.5621959	1.621624849	0.283119639	5.728882777	1.01E-08	2.20E-08	7.657577139
ABUW_RS1970	ABUW_1063	N2_CP008706.1	2045222	2045809	+	WP_000582742.1	uracil-DNA glycosylase family protein	258.6888308	1.621613107	0.162999998	6.191276307	5.95E-10	1.38E-09	8.860120094
ABUW_RS0290	no	N2_CP008706.1	255035	255300	+	WP_000000000.1	hypothetical protein	249.0829337	1.62053121	0.200264313	8.019602005	5.87E-16	1.90E-15	14.7212464
ABUW_RS0145	ABUW_1596	N2_CP008706.1	142552	142324	+	WP_000993156.1	acyl-CoA thioesterase II	222.9118442	1.619718219	0.131523931	12.4640188	4.41E-34	3.40E-33	32.44885108
ABUW_RS1910	ABUW_1328	N2_CP008706.1	1363788	1363168	+	WP_000689220.1	copper resistance protein CopC	713.1958368	1.61799819	0.296893699	5.449695675	5.05E-08	1.05E-07	6.978819701
ABUW_RS1975	ABUW_1216	N2_CP008706.1	2099920	2100869	+	WP_001186388.1	chrA chromate efflux transporter	87.2544658	1.617412142	0.196359117	8.237016877	1.77E-16	6.88E-16	8.23062287
ABUW_RS1810	ABUW_1284	N2_CP008706.1	2371998	2372862	+	WP_000107065.1	MFS transporter	48.41502282	1.617730034	0.21914219	5.555018805	2.78E-08	5.87E-08	7.231681899
ABUW_RS0285	ABUW_1075	N2_CP008706.1	1174330	1175260	+	WP_000600982.1	DUF3360 domain-containing protein	100.43348	1.616717473	0.203537578	7.943370906	1.97E-15	6.16E-15	10.20901762
ABUW_RS1760	ABUW_1325	N2_CP008706.1	1358092	1358240	-	WP_000033441.1	polyporphosphate-AMP phosphotransferase	23.91475915	1.616557247	0.193585884	8.338627185	7.84E-17	2.65E-16	15.67671413
ABUW_RS1145	ABUW_1253	N2_CP008706.1	1233618	1233618	+	WP_000451873.1	LysE family translocator	85.50730511	1.616490329	0.306939437	5.258666017	1.45E-07	2.93E-07	6.153112328
ABUW_RS0260	ABUW_1420	N2_CP008706.1	141099	141274	+	WP_001023191.1	head-tail connector protein	41829.0448	1.610675898	0.314073354	5.039327261	3.70E-07	7.23E-07	6.160637013
ABUW_RS1910	ABUW_1405	N2_CP008707.1	14320	14549	+	WP_001024021.1	hypothetical protein	648.6433325	1.60999048	0.22256831	7.328186544	4.55E-13	1.26E-12	11.89914645
ABUW_RS1835	ABUW_1776	N2_CP008706.1	1836104	1836870	+	WP_000387873.1	acyl-homoserine-coenzyme synthase Abal	45.9164997	1.607195898	0.353569394	4.54528810	5.48E-06	9.83E-06	5.00746482
ABUW_RS1880	ABUW_1462	N2_CP008706.1	1454676	1455293	+	WP_000418291.1	MFS transporter	25.30182738	1.605749987	0.332731075	4.822993843	1.39E-06	2.63E-06	5.580044252
ABUW_RS1930	ABUW_1410	N2_CP008706.1	1410925	1411032	+	WP_000733335.1	type-F conjugative transfer system pilin assembly protein TrcC	103.8727321	1.604462804	0.253110012	6.339614364	2.30E-10	5.43E-10	9.26520707
ABUW_RS1295	ABUW_1739	N2_CP008706.1	2728902	2728927	+	WP_001626236.1	GNAT family N-acyltransferase	233.618266	1.602818204	0.220367687	7.273345616	3.15E-13	9.72E-13	12.0233374
ABUW_RS0760	ABUW_1280	N2_CP008706.1	128431	129111	+	WP_000744369.1	basE (2,3-bisphosphoglycerate) pyruvate synthase BasE	272.1624645	1.601733092	0.713809314	2.198413309	0.028566807	0.036403969	1.477718901
ABUW_RS1285	ABUW_1230	N2_CP008706.1	1230476	1230905	+	WP_001015553.1	LysE family transcriptional regulator	220.1324792	1.599289228	0.249076781	6.420683819	1.35E-10	3.25E-10	9.488116039
ABUW_RS0840	ABUW_1837	N2_CP008706.1	1833377	1833790	+	WP_000997505.1	pcaC 4-carboxymuconolactone decarboxylase	56.01268362	1.595891991	0.318236993	5.016873019	9.31E-07	1.03E-06	5.987162775
ABUW_RS1240	no	N2_CP008706.1	2573969	2574660	+	WP_000000000.1								

ABUW_RS06275	ABUW_1287	NZ_CP008706.1	1306740	1060976	+	WP_000_62667.1		hypothetical protein	165.8330551	15280.9323	0.340388552	4.489035589	7.65E-06	1.27E-05	4.896196279	
ABUW_RS0630	ABUW_4001	NZ_CP008707.1	1	1076	+	WP_00203_424.1		replication initiation protein	414.2895856	15280.9297	0.332166747	4.60027662	4.22E-06	7.66E-06	5.1677123	
ABUW_RS0625	ABUW_2805	NZ_CP008706.1	28033.8	2804025	+	WP_000_919.6.1		POC sensor domain-containing protein	307.5839368	15260.9831	0.206046491	7.406541231	1.30E-03	3.70E-03	12.43197828	
ABUW_RS0300	ABUW_300	NZ_CP008706.1	30097.8	311945	+	WP_000_62080.1	terL	phage terminase large subunit	102.2523942	1522370889	0.256738619	5.920652879	3.04E-09	6.80E-09	8.674091087	
ABUW_RS02975	ABUW_6005	NZ_CP008706.1	603070	605451	+	WP_00103422.1		acyl-CoA dehydrogenase C-terminal domain-containing protein	4097.43123	1522263486	0.19272739	7.89853216	2.82E-05	8.80E-05	14.0055573	
ABUW_RS06020	ABUW_5332	NZ_CP008706.1	527214	527560	+	WP_000097626.1		MPS transporter	65.9763493	1519067651	0.240762588	6.31437383	2.71E-04	6.37E-04	9.165060568	
ABUW_RS0690	ABUW_3310	NZ_CP008706.1	3346077	3347531	+	WP_000394405.1		NAD(P)+ transhydrogenase (NtrB-specific) subunit beta	8657.780479	1518794792	0.271434375	5.595440125	2.20E-08	4.70E-08	7.327992142	
ABUW_RS0045	ABUW_2688	NZ_CP008706.1	2677144	2677959	+	WP_000932376.1		NAD(P)+ binding domain-containing protein	1219.457287	151647033	0.15311025	9.97083357	3.55E-23	1.09E-22	21.79680288	
ABUW_RS00050	ABUW_0010	NZ_CP008706.1	14576	14580	+	WP_001210355.1		hypothetical protein	10.4010563	1516097489	0.23882092	6.346216574	2.21E-04	5.22E-04	9.282329497	
ABUW_RS1285	ABUW_2504	NZ_CP008706.1	2498560	2499624	+	WP_000_061472.1		catalase family peroxidase	1074.815742	1514126567	0.222854169	6.719424867	1.00E-11	2.76E-11	10.55900902	
ABUW_RS07825	ABUW_1602	NZ_CP008706.1	1597969	1598673	+	WP_000923629.1		rRNA pseudotidine synthase	4913674852	1514101281	0.232029791	6.5254607	6.78E-11	1.65E-10	9.782516056	
ABUW_RS0035	ABUW_3301	NZ_CP008706.1	3332605	3333378	+	WP_000682841.1		SDR family oxidoreductase	208.0228595	1514069619	0.179070895	8.45529381	2.78E-07	9.59E-07	16.0189139	
ABUW_RS09070	ABUW_1863	NZ_CP008706.1	1858980	1859179	+	WP_000816905.1		SDR family oxidoreductase	3855863172	1512483423	0.43407335	3.484845653	0.000492421	0.000744731	3.128000568	
ABUW_RS02445	ABUW_0970	NZ_CP008706.1	981821	981907	+	WP_00069195.1		hypothetical protein	317491507	1507785793	0.222178467	6.786372286	1.15E-11	2.91E-11	10.03610701	
ABUW_RS0395	ABUW_2759	NZ_CP008706.1	2749545	2750507	+	WP_000226456.1		metal-dependent hydrolase	3936014067	1507729724	0.308109969	4.89347958	9.91E-07	1.89E-06	5.72358196	
ABUW_RS0035	ABUW_2188	NZ_CP008706.1	2172182	2173615	+	WP_000883676.1		SidA/RacD/PsA family monooxygenase	174.867092	1507507711	0.544720636	2.767487793	0.005649016	0.007775841	2.10925028	
ABUW_RS0080	ABUW_2088	NZ_CP008706.1	2068999	2069784	+	WP_001071885.1		SDR family oxidoreductase	1550614043	1507151667	0.424829187	3.547664837	0.000388662	0.000594905	3.22515881	
ABUW_RS0275	ABUW_1346	NZ_CP008706.1	1319331	1319380	+	WP_00018707.1	apbC	iron-sulfur cluster center protein ApbC	1991278012	1506510709	0.500909732	9.982817965	1.85E-23	8.37E-23	22.07277454	
ABUW_RS1745	ABUW_3524	NZ_CP008706.1	3580463	3580969	+	WP_000687235.1		hypothetical protein	3336.22511	1506080491	0.32080422	4.06965567	3.86E-06	7.03E-06	6.153044765	
ABUW_RS01720	ABUW_2409	NZ_CP008706.1	2395759	2395664	+	WP_00094097.1		LysR family transcriptional regulator	866.9534798	1504996187	0.17307458	8.65955126	3.45E-09	1.24E-07	16.90057631	
ABUW_RS07380	no	NZ_CP008706.1	1498801	1499580	+	WP_000498738.1		DUF1295 domain-containing protein	97.19004677	1504095106	0.316088003	4.752114577	2.01E-06	3.74E-06	8.427128398	
ABUW_RS0225	ABUW_4040	NZ_CP008707.1	23711	23893	+	WP_000373385.1		hypothetical protein	192.3356475	1504458932	0.388816575	3.869337141	0.000109102	0.000716017	10.4344585	
ABUW_RS0730	ABUW_2623	NZ_CP008706.1	2619612	2620562	+	WP_000394495.1		3-hydroxyacyl-CoA dehydrogenase	448.3122468	1500777222	0.200816453	7.473377808	7.82E-04	2.26E-03	12.04589106	
ABUW_RS0420	ABUW_2933	NZ_CP008706.1	2947306	2948451	+	WP_000394495.1		galactose mutarotase	1314.777044	150017383	0.274771846	5.459711883	4.77E-08	9.96E-08	7.004704662	
ABUW_RS0210	ABUW_0433	NZ_CP008706.1	445900	447390	+	WP_000415133.1		NAD(P)+FAD-dependent oxidoreductase	16015178082	1499099543	0.180263582	8.31953082	9.09E-07	3.06E-06	15.51427187	
ABUW_RS0640	ABUW_3623	NZ_CP008706.1	3681056	3682135	+	WP_000722631.1		hypothetical protein	317491507	15065684	149742736	0.173491938	8.6310185	6.07E-08	2.16E-07	16.62756164
ABUW_RS0755	ABUW_2629	NZ_CP008706.1	2620050	2620604	+	WP_003211004.1		TerR/AcrR family transcriptional regulator	27.46681933	1497196487	0.48743751	3.06837262	0.002152233	0.00307059	2.52177189	
ABUW_RS0060	ABUW_0333	NZ_CP008706.1	147654	148204	+	WP_00019316.1		HPH/RaA family tyrosine-associated protein	7974.211048	149124574	0.293188289	5.086307317	3.65E-07	7.16E-07	6.45693958	
ABUW_RS0575	ABUW_2176	NZ_CP008706.1	2165699	2167585	+	WP_000249278.1		2'-5' RNA ligase family protein	350.0841259	1490505162	0.18513967	6.620749608	9.06E-02	2.32E-11	10.43451002	
ABUW_RS02425	ABUW_0861	NZ_CP008706.1	840917	841004	+	WP_000482017.1		DUF483 domain-containing protein	25.86103308	1483436287	0.245289552	6.051477822	1.44E-09	3.27E-09	4.885442767	
ABUW_RS0590	ABUW_3210	NZ_CP008706.1	3243636	3243665	+	WP_000501127.1		CoA transferase	8571572692	1482863406	0.177764638	8.34715827	7.32E-07	2.49E-06	15.60380055	
ABUW_RS06020	ABUW_1948	NZ_CP008706.1	1914334	1916031	+	WP_000106144.1		BCTC family transporter	870.3734275	148102037	0.187770004	8.751079961	3.18E-26	2.55E-26	25.50723961	
ABUW_RS05840	ABUW_1896	NZ_CP008706.1	1828881	1830380	+	WP_000893677.1	xdtA	xanthine dehydrogenase small subunit	308.411144	1480934273	0.207992898	7.10116417	1.08E-02	2.91E-02	11.53610701	
ABUW_RS1260	ABUW_2497	NZ_CP008706.1	2493132	2494349	+	WP_001021565.1		LLMase flavin-dependent oxidoreductase	82.01583624	1480209939	0.250816357	5.90198048	3.41E-09	8.05E-09	8.09420412	
ABUW_RS0390	ABUW_1864	NZ_CP008706.1	1819056	1819595	+	WP_0002071557.1		hypothetical protein	134.5997896	1479004186	0.284978288	5.98883173	2.11E-07	4.19E-07	6.73778977	
ABUW_RS0430	ABUW_2954	NZ_CP008706.1	2967309	2968721	+	WP_000051057.1		kRr family transcriptional regulator	302.2749882	1478436251	0.193219317	8.069612429	7.05E-06	2.28E-05	16.44200515	
ABUW_RS05965	ABUW_1967	NZ_CP008706.1	1969305	1970147	+	WP_0004019720.1		SDR family NAD(P)+ dependent oxidoreductase	618.25559783	1478039008	0.25840106	5.78935084	1.07E-08	2.32E-08	7.63451015	
sRNA82	no	no	no	no	no	no	no	no	828.2585303	1478024173	0.204670592	7.221466238	5.14E-03	1.41E-02	11.85070809	
ABUW_RS0275	ABUW_2735	NZ_CP008706.1	2723589	2724005	+	WP_001060738.1		hypothetical protein	4019332844	1476262776	0.16261006	9.072004982	1.17E-09	4.45E-09	16.35193999	
ABUW_RS01765	ABUW_0360	NZ_CP008706.1	382756	383175	+	WP_000644154.1		hypothetical protein	5142544468	1473687485	0.230437742	6.395165433	1.60E-10	8.82E-10	4.971936637	
ABUW_RS0390	ABUW_2758	NZ_CP008706.1	2748649	2749479	+	WP_00059996.1		SDR family NAD(P)+ dependent oxidoreductase	53.175338352	1470047777	0.306296882	4.799416723	1.59E-06	2.98E-06	5.525787376	
ABUW_RS0685	ABUW_3432	NZ_CP008706.1	3476774	3478483	+	WP_001198008.1		cation proton antiporter	4610.097036	1466005505	0.242471444	6.049807278	1.45E-09	3.30E-09	8.48148606	
ABUW_RS0245	ABUW_2475	NZ_CP008706.1	2464645	2464554	+	WP_000188158.1		enoyl-CoA hydratase	48.78291743	1464666277	0.362194897	4.043862265	5.26E-05	8.72E-05	4.094943515	
ABUW_RS0440	ABUW_4092	NZ_CP008706.1	40584	40722	+	WP_00095382.1		nicotinamide family protein	1737.209632	1463363184	0.209831643	6.975326144	3.05E-02	8.02E-02	11.09580563	
ABUW_RS0690	ABUW_839	NZ_CP008706.1	835451	8351970	+	WP_00067206.1	pcgA	peritricate/steal 3,4-dioxygenase subunit alpha	72.93569589	1460641447	0.339664522	4.107208651	3.39E-06	1.66E-05	4.778991910	
ABUW_RS00335	ABUW_0508	NZ_CP008706.1	72582	73101	+	WP_000161645.1		VOC family protein	24.9616693	1460210158	0.35520723	4.10876793	3.94E-05	6.60E-05	4.180456064	
ABUW_RS08290	ABUW_1703	NZ_CP008706.1	1699929	1699970	+	WP_00014555.1		hypothetical protein	5.11636546	1459745746	0.795235469	183561484	0.060416893	0.08107495	1.698602432	
ABUW_RS02840	ABUW_0578	NZ_CP008706.1	573382	574091	+	WP_0001059474.1		tail protein X	37.23191185	1459440005	0.307302102	4.749210279	2.04E-06	3.79E-06	4.52103079	
ABUW_RS07830	ABUW_1603	NZ_CP008706.1	1598666	1599109	+	WP_000637089.1		GNA1 family N-acetyltransferase	482.5049476	145885733	0.20095853	7.049032126	1.80E-02	4.81E-02	11.37185492	
ABUW_RS06380	ABUW_1008	NZ_CP008706.1	1020064	1021161	+	WP_000125008.1		hypothetical protein	617.674699	1458754287	0.20541664	7.1014167	1.23E-02	3.33E-02	11.77555577	
ABUW_RS06900	ABUW_829	NZ_CP008706.1	825835	826224	+	WP_000895054.1	ftsB	cell division protein FtsB	555.1847285	1457545864	0.16288854	9.533388602	1.52E-21	6.36E-21	20.9654288	
ABUW_RS0290	ABUW_2118	NZ_CP008706.1	2102049	2102903	+	WP_000331092.1		Aac family transcriptional regulator	427.9809079	1454294574	0.149565643	9.723453468	2.40E-22	1.04E-21	20.98296666	
ABUW_RS00005	ABUW_0122	NZ_CP008706.1	116197	117340	+	WP_001199635.1		hypothetical protein	314.418591	1450384733	0.181202338	7.977025798	1.50E-05	4.75E-05	14.32303039	
ABUW_RS02985	ABUW_0607	NZ_CP008706.1	607711	608091	+	WP_000784270.1		hypothetical protein	60.40225408	1450097673	0.395645058	3.665104522	0.000247209	0.000386497	3.43803873	
ABUW_RS0695	ABUW_2261	NZ_CP008706.1	2246373	2247008	+	WP_000264044.1		MoxA/TcoX/ElxR channel channel family protein	104.525071	1448424219	0.170102025	8.5141193	1.68E-07	5.84E-07	12.57196271	
ABUW_RS0260	ABUW_1343	NZ_CP008706.1	139366	139399	+	WP_000628777.1		YnfL family transporter	942.3277777	1447611916	0.129536026	111779592	5.23E-29	3.04E-28	27.21575642	
ABUW_RS0930	ABUW_0393	NZ_CP008706.1	417778	418093	+	WP_000547775.1		NAD(P)+ binding protein	647.9837992	1444900348	0.156665663	9.222878912	2.89E-20	1.15E-19	16.94902156	
ABUW_RS0685	ABUW_3311	NZ_CP008706.1	3345204	3346025	+	WP_000697823.1		SDR family NAD(P)+ dependent oxidoreductase	276.0305649	1440805898	0.218975491	6.519758733	4.71E-11	1.16E-10	9.93930212	

ABUW_RS0955	ABUW_2669	N2_CP008706.1	2662975	2664465	-	WP_001863469.1	terL	phage terminase large subunit	615922403	1.376086222	0.321692988	4.27896836	1886-05	3.22E-05	4.492141928
ABUW_RS0265	ABUW_2110	N2_CP008706.1	2096773	2098066	-	WP_000428993.1		fumarate reductase/succinate dehydrogenase flavoprotein subu	68.2217779	1.37490565	0.2460401	5.58906198	2.28E-08	4.87E-08	7.31427039
ABUW_RS0406	ABUW_0256	N2_CP008706.1	0292990	0293886	-	WP_00156663.1		hypothetical protein	72.32947648	1.374830586	0.247050388	5.564809485	2.62E-08	5.57E-08	7.254148005
ABUW_RS0750	ABUW_2628	N2_CP008706.1	2624476	2625780	-	WP_000659371.1		MFS transporter	81.18136458	1.37006662	0.299491464	4.580433264	6.44E-06	8.39E-06	5.07230239
ABUW_RS0385	ABUW_4077	N2_CP008707.1	419483	419608	-	WP_000261991.1		hypothetical protein	404.6337669	1.3691006	0.319856325	4.280454989	1.87E-05	3.21E-05	4.401489668
ABUW_RS0245	ABUW_3344	N2_CP008706.1	3377501	3378400	-	WP_00185467.1		LyfR family transcriptional regulator	244.838216	1.36773991	0.27160528	5.04239529	4.58E-07	8.94E-07	6.048664481
ABUW_RS0760	ABUW_2210	N2_CP008706.1	2209156	2209908	-	WP_085920589.1		glutathione S-transferase C-terminal domain-containing protein	366.1264102	1.366571891	0.156837161	8.71331009	2.95E-16	1.06E-17	8.57469113
ABUW_RS0945	ABUW_0663	N2_CP008706.1	666685	666672	+	WP_001033591.1		hypothetical protein	94.0236674	1.366418435	0.27862216	4.900680964	9.50E-07	1.82E-06	5.73992812
ABUW_RS0615	ABUW_0255	N2_CP008706.1	0292728	0292885	-	WP_001600839.1		hypothetical protein	41.97110178	1.364030317	0.379440367	3.594847759	0.000324581	0.000500091	3.300950961
ABUW_RS0065	ABUW_2479	N2_CP008706.1	2473316	2474565	+	WP_000224801.1		MFS transporter	57.29549307	1.362601401	0.28341265	4.807835508	1.53E-06	2.87E-06	5.542189103
ABUW_RS0760	ABUW_0623	N2_CP008706.1	617656	618824	-	WP_001098135.1		alpha/beta hydrolase	587.641659	1.36241777	0.171010551	7.952888876	1.82E-15	5.74E-15	1.24408811
ABUW_RS0380	ABUW_2547	N2_CP008706.1	2538800	2539903	-	WP_001058339.1		FAD-binding oxidoreductase	610.1490195	1.362208197	0.35009795	3.809034515	9.99E-05	0.00016979	3.791615084
ABUW_RS0390	ABUW_0628	N2_CP008706.1	629273	629914	-	WP_001075332.1		peroxiredoxin	59.451628	1.361980022	0.370182683	3.680006801	0.000233228	0.000365206	3.437462096
ABUW_RS0380	ABUW_3771	N2_CP008706.1	3829054	3829814	-	WP_001306990.1		acyl carrier protein	70.19225346	1.359500064	0.237845922	5.71885529	1.09E-08	2.37E-08	7.625251604
ABUW_RS0385	ABUW_2963	N2_CP008706.1	2975954	2977216	+	WP_000267738.1	dctA	C4-dicarboxylate transporter DctA	81.951705	1.359440524	0.36456919	3.72881039	0.00192385	0.000302427	3.91973439
ABUW_RS0190	ABUW_4029	N2_CP008707.1	41262	48542	+	WP_001693070.1		hypothetical protein	285.0588409	1.358497841	0.263228985	5.4089762	2.46E-07	4.87E-07	6.31247039
ABUW_RS0225	ABUW_2499	N2_CP008706.1	2495135	2496106	-	WP_000987216.1		alpha/beta hydrolase	70.19077252	1.357414123	0.310547197	4.37399686	1.24E-05	2.16E-05	4.66546249
ABUW_RS0430	ABUW_2559	N2_CP008706.1	2548324	2549481	-	WP_000204305.1		winged helix-helix domain-containing protein	197.848816	1.355730107	0.15094194	8.98789663	2.66E-19	1.01E-19	17.69567663
ABUW_RS0195	ABUW_0870	N2_CP008706.1	868696	870758	-	WP_000935101.1		penicillin acylase family protein	68.6777096	1.352509027	0.254919168	3.506827663	1.12E-07	2.28E-07	6.64260193
ABUW_RS0190	ABUW_0545	N2_CP008706.1	052191	053207	-	WP_000448549.1		diglycan lyase	386.548462	1.352424707	0.1847206	7.321461015	2.45E-10	8.65E-10	12.16430493
ABUW_RS0270	ABUW_2645	N2_CP008706.1	2537307	2538969	-	WP_000415250.1		NAD(P)FAD-dependent oxidoreductase	80.3579149	1.349067949	0.242961661	5.552299289	2.81E-08	5.95E-08	7.225483034
ABUW_RS0275	ABUW_0260	N2_CP008706.1	0276884	277874	-	WP_001035486.1		SDR family NAD(P)-dependent oxidoreductase	1479.56875	1.347156131	0.461618602	2.920486263	0.003494856	0.004897661	3.21001679
ABUW_RS0808	ABUW_0879	N2_CP008706.1	8712243	8737121	+	WP_001070306.1	amA	multidrug eflux MFS transporter AmA	20.82325692	1.346197683	0.191048677	7.038896693	1.94E-12	5.16E-12	11.28890277
ABUW_RS0240	ABUW_0897	N2_CP008706.1	898040	898843	+	WP_000056614.1		SDR family oxidoreductase	24.407674	1.345871687	0.326431981	4.12927472	3.74E-05	6.28E-05	3.402460369
ABUW_RS0085	ABUW_0866	N2_CP008706.1	861903	862817	+	WP_001077869.1	feaR	transcriptional regulator FeaR	89.07902845	1.344363226	0.306484836	4.386393932	1.16E-05	2.01E-05	4.696801943
sRNA7	no	no	no	no	no	no	no	no	1068.471058	1.340224895	0.41585485	3.25640793	0.00102308	0.001653074	7.281707705
ABUW_RS0870	ABUW_0339	N2_CP008706.1	361932	362007	-	WP_001438851.1		superoxide dismutase family protein	6022.173678	1.337463887	0.242806635	5.508349828	3.62E-08	7.62E-08	7.118045029
ABUW_RS0730	ABUW_3573	N2_CP008706.1	3632075	3633247	+	WP_000212712.1	fadA	acetyl-CoA C-acyltransferase FadA	59.82000559	1.334460305	0.257611835	5.81010335	2.22E-07	4.40E-07	5.654547324
ABUW_RS0700	ABUW_2819	N2_CP008706.1	2824478	2824744	+	WP_000703423.1		hypothetical protein	227.9271978	1.332106383	0.426399909	3.104147908	0.001978308	0.002558599	2.591997774
ABUW_RS0620	ABUW_0878	N2_CP008706.1	882696	884108	-	WP_001697729.1		NAD(P)FAD-dependent oxidoreductase	524.2164710	1.331915142	0.18791482	7.086996872	1.37E-12	3.68E-12	11.41421828
ABUW_RS0055	ABUW_0011	N2_CP008706.1	13605	13940	-	WP_000993572.1	epaA	iron-sulfur cluster insertion protein EpaA	916.716181	1.330366471	0.239265804	5.583359264	2.36E-08	5.02E-08	7.289269283
ABUW_RS0265	ABUW_0261	N2_CP008706.1	0275405	0276394	-	WP_001643259.1		phage major capsid protein, P2 family	9118.832674	1.329832411	0.180828439	7.343716594	2.08E-10	8.83E-10	12.23431415
ABUW_RS0420	ABUW_1144	N2_CP008706.1	1209945	1210086	-	WP_000367442.1		hypothetical protein	1326.884811	1.329741485	0.21063482	6.224366824	4.84E-10	1.12E-09	8.950781977
ABUW_RS0905	ABUW_3071	N2_CP008706.1	3099196	3099242	-			tRNA-Met	97.95217399	1.328694115	0.404403674	3.285563911	0.001017784	0.001497682	2.824488039
ABUW_RS0365	ABUW_0744	N2_CP008706.1	744323	744514	-	WP_001076181.1			59.99214638	1.328181342	0.279038026	4.760341662	1.93E-06	3.60E-06	4.940997499
ABUW_RS0350	ABUW_2849	N2_CP008706.1	2861937	2862827	-	WP_000887362.1		LyfR family transcriptional regulator ArpR	120.053214	1.326627921	0.233341466	5.685300081	1.13E-08	2.83E-08	7.548212564
ABUW_RS1925	ABUW_3520	N2_CP008706.1	3569079	3570377	+	WP_00089282.1		EstA family serine hydrolase	67.6987073	1.32425464	0.207302315	6.388039932	1.68E-10	4.00E-10	9.39740009
ABUW_RS0430	ABUW_3056	N2_CP008706.1	3082659	3083474	-	WP_000844343.1		acylglycerol transferase	167.7122283	1.322137988	0.42885193	9.246677656	2.32E-20	1.08E-20	10.0419146
ABUW_RS0745	ABUW_3243	N2_CP008706.1	327202	3273307	+	WP_000370427.1		hypothetical protein	503.1004285	1.321942611	0.16882146	3.84019668	4.86E-16	1.50E-16	11.823909874
ABUW_RS0416	ABUW_2556	N2_CP008706.1	2546100	2546387	-	WP_000342966.1		hypothetical protein	10.4437984	1.320782764	0.319160558	4.08333299	3.50E-05	5.88E-05	4.230622674
ABUW_RS0700	ABUW_0441	N2_CP008706.1	413314	4133308	+	WP_000084540.1		hypothetical protein	107.6863422	1.319267693	0.25348531	5.204514041	1.95E-07	3.89E-07	5.410050399
ABUW_RS0248	ABUW_4010	N2_CP008707.1	6270	6410	+	WP_000691626.1		hypothetical protein	69.58426426	1.319054257	0.433708986	3.041391658	0.002354873	0.003325274	2.474621627
ABUW_RS0225	ABUW_2471	N2_CP008706.1	2464021	2465226	+	WP_000930806.1		3'-oxoacyl-CoA thiolase	59.01489803	1.319037779	0.372875756	5.53747253	0.000403876	0.000617693	3.0292732
ABUW_RS0690	ABUW_0338	N2_CP008706.1	0380744	0381668	+	WP_000554500.1		Aac family transcriptional regulator	286.7951696	1.318820434	0.192622816	7.221953511	5.16E-13	1.41E-12	11.85071089
ABUW_RS0225	ABUW_3340	N2_CP008706.1	3374993	3374365	+	WP_000538099.1		pyocin activator PtiB family protein	286.2591919	1.31640095	0.192261732	6.606642122	3.93E-11	9.68E-11	10.0141684
ABUW_RS0145	ABUW_2355	N2_CP008706.1	2337728	2338213	-	WP_000666032.1		glutathione peroxidase	698.407007	1.316326885	0.256843882	5.1250184	2.98E-07	5.86E-07	6.232102384
ABUW_RS0340	ABUW_0069	N2_CP008706.1	73148	73780	-	WP_000719235.1	malA	malicylacetate carboxyl isomerase	44.47188604	1.315646064	0.374640374	3.91638414	0.000445021	0.000877357	3.16182217
ABUW_RS0280	ABUW_0080	N2_CP008706.1	076468	075394	-	WP_000095041.1		terminase	79.1794326	1.31500601	0.272337143	4.810861339	1.50E-06	2.82E-06	5.549750892
ABUW_RS0965	ABUW_0842	N2_CP008706.1	837597	838816	-	WP_001042561.1		carboxyl diol porin	249.4563322	1.310047131	0.191528881	6.839952779	7.92E-12	2.03E-11	10.69250960
ABUW_RS0175	ABUW_1025	N2_CP008706.1	1046270	1046734	+	WP_001041863.1	bfr	bacterioferritin	12989.31849	1.308126895	0.402854664	3.247143483	0.00165596	0.001904193	7.084969515
ABUW_RS0405	ABUW_0082	N2_CP008706.1	89373	91199	+	WP_000797607.1		DUF185 domain-containing protein	346.606194	1.307572169	0.250658577	5.21862865	1.80E-07	3.62E-07	6.441029429
ABUW_RS0895	ABUW_3880	N2_CP008706.1	3948566	3949473	+	WP_000714235.1		main family metalloprotease	514.44406483	1.306830719	0.373999246	3.491533027	0.000480257	0.000727974	3.17884131
ABUW_RS0195	ABUW_3333	N2_CP008706.1	3367191	3368264	-	WP_001893743.1		hypothetical protein	316.0120858	1.305591598	0.489184102	2.668916514	0.007160936	0.010364849	1.984437021
ABUW_RS07435	ABUW_0623	N2_CP008706.1	608451	609653	-	WP_001066101.1		MFS transporter	120.0376374	1.304821593	0.373840967	3.488870159	0.000485067	0.00073416	3.104209281
ABUW_RS0275	ABUW_2546	N2_CP008706.1	2538569	2538799	+	WP_000619330.1		GFx-25p-binding protein	36.8866973	1.30350212	0.363351966	3.585462996	0.000336481	0.000517831	3.285815064
ABUW_RS0435	ABUW_0274	N2_CP008706.1	029407	0293291	-	WP_001868687.1		hypothetical protein	187.6162873	1.302291952	0.258858001	5.030631622	4.88E-07	9.52E-07	6.281030502
ABUW_RS0675	ABUW_0387	N2_CP008706.1	0398166	0398321	-	WP_001922564.1		hypothetical protein	78.5555198	1.301367556	0.244396241	5.325102128	1.01E-07	2.06E-07	6.68619378
ABUW_RS02710	ABUW_0652	N2_CP008706.1	054968	055162	-	WP_000696053.1		hypothetical protein	162.8780432	1.301075642	0.364833243	3.566220092	0.000362187	0.000505575	3.250502258
ABUW_RS															

ABUW_RS08960	ABUW_2031	NZ_CP008706.1	206476	201976	-	WP_005142463.1	replication initiation factor domain-containing protein	458.167691	1244655349	0.232666949	5.349744998	8.81e-08	1.81e-07	6.74232425
ABUW_RS1415	ABUW_2989	NZ_CP008706.1	3007583	3008527	+	WP_000050879.1	dihydrodipicolinate synthase family protein	48.66902462	1243180291	0.39140644	3.175483210	0.001495872	0.002160942	2.665358889
ABUW_RS08818	ABUW_0397	NZ_CP008706.1	402372	402569	-	WP_00084983.1	hypothetical protein	15.34859244	1241985812	0.491008844	2.527910588	0.019474292	0.019338394	18.14220111
ABUW_RS00555	ABUW_0239	NZ_CP008706.1	526363	526379	+	WP_001091858.1	Arc family ABC transporter permease	64.45730410	1241894996	0.367846676	3.37557739	0.000736609	0.00098371	2.959250942
ABUW_RS14960	ABUW_3088	NZ_CP008706.1	310214	310709	+	WP_001007221.1	DNA primase	231.182386	1239881843	0.134023933	9.251950003	2.232e-20	8.71e-20	9.0599184
ABUW_RS1190	ABUW_2300	NZ_CP008706.1	2286568	2287482	+	WP_001021779.1	OXA-51 family carbapenem-hydrolyzing class D beta-lactamase OX	320.3038308	1238453941	0.22164949	5.619196923	2.255e-08	4.796e-08	7.31664487
ABUW_RS09360	ABUW_0922	NZ_CP008706.1	902070	902182	-	WP_000959626.1	amidohydrolase family protein	18.1866527	1238655871	0.294433422	4.206910279	2.595e-05	4.396e-05	4.35753548
ABUW_RS1525	ABUW_2369	NZ_CP008706.1	2356407	2357441	-	WP_001866574.1	arsB	28.28076534	1238207539	0.378279723	3.273259079	0.00100315	0.00106166	2.806434093
ABUW_RS1524	ABUW_3224	NZ_CP008706.1	3253704	3254183	-	WP_0009217483.1	methylated-DNA-(protein)-cytisine S-methyltransferase	332.9229951	1237144688	0.13794374	8.970663383	2.955e-19	1.11e-18	17.95467702
ABUW_RS03495	ABUW_0710	NZ_CP008706.1	716525	717043	+	WP_000868443.1	hypothetical protein	621.5008335	1234999448	0.194978185	6.334039102	2.396e-10	5.622e-10	9.250263684
ABUW_RS07735	ABUW_0584	NZ_CP008706.1	572455	575109	+	WP_001191611.1	sensor histidine kinase KdpD	494.4283301	1232527337	0.145567137	8.467048118	2.525e-17	8.695e-17	6.060980022
ABUW_RS08985	ABUW_0446	NZ_CP008706.1	843079	843492	+	WP_000789128.1	YeeE/YeeD family protein	86.70647978	1232261592	0.269026256	4.577388392	4.71e-06	8.505e-06	5.070581074
ABUW_RS06350	ABUW_0302	NZ_CP008706.1	3137877	3138245	+	WP_001052442.1	hypothetical protein	21.556055797	1231594936	0.149974382	2.960747079	0.0003088938	0.00431881	2.3644035902
ABUW_RS09580	ABUW_0172	NZ_CP008706.1	973736	974821	-	WP_000837449.1	adeS	204.9191899	1226462302	0.16677085	7.3541976726	1.925e-13	5.41e-13	5.216680273
ABUW_RS04065	ABUW_0830	NZ_CP008706.1	807188	807886	-	WP_001844466.1	phosphatase PAP2 family protein	97.35442316	1224550499	0.268998761	4.552625056	5.306e-06	9.535e-06	5.029070799
ABUW_RS09660	ABUW_0886	NZ_CP008706.1	9902238	991866	+	WP_038405894.1	replication initiation factor domain-containing protein	454.6604761	1222918140	0.282603327	4.327331031	11.51e-05	2.61e-05	4.583359493
ABUW_RS03050	ABUW_0620	NZ_CP008706.1	621075	622150	+	WP_000091028.1	metal-dependent hydrolase	304.3910027	1221009098	0.235625401	5.18281417	2.16e-07	4.346e-07	3.36251027
ABUW_RS15610	ABUW_3216	NZ_CP008706.1	3247773	3248549	+	WP_000843791.1	zinc-binding dehydrogenase	97.2610178	1221069118	0.30227145	4.03964468	5.335e-05	8.875e-05	4.02507638
ABUW_RS10505	ABUW_2781	NZ_CP008706.1	2718038	2717197	+	WP_001051439.1	acyl-CoA dehydrogenase family protein	158.856032	122080064	0.345212211	3.536314025	0.00405929	0.000619895	3.20176188
ABUW_RS01950	ABUW_0397	NZ_CP008706.1	423531	424796	+	WP_002000599.1	dicarboxylate/amino acid:cation symporter	7045.597729	1220277895	0.139102651	8.772488902	1.755e-18	6.37e-18	97.8566007
ABUW_RS15710	ABUW_3208	NZ_CP008706.1	3237843	3238637	+	WP_000749505.1	substrate-binding domain-containing protein	38.45587459	1219566387	0.302780668	4.028100802	5.625e-05	9.29e-05	4.031984288
ABUW_RS10065	ABUW_3307	NZ_CP008706.1	3341693	3342781	+	WP_001861724.1	crotonase/enoyl-CoA hydratase family protein	339.0483809	1216203788	0.170398175	7.17422611	9.51e-13	2.575e-12	1159006688
ABUW_RS14210	ABUW_2927	NZ_CP008706.1	2941889	2942593	-	WP_000808241.1	transketolase	99.89030925	1216532696	0.22154755	5.496299173	3.888e-08	8.135e-08	7.089901454
ABUW_RS10015	ABUW_2062	NZ_CP008706.1	2043454	2044310	+	WP_000809993.1	phospholipase A family protein	9332.2645782	12164902	0.149974382	6.703557097	2.038e-11	5.081e-11	10.29410629
ABUW_RS09305	ABUW_1416	NZ_CP008706.1	140607	1410270	+	WP_000510483.1	hypothetical protein	86.73105249	1210330399	0.283793777	4.27433554	1.932e-05	3.296e-05	4.442804102
ABUW_RS11510	ABUW_2170	NZ_CP008706.1	2693006	2694388	+	WP_001157401.1	benA	97.45225423	1210616565	0.299707316	4.039322698	5.366e-05	8.886e-05	4.051987034
ABUW_RS01665	ABUW_0338	NZ_CP008706.1	355989	357139	+	WP_001061826.1	yccS	740.35361	1209537361	0.192709894	6.27647833	3.446e-10	8.10e-10	9.00915981
ABUW_RS07280	ABUW_1493	NZ_CP008706.1	1480558	1481400	+	WP_000821899.1	hypothetical protein	162.5476693	1206872526	0.312739327	3.859036656	0.000103835	0.000193763	2.737162252
ABUW_RS14545	ABUW_2151	NZ_CP008706.1	2105552	2106371	+	WP_000828833.1	alpha/beta fold hydrolase	254.2297825	1204988584	0.15089919	7.480971409	6.945e-14	2.01e-13	1.021668034
ABUW_RS09445	ABUW_2048	NZ_CP008706.1	2027330	2028487	+	WP_001050023.1	replication initiation factor domain-containing protein	400.4096723	1204822568	0.224636473	5.363432531	8.17e-08	1.685e-07	6.77460719
ABUW_RS08715	ABUW_0790	NZ_CP008706.1	795435	796031	+	WP_001029431.1	nitroreductase family protein	151.1025667	1202655639	0.216954826	5.543233896	2.975e-08	6.275e-08	7.1027732459
ABUW_RS10925	ABUW_2896	NZ_CP008706.1	2876028	2876507	+	WP_000702193.1	dmh	238.0802382	1202080749	0.135417481	8.873094102	7.11e-19	2.64e-18	97.8738067
ABUW_RS02235	ABUW_0450	NZ_CP008706.1	467383	468297	+	WP_000392876.1	DMT family transporter	219.9102858	120146207	0.192699238	6.235023146	4.432e-10	1.055e-09	8.97881071
ABUW_RS10850	ABUW_2232	NZ_CP008706.1	2221003	222116	+	WP_000525676.1	bicopolymer transporter BxbD	44.89901605	1201734574	0.343985675	3.490652841	0.00044942	0.000730102	3.15661462
ABUW_RS04725	ABUW_0963	NZ_CP008706.1	973225	974205	+	WP_001022403.1	glycylcysteine family 2 protein	90.86496627	1200564518	0.263177076	4.56610568	5.075e-06	9.105e-06	5.039520222
ABUW_RS10730	ABUW_3240	NZ_CP008706.1	3267189	3269044	+	WP_001035109.1	hypothetical protein	234.9356208	1199024259	0.10265493	10.62437959	2.326e-25	1.205e-25	14.20281875
ABUW_RS09495	ABUW_0952	NZ_CP008706.1	953073	954659	+	WP_000841603.1	GHD auxin-responsive promoter family protein	86.49374677	1198853819	0.255416205	4.69372652	2.688e-06	4.955e-06	5.303594801
ABUW_RS11460	ABUW_2978	NZ_CP008706.1	2995619	2996326	+	WP_001185351.1	DUF1275 domain-containing protein	47.50594831	1197916259	0.332730127	3.599551591	0.000318766	0.000441939	3.38083578
ABUW_RS09050	ABUW_0859	NZ_CP008706.1	856569	856628	+	WP_000387550.1	hypothetical protein	559.554375	119728952	0.546527269	2.0172238	0.028471889	0.036416901	14.68697014
ABUW_RS10090	ABUW_2078	NZ_CP008706.1	2050405	2050997	-	WP_000971688.1	modB	68.9416177	1196350073	0.265294819	4.05591626	6.505e-06	1.165e-05	4.93542011
ABUW_RS10415	ABUW_2763	NZ_CP008706.1	2759178	2754811	+	WP_000600019.1	SDR family NAD(P)-dependent oxidoreductase	97.83144073	1194110623	0.253378526	5.053194258	4.355e-07	8.48e-07	6.071604148
ABUW_RS10525	ABUW_1409	NZ_CP008707.1	68467	69510	+	WP_001732320.1	TafA family protein	186.1718964	1196688556	0.17761148	6.81261437	2.375e-11	5.905e-11	10.2294799
ABUW_RS03685	ABUW_0749	NZ_CP008706.1	744222	744858	+	WP_000051086.1	hypothetical protein	210.7037108	119485742	0.266544916	4.445244869	8.785e-06	1.555e-05	4.809668302
ABUW_RS10715	ABUW_0159	NZ_CP008706.1	905450	9055268	+	WP_000848611.1	aspartate/gluamate racemase family protein	122.6529487	1193204882	0.24619328	4.807445938	1.533e-06	2.875e-06	5.54219193
ABUW_RS02810	ABUW_0572	NZ_CP008706.1	571795	571087	-	WP_000990625.1	phage baseplate assembly protein V	67.26840021	1192961854	0.310227172	3.788734033	0.000191086	0.000241931	3.617937018
ABUW_RS11780	no	NZ_CP008706.1	1745301	1745397	+	Rs	signal recognition particle rRNA small type	9311.663398	1182850142	0.357227925	3.31191707	0.000928995	0.00103736	2.8627912789
ABUW_RS10095	ABUW_3310	NZ_CP008706.1	3347544	3347858	+	WP_000230434.1	NAD(P) transhydrogenase subunit alpha	9342.924705	1182519606	0.301506669	3.924055016	8.71e-05	0.000115485	3.844931897
sRNA37	no	no	no	no	no	no	no	9340.447729	1181400056	0.3557144	3.320208612	0.000899502	0.001033019	2.875848375
ABUW_RS06305	ABUW_0293	NZ_CP008706.1	311192	312593	+	WP_000126352.1	DUF4055 domain-containing protein	61.8254398	1179191862	0.252503961	4.669638302	3.025e-06	5.555e-06	5.25507017
ABUW_RS03995	ABUW_0752	NZ_CP008706.1	749841	751166	+	AAA family ATPase	87.41710203	1177166344	0.269956151	3.60583324	1.305e-05	2.265e-05	4.645891651	
ABUW_RS18945	ABUW_3891	NZ_CP008706.1	3959197	3960163	+	WP_000447690.1	Tec family protein	276.5886274	1174346195	0.239404018	4.01956066	9.15e-07	1.825e-06	7.139926162
ABUW_RS02585	ABUW_0526	NZ_CP008706.1	534124	534975	+	WP_001161539.1	PHP domain-containing protein	863.8062704	1173137873	0.178098555	5.687239482	4.448e-11	1.105e-10	9.958607135
ABUW_RS10095	ABUW_2079	NZ_CP008706.1	2060094	2060879	+	WP_000251953.1	modA	243.5259999	1171077355	0.192207256	6.092784325	1.11e-09	2.555e-09	8.59345982
ABUW_RS07190	ABUW_1475	NZ_CP008706.1	1462778	1463164	+	WP_000907870.1	Aac family transcriptional regulator	133.955133	116497113	0.22421528	5.95857424	2.046e-07	4.076e-07	4.000405911
ABUW_RS09335	ABUW_1623	NZ_CP008706.1	1419352	1419751	+	WP_001262762.1	hypothetical protein	49.07522788	1158632924	0.289252251	4.005614893	6.165e-05	0.00019764	3.992405831
ABUW_RS09720	ABUW_2000	NZ_CP008706.1	919857	9199723	+	WP_0001471909.1	hypothetical protein	335.06638	1158238578	0.204483988	5.664916758	1.475e-08	3.185e-08	7.49757288
ABUW_RS09780	ABUW_2014	NZ_CP008706.1	2005890	2007194	+	WP_000695268.1	hypothetical protein	484.2183719	1158048294	0.174724985	6.627834573	3.41e-11	8.405e-11	10.07572071
ABUW_RS06545	no	NZ_CP008706.1	1354858	1355364	+		ATP-binding cassette domain-containing protein	78.16625224	1157688746	0.243996041	4.744702987	2.095e-06	3.885e-06	5.41168274
ABUW_RS18680	ABUW_3467	NZ_CP008706.1	3516928	3515143	+	WP_000567254.1	RNA pyrophosphohydrolase	1483.687448	115726563	0.16610941	5.902917189	3.575e-09	7.975e-09	8.018815979
ABUW_RS06520	ABUW_0336	NZ												

ABUW_RS03616	ABUW_0734	NZ_CP008706.1	739888	74012	-	WP_00288394.1		hypothetical protein	129.589 9'45	1.07293358	0.218596407	5.085499 6'53	4.07E-07	7.96E-07	6.099086932
ABUW_RS08275	ABUW_1699	NZ_CP008706.1	965982	969730	-	WP_000652017.1		Y-family DNA polymerase	210.358 6'49	1.04835856	0.207170492	5.332978867	9.66E-08	1.79E-07	6.705233774
ABUW_RS02325	ABUW_0473	NZ_CP008706.1	484634	485701	+	WP_01025222.1		hypothetical protein	740.83657 2'5	1.04319355	0.23546232	4.689973044	2.73E-06	5.03E-06	5.2984320 5
ABUW_RS09365	ABUW_1923	NZ_CP008706.1	922990	922379	-	WP_00026040.1		SLC10 family permease	42.596 12'92	1.0126 5'06	0.364538764	3.020972292	0.002519644	0.003573265	2.446934775
ABUW_RS04440	ABUW_0899	NZ_CP008706.1	895 88	897083	+	WP_00286662.1	ftsH	ATP-dependent zinc metalloprotease FtsH	66757 44407	1.00868348	0.22 8'10044	4.96310 5'4	6.94E-07	1.53E-06	5.876 14'559
ABUW_RS14930	ABUW_3076	NZ_CP008706.1	3104064	310578	-	WP_00984224.1		BCCIT family carnitine transporter	5 52.6409791	1.08991161	0.2445 10934	4.94325028	6.98E-06	1.24E-05	4.9065783 5
ABUW_RS08805	ABUW_1609	NZ_CP008706.1	904561	906081	-	WP_000886877.1		hypothetical protein	892.1267689	1.09705101	0.114954798	4.94327604	1.38E-21	5.79E-21	20.2372144
ABUW_RS05740	ABUW_1076	NZ_CP008706.1	1020000	1020568	+	WP_00104131.1	baaB	siderophore-binding periplasmic lipoprotein BaaB	239.2225961	1.0955996 8	0.349929496	3.1009 53'9	0.001742824	0.0025025	6.807886659
ABUW_RS09570	ABUW_1668	NZ_CP008706.1	970 83	971053	-	WP_000872857.1		SDR family NAD(P)-dependent oxidoreductase	16.75599531	1.095485189	0.48232 991	2.22519682	0.02607 963	0.033453355	1475560321
ABUW_RS06840	ABUW_1402	NZ_CP008706.1	9044450	9044785	+	WP_000819542.1		ribbin-helix-helix protein, CspG family	63.9308493	1.094220882	0.30 0'429 9	3.632590289	0.000286959	0.0004358 9	3.3605989 9
ABUW_RS15300	ABUW_2780	NZ_CP008706.1	2774078	2775964	+	WP_07019699.1		AMP-binding protein	860.1609104	1.093127937	0.33791863	3.234951785	0.00 1'26633	0.00 7'77307	2.750237349
ABUW_RS00910	ABUW_0184	NZ_CP008706.1	204604	2063 9	+	WP_000871885.1		cation acetate symporter	3826.3 15546	1.090827046	0.387074655	2.818109091	0.004830411	0.00669478	2.17426369
ABUW_RS12570	ABUW_2587	NZ_CP008706.1	2580966	2581400	-	WP_00118705.1		transcriptional regulator	23.416 5'06	1.090643867	0.39031431	2.784269904	0.005201704	0.007 87'29	2.1344456
ABUW_RS02800	ABUW_0570	NZ_CP008706.1	569512	5704 14	-	WP_000169738.1		baseplate JigB4 family protein	118.0727966	1.08894268	0.266287141	4.0898 8'451	4.32E-05	7.2E-05	4.1620647 35
ABUW_RS09090	ABUW_1867	NZ_CP008706.1	1863026	1865341	+	WP_00909098.1	lynA	primary-amine oxidase	102.160913	1.087691106	0.2808 9003	3.873281324	0.00019738	0.000 9'73331	3.761023757
ABUW_RS05640	ABUW_1152	NZ_CP008706.1	1800383	181 699	+	WP_000561082.1		FAD-binding oxidoreductase	108.78377 9	1.086897098	0.12832001	5.107254046	3.27E-07	6.42E-07	6.192464072
ABUW_RS05850	ABUW_1188	NZ_CP008706.1	1232764	1233747	+	WP_00164227.1	xdhC	xanthine dehydrogenase accessory protein XdhC	292.0939764	1.0853225	0.1752 8604	6.194105408	5.86E-10	1.36E-09	8.86646 092
ABUW_RS01480	ABUW_0301	NZ_CP008706.1	325229	3258 9	+	WP_000846931.1		LeuM family protein	2088.037787	1.084003571	0.194745604	5.566254372	2.80E-08	5.53E-08	7.257274869
ABUW_RS15930	ABUW_2867	NZ_CP008706.1	2876620	2877396	+	WP_000423004.1		deoxygenase	316.0237624	1.082679962	0.29084262	3.722541937	0.000 9'7227	0.000309676	3.509092451
ABUW_RS05800	ABUW_1188	NZ_CP008706.1	12 844	1220581	+	WP_000983826.1	basJ	acinetobactin biosynthesis isochorismate synthase BasJ	175.9262843	1.08267 9'83	0.495024775	2.187 96259	0.028734768	0.03694891	1.353349398
ABUW_RS15355	ABUW_4111	NZ_CP008707.1	927272	72286	+	WP_002072594.1	tsaN	conjugial transfer protein TsaN	1047.5 921	1.08194785	0.146547682	3.782306603	1.55E-13	4.39E-13	4.14359434
ABUW_RS12145	ABUW_2496	NZ_CP008706.1	249 931	2493300	-	WP_00023063.1		aldehyde dehydrogenase	103.8653568	1.08 9'8025	0.237234643	4.559275213	5.15E-06	9.24E-06	5.034282629
ABUW_RS08355	ABUW_0716	NZ_CP008706.1	97 8421	17 07284	+	WP_00168993.1		DMT family transporter	112.5993598	1.08 0'10408	0.254851486	4.24268761	2.2E-05	3.76E-05	4.4248 2'55
ABUW_RS08725	ABUW_1792	NZ_CP008706.1	1786986	187285	+	WP_08591945.1		cyd operon YbgE family protein	324.3220714	1.079829743	0.42 65496	5.09932148	0.01439174	0.0140 0'471	1.85347264
ABUW_RS03880	ABUW_0791	NZ_CP008706.1	771497	7724 14	+	WP_000094258.1		hypothetical protein	17.64543608	1.077878123	0.420287839	2.564143007	0.01343092	0.01890772	1.857273617
ABUW_RS12595	ABUW_2592	NZ_CP008706.1	2586352	2587005	-	WP_000217385.1		DUF1988 domain-containing protein	3.4480806784	1.07664206	1072590154	1.00038263	3.64624345	0.34992791	4.58002417
ABUW_RS15300	ABUW_151	NZ_CP008706.1	3177437	3178006	+	WP_000044599.1		TetR/AcrR family transcriptional regulator	795.0830323	1.076072542	0.296162292	3.6335 0765	0.000279591	0.000434428	3.26082 91
ABUW_RS07765	ABUW_1590	NZ_CP008706.1	1580470	1583190	+	WP_001039432.1		outer membrane protein assembly factor	3874.665882	1.07467438	0.145278744	3.793727024	1.39E-13	3.96E-13	2.40230481
sRNA H	no	no	no	no	no	no	no	no	23.9158784	1.074648905	0.549345394	1.956235396	0.050437431	0.06268187	1.022862788
ABUW_RS19375	ABUW_4075	NZ_CP008707.1	43946	46305	+	WP_000644960.1		type IV secretion system DNA-binding domain-containing protein	454.0738857	1.07473458	0.251934662	4.273537031	1.92E-05	3.30E-05	4.48488606
ABUW_RS14610	ABUW_3011	NZ_CP008706.1	3037311	30378 6	-	WP_000787 49.1		hypothetical protein	479.9532054	1.07394025	0.277766786	3.864931625	0.0001112	0.00017901	3.747122707
ABUW_RS16040	ABUW_2189	NZ_CP008706.1	2173608	2175192	-	WP_01056890.1		siderophore biosynthesis protein	2465.579795	1.073933572	0.629328579	1.70647515	0.087196652	0.06374858	0.973167007
ABUW_RS19900	no	NZ_CP008706.1	2843929	2844051	+			glutathione S-transferase	1413323059	1.072814599	0.24182407	4.44816618	8.66E-06	153E-06	8.425308569
ABUW_RS12610	ABUW_2596	NZ_CP008706.1	2589493	2589924	+	WP_000921226.1		SPRRCC family protein	20.15594878	1.070314457	0.210581992	5.082649501	3.72E-07	7.28E-07	6.17686821
ABUW_RS11065	ABUW_2275	NZ_CP008706.1	22605 9	2261092	+	WP_0000337059.1		TetR/AcrR family transcriptional regulator	889.1953061	1.068682058	0.252662197	2.22695819	2.34E-05	3.98E-05	4.400178028
ABUW_RS15065	ABUW_2692	NZ_CP008706.1	2680084	2680629	-	WP_0010 9681.1		N-acetyltransferase	177.5177091	1.068040 1	0.242955594	4.396030089	1.10E-05	1.93E-05	4.714442691
ABUW_RS06550	ABUW_1343	NZ_CP008706.1	1355706	1356035	-	WP_000210131.1	abeS	multidrug efflux SAMr transporter AbeS	97.71146051	1.066229764	0.248366371	4.292971549	1.76E-05	3.04E-05	4.517 054 16
ABUW_RS14920	ABUW_3074	NZ_CP008706.1	3101920	3103035	-	WP_001277084.1		Rieske 2Fe-2S domain-containing protein	886.4704893	1.066165655	0.18297748	5.880740489	4.08E-09	9.08E-09	8.041914 51
ABUW_RS03605	ABUW_0732	NZ_CP008706.1	738671	739546	+	WP_001995768.1	hchA	phage tail sheath-like HchA	367.2567347	1.06304 96	0.248485141	2.478900664	1.89E-05	3.24E-05	4.48549549
ABUW_RS02785	ABUW_0567	NZ_CP008706.1	565518	566793	+	WP_00096331.1		phage tail sheath protein	162.3637995	1.061942889	0.302423798	5.11439562	0.000445687	0.000767357	3.195928377
ABUW_RS02845	ABUW_0579	NZ_CP008706.1	574092	574544	-	WP_000015691.1		head completion/stabilization protein	50.45212328	1.06 9'29014	0.300827887	3.52935702	0.000445571	0.000635985	3.96553 97
ABUW_RS08405	ABUW_1395	NZ_CP008706.1	1401004	1402059	-	WP_00037 648.1		hypothetical protein	5139063097	1.059 9 47	0.2965 9961	3.572074763	0.000354 84	0.000543799	3.26456 95
ABUW_RS09430	ABUW_1936	NZ_CP008706.1	1936251	1937 886	+	WP_000774595.1		LyxR family transcriptional regulator	72.1916392	1.0590 14781	0.287003643	3.689900134	0.000223432	0.00035 839	3.45366022
ABUW_RS08865	ABUW_1822	NZ_CP008706.1	1819655	1819749	-	WP_000510050.1		alpha-beta hydrolase	5 16.021924	1.058153959	0.16410165	7.757148898	8.89E-15	2.65E-14	0.517574 13
ABUW_RS10210	ABUW_2102	NZ_CP008706.1	2105633	2108545	-	WP_000661858.1		hypothetical protein	30.102057414	1.05818233	0.59401731	1.781002469	0.074863022	0.0913062	1.039638228
ABUW_RS06030	ABUW_1294	NZ_CP008706.1	1212595	1213688	+	WP_00019793.1		minor capsid protein	99.042859	1.055374531	0.22776848	4.633540742	3.99E-06	6.57E-06	5.12403465
ABUW_RS16155	ABUW_3321	NZ_CP008706.1	33553 8	3357433	-	WP_004571201.1		copper resistance protein multicopper oxidase	1475.605001	1.0521555	0.203223344	3.482589356	0.000496589	0.000750754	3.92423425
ABUW_RS17930	ABUW_3621	NZ_CP008706.1	3679468	3680371	-	WP_000626455.1		EamA family transporter	95.48020084	1.05 9'28688	0.262443773	4.008205927	6.12E-05	0.00010777	3.996638574
ABUW_RS11630	ABUW_2370	NZ_CP008706.1	2357546	2357875	-	WP_000610147.1		metalloreductase AnrS/Met family transcription factor	19.00867301	1.048846026	0.42613797	2.454287195	0.0184395	0.018253825	1.736273414
ABUW_RS12335	ABUW_2537	NZ_CP008706.1	2528673	2530052	-	WP_0004710954.1		L-serine ammonia-lyase	1739.075033	1.047496769	0.16885 905	6.687827516	2.42E-11	6.01E-11	10.2210253
ABUW_RS12220	ABUW_3339	NZ_CP008706.1	3373094	3374074	+	WP_000170388.1		hypothetical protein	571.6 20489	1.046327463	0.194629207	3.576004338	7.62E-08	157E-07	6.804 100348
ABUW_RS09555	ABUW_0336	NZ_CP008706.1	357587	357952	+	WP_0007 8497.1		hypothetical protein	989.230882	1.043528021	0.264356197	3.947431666	7.90E-05	0.00028957	3.889555079
ABUW_RS09730	ABUW_2003	NZ_CP008706.1	1999414	2000558	-	WP_000609268.1		hypothetical protein	482.4474793	1.04 931529	0.165 86524	3.608368995	2.82E-10	6.8E-10	9.97196541
ABUW_RS09930	ABUW_1422	NZ_CP008706.1	1413217	1418840	+	WP_000933 0282.1		hypothetical protein	18.38272202	1.041901147	0.4899907483	2.1 067302	0.033442488	0.042371002	1.372931266
ABUW_RS19335	no	NZ_CP008707.1	193232	395 16	+			hypothetical protein	214.1260308	1.041101614	0.20816 9782	5.001406142	5.69E-07	1.16E-06	0.9586073 5
ABUW_RS03720	ABUW_0758	NZ_CP008706.1	752840	753025	+	WP_001278405.1		hypothetical protein	25.83921457	1.041007428	0.403543744	2.579964395	0.000889637	0.01326204	1.735293543
ABUW_RS06205	ABUW_1271	NZ_CP008706.1	1299912	1301237	+	WP_000106166.1		AAA family ATPase	90.23406825	1.039244361	0.2836422 9	3.869136994	0.000248378	0.000388024	3.11411412
ABUW_RS09810	ABUW_2020	NZ_CP													

Table S6. RNA-seq data: Absolute and relative expression (LSP/MEP > 2-fold down)

ABUW_RS05335	ABUW_5887	NZ_CP008706.1	110936	110261	+	WP_000436801.1	cas F	type I-F CRP6P-associated endonuclease Cas1	929.8947727	-1.000005679	0.12978957	-7.70916614	1276.74	3.625E-16	0.14793664
ABUW_RS17020	ABUW_3499	NZ_CP008706.1	3546228	3547232	-	WP_000878662.1		DUF4062 domain-containing protein	243.8474462	-0.000000386	0.20189953	-0.4734381	6.55E-07	1.28E-06	5.69962455
ABUW_RS04495	ABUW_531	NZ_CP008706.1	134596	134282	-	WP_001478304.1		DUF3820 family protein	236.8897399	-1.00547339	0.95376249	-0.07994107	1.20E-09	2.75E-09	8.560667306
ABUW_RS08016	ABUW_064	NZ_CP008706.1	82957	83610	+	WP_0008616.1	pdhH	pyridoxamine 5'-phosphate oxidase	2905.41624	-1.005518991	0.15519334	-6.4791607	9.22E-11	2.23E-10	9.65165137
ABUW_RS03030	ABUW_186	NZ_CP008706.1	67839	61498	+	WP_000083551.1		phosphoribosylthiamine isomerase	194.387033	-1.007049996	0.56227259	-6.46005815	1.9E-10	2.76E-10	9.55500919
ABUW_RS17285	ABUW_3552	NZ_CP008706.1	3609997	361293	+	WP_000874105.1		dephospho-CoA kinase	110.64972	-1.008003059	0.18125262	-5.56217396	2.66E-08	5.65E-08	7.247951652
ABUW_RS00976	ABUW_0197	NZ_CP008706.1	22245	222728	+	WP_001216380.1	sab	single-stranded DNA-binding protein	540.1256462	-1.016079312	0.18861822	-7.330034708	2.30E-15	6.44E-15	0.1911418
ABUW_RS09035	ABUW_856	NZ_CP008706.1	1853329	853796	-	WP_000884019.1		winged-helix-helix transcriptional regulator	605.8915699	-1.017181086	0.1454893	-7.986075436	6.67E-10	1.60E-10	11.73992861
iRNA33	no	no	no	no	no	no	no		524.991025	-1.020552355	0.40578259	-2.51680988	0.01880293	0.01684857	1.799992516
ABUW_RS04485	ABUW_1742	NZ_CP008706.1	174189	1741932	+	WP_001037943.1		OmpH family outer membrane protein	5896.748467	-1.02145544	0.18303276	-6.069195814	1.29E-09	2.94E-09	8.53165267
ABUW_RS03860	ABUW_0787	NZ_CP008706.1	769195	769638	+	WP_0002039334.1		hypothetical protein	93.7914955	-1.024181621	0.239875682	-4.2694106	1.96E-05	3.35E-05	4.474935193
ABUW_RS0200	ABUW_0245	NZ_CP008706.1	261788	262339	+	WP_000083594.1		helic-helix transcriptional regulator	209.544663	-1.02896365	0.205898864	-4.997417888	5.81E-07	1.02E-06	9.550781977
ABUW_RS16555	ABUW_3406	NZ_CP008706.1	345484	345344	+	WP_000090638.1		homoserine O-acetyltransferase	519.018919	-1.033483999	0.19581405	-6.4633685405	1.02E-10	2.47E-10	9.607303047
ABUW_RS05625	ABUW_198	NZ_CP008706.1	3226652	3227638	-	WP_000031556.1		DUF1852 domain-containing protein	3267.508637	-1.032419502	0.41851183	-2.478110516	0.01915377	0.019127302	1.76263493
ABUW_RS17050	ABUW_3505	NZ_CP008706.1	3553931	3552670	+	WP_001548909.1		CBS domain-containing protein	4603.487446	-1.033180244	0.92319328	-10.10143	4.98E-24	2.35E-23	22.63892334
ABUW_RS00965	ABUW_0216	NZ_CP008706.1	247936	241479	+	WP_0000937378.1		hypothetical protein	437.374504	-1.033834266	0.17991197	-6.746359679	9.12E-09	2.00E-08	7.698970004
ABUW_RS07755	ABUW_1739	NZ_CP008706.1	174762	1791650	+	WP_000142003.1		Nucleo (DPE-25) protein	2.65127229	-1.034401594	0.10009016	-6.464662991	1.02E-10	2.45E-10	9.616833916
ABUW_RS01730	ABUW_0353	NZ_CP008706.1	375196	376697	+	WP_000071653.1	astD	succinylglutamate semialdehyde dehydrogenase	5426.972402	-1.034509005	0.24216054	-4.272159862	1.94E-05	3.32E-05	4.473981916
ABUW_RS05015	ABUW_0064	NZ_CP008706.1	68034	69377	+	WP_001071753.1		MATE family efflux transporter	92.5437999	-1.035788537	0.19538869	-5.302419037	1.14E-07	2.32E-07	6.63451016
ABUW_RS01040	ABUW_0083	NZ_CP008706.1	9199	91937	+	WP_000414387.1		HAD family hydrolase	278.3167724	-1.039529688	0.239731428	-4.336224067	1.45E-05	2.52E-05	4.598958499
ABUW_RS13835	ABUW_2346	NZ_CP008706.1	280022	280423	+	WP_000599396.1		YnfK family protein	355.665168	-1.039842493	0.22106638	-4.700781718	2.59E-06	4.79E-06	5.139664487
ABUW_RS1450	ABUW_2160	NZ_CP008706.1	2194231	215418	-	WP_001076388.1		O-succinylhomoserine sulphydrolase	296.1042308	-1.04168851	0.23589695	-8.424323789	3.63E-17	1.25E-16	9.53039999
ABUW_RS03455	ABUW_943	NZ_CP008706.1	941281	943774	+	WP_000520862.1		nicotinamide phosphoribosyltransferase	3526.543565	-1.041607809	0.397744788	-2.618281875	0.008837387	0.01984029	102.62783
ABUW_RS17337	ABUW_2837	NZ_CP008706.1	2847054	2848064	+	WP_000008520.1		ABC transporter permease	272.519182	-1.045841816	0.170523852	-6.133193777	8.62E-10	1.99E-09	8.701466294
ABUW_RS01845	ABUW_0376	NZ_CP008706.1	401038	401928	+	WP_000166010.1	aoeE	shikimate dehydrogenase	933.189617	-1.048291324	0.244326663	-4.290531939	1.78E-05	3.07E-05	4.519261625
ABUW_RS03030	ABUW_0006	NZ_CP008706.1	6870	7427	-	WP_001009202.1		VTT domain-containing protein	532.017163	-1.049582269	0.16040326	-6.543397382	6.01E-11	1.66E-11	9.635647144
ABUW_RS1765	ABUW_3247	NZ_CP008706.1	3277080	3278165	-	WP_000218880.1		histidinol-phosphate transaminase	765.5957587	-1.049755141	0.17434828	-6.021023785	1.73E-09	3.93E-09	8.40560745
ABUW_RS00925	ABUW_0052	NZ_CP008706.1	57176	58452	-	WP_000100767.1		dienelactone hydrolase family protein	1902.252445	-1.05010903	0.299030699	-4.053961304	6.04E-05	8.36E-05	4.077793723
ABUW_RS10080	ABUW_2076	NZ_CP008706.1	2057651	2058421	-	WP_001027948.1		SDR family oxidoreductase	273.1469539	-1.053370394	0.69483574	-1.516999165	0.10519566	0.15310403	0.14966937
ABUW_RS14985	ABUW_3087	NZ_CP008706.1	318988	319055	+	WP_00005681.1		outer membrane protein assembly factor BamD	51.7046648	-1.056489326	0.128405485	-8.227758511	1.91E-16	5.70E1074	
ABUW_RS1616	ABUW_3317	NZ_CP008706.1	3330567	3331841	+	WP_000106691.1		MFS transporter	75.3848778	-1.04059433	0.19371472	-5.49316426	3.95E-08	8.27E-08	7.08249446
ABUW_RS185	ABUW_980	NZ_CP008706.1	973895	974045	+	WP_045887671.1		DNA polymerase β -subunit gamma β	3039.780533	-1.050554109	0.40450332	-9.73493791	2.14E-22	9.33E-22	21.0301836
ABUW_RS1930	ABUW_925	NZ_CP008706.1	924022	924252	+	WP_000082897.1		AAA family ATPase	1287.461335	-1.046384846	0.094576311	-11.29610579	1.37E-29	8.17E-29	28.0877794
ABUW_RS19035	ABUW_4057	NZ_CP008706.1	34574	33366	-	WP_001016740.1	ANT(1) ⁺ is family antitoxin-specific nucleoside transferase AadaJ	653.4054952	-1.06829195	0.425782102	-2.509802819	0.01079859	0.01810478	17.9289174	
ABUW_RS03935	ABUW_016	NZ_CP008706.1	1232902	1232977	-		tRNA-Asn	114.8801338	-1.067698963	0.424823605	-2.52020712	0.019126881	0.016654869	1.800350662	
ABUW_RS04050	ABUW_0091	NZ_CP008706.1	93891	94106	-	WP_000308076.1		phosphatidylglycerophosphatase A	3233.298665	-1.070496165	0.172934232	-6.244887635	4.82E-10	1.02E-09	8.950781977
ABUW_RS01740	ABUW_0960	NZ_CP008706.1	964823	971137	+	WP_001164445.1	gyrA	DNA gyrase subunit A	5938.58875	-1.07788839	0.14743289	-7.311620432	2.64E-10	7.36E-10	0.1332922
ABUW_RS17375	ABUW_3848	NZ_CP008706.1	3913636	3917067	+	WP_000973871.1		HAD-A family hydrolase	1200.667671	-1.080573708	0.24184924	-4.467564524	7.90E-06	1.40E-05	4.853871964
ABUW_RS10880	ABUW_2611	NZ_CP008706.1	2604316	2604852	-	WP_001955449.1		hypothetical protein	488.541047	-1.081033071	0.239305926	-3.262762277	0.01027953	0.01052093	2.82041407
iRNA37	no	no	no	no	no	no	no		18.0210697	-1.084054112	0.187971048	-1.232199838	0.219744444	0.248205169	0.60586869
ABUW_RS01600	ABUW_0225	NZ_CP008706.1	244647	244691	-	WP_000109713.1		hypothetical protein	129.146697	-1.085068198	0.384604086	-2.18216019	0.004783339	0.006136256	2.19878689
ABUW_RS10230	ABUW_0339	NZ_CP008706.1	331929	331934	-	WP_001191590.1	junctional (p)ppGpp synthetase/allophanine-3'-phosphatase (3'-pyrophosphatase)	4235.696217	-1.08811977	0.19504828	-8.574233893	9.97E-18	3.49E-17	6.4571467	
ABUW_RS1435	ABUW_3382	NZ_CP008706.1	341182	342182	+	WP_000524329.1	lacX	Fe-S cluster assembly protein lacX	657.0273216	-1.088368181	0.16619309	-6.551325901	5.70E-11	1.39E-10	9.8568562
ABUW_RS19575	ABUW_4120	NZ_CP008706.1	41918	42325	+	WP_000272586.1		hypothetical protein	636.7803888	-1.090019929	0.248095008	-4.393534033	1.92E-05	1.95E-05	4.79966389
ABUW_RS14585	ABUW_3005	NZ_CP008706.1	3013970	3013999	-	WP_000084810.1		Fts family protein	553.351466	-1.090426679	0.145336301	-7.101544116	6.31E-16	1.84E-15	0.73518218
ABUW_RS01860	ABUW_2851	NZ_CP008706.1	2863987	2864328	+	WP_000968578.1		cation transporter	240.2621055	-1.090433668	0.17933868	-6.017412516	5.24E-07	1.02E-06	5.91918938
ABUW_RS15955	ABUW_2793	NZ_CP008706.1	2790664	2797374	+	WP_001255651.1		AraC family transcriptional regulator	283.0437782	-1.092056685	0.19177333	-6.088861506	1.87E-09	4.23E-09	8.373516933
ABUW_RS04005	ABUW_1903	NZ_CP008706.1	191979	191761	-	WP_000578663.1	nuvA	Holliday junction branch migration protein NuvA	1065.10194	-1.092296511	0.19295165	-7.844606409	4.36E-15	1.35E-14	0.88965623
ABUW_RS14440	ABUW_2974	NZ_CP008706.1	299022	299162	+	WP_001099229.1		hypothetical protein	85.02492676	-1.092482876	0.21514033	-4.35292959	1.34E-05	2.34E-05	4.630744163
ABUW_RS01960	ABUW_2337	NZ_CP008706.1	2395468	2396027	-	WP_000181005.1	ampD	1,6-anhydro-D-acetylmuramyl-L-alanine amidase AmpD	225.3410319	-1.095758743	0.21401716	-5.16077407	3.21E-07	6.32E-07	0.80292922
ABUW_RS05580	ABUW_140	NZ_CP008706.1	185053	186079	+	WP_000161079.1	epmB	EF-P-beta-lysylase protein EpmB	1740.176242	-1.09909657	0.114545889	-8.595267873	8.37E-22	3.55E-21	20.44077165
ABUW_RS0350	ABUW_0071	NZ_CP008706.1	75433	75821	+	WP_000107088.1		amino acid permease	2930.899722	-1.101694232	0.306357053	-3.595785451	0.000223414	0.000494884	3.302347777
ABUW_RS01705	ABUW_043	NZ_CP008706.1	1284655	1285656	-	WP_000595108.1	mfb	lytic murein transglycosylase B	1049.730951	-1.102516879	0.205577006	-5.363303044	8.18E-08	1.68E-07	6.77406718
ABUW_RS17075	ABUW_2202	NZ_CP008706.1	2197829	2199193	+	WP_000283930.1		lacS sulfamoyl cyclase desulfurase	5405.00116	-1.102960303	0.18993246	-6.86800819	6.32E-09	1.39E-08	7.8668562
ABUW_RS14315	ABUW_0688	NZ_CP008706.1	700215	702761	+	WP_000473052.1		PeptS domain-containing protein	1695.183703	-1.102991276	0.33207916	-8.332146632	0.008954548	0.001525889	2.877442832
ABUW_RS19210	ABUW_3337	NZ_CP008706.1	3369088	3371761	+	WP_001791572.1		hypothetical protein	1977.339983	-1.10455877	0.221838022	-4.985886447	6.17E-07	1.96E-06	5.424413039
ABUW_RS01880	ABUW_2029	NZ_CP008706.1	2016665	2018859	+	WP_000367699.1		hypothetical protein	10.5140711	-1.106204085	0.250800549	-4.407529195	1.05E-05	1.84E-05	4.73518217
ABUW_RS03080	ABUW_0626	NZ_CP008706.1	627624	623202	-	WP_000714606.1		dual specificity protein phosphatase family protein	422.3088543	-1.106334752	0.14965433</				

ABUW_RS1810	ABUW_2326	N2_CP008706.1	2309736	2330281	+	WP_00075973.1		1-acyl-sn-glycerol-3-phosphate acyltransferase	352.2496348	-1.177623439	0.31490588	-3.739604481	0.0008431	0.00029086	3.537323544
ABUW_RS07465	ABUW_829	N2_CP008706.1	95471	95496	-	WP_000940225.1		methionine ABC transporter ATP-binding protein	552.750896	-1.98025462	0.9420962	-6.40737795	1.48E-06	0.450996738	
ABUW_RS0565	ABUW_214	N2_CP008706.1	255395	256450	-	WP_00104730.1	cobT	nucleo-nucleotide-diphosphatidylzinc phosphoribosyltransferase	1082.848111	-1.98055251	0.90003404	-7.378282079	1.60E-06	4.54E-03	12.3429445
ABUW_RS0405	ABUW_598	N2_CP008706.1	62335	62569	+	WP_001274623.1	gntJ	chaperonin GroEL	52679.22472	-1.980747978	0.300476589	-3.925953944	8.5E-05	0.000198402	3.85857634
ABUW_RS1785	ABUW_3251	N2_CP008706.1	328762	329327	-	WP_00183380.1	baaG	BolA family non-metabolism protein baaG	2877.662122	-1.98190029	0.17102655	-6.90371273	5.00E-02	1.32E-01	10.8794207
ABUW_RS0480	ABUW_5995	N2_CP008706.1	507534	507986	-	WP_001507664.1	tolR	protein TolR	338.660339	-1.98240008	0.21184256	-5.59767116	2.17E-08	6.46E-08	7.333452919
ABUW_RS0545	ABUW_5084	N2_CP008706.1	93961	93761	+	WP_00166379.1	murI	glutamate racemase	408.222369	-1.983355083	0.9798386	-5.97900630	2.25E-09	5.06E-09	8.29584483
ABUW_RS20335	ABUW_3639	N2_CP008706.1	3907041	3907208	-	WP_000938839.1		hypothetical protein	37.2966124	-1.98351214	0.358100271	-3.304687231	0.000950791	0.0040859	2.85335763
ABUW_RS05365	ABUW_5991	N2_CP008706.1	10849	109162	+	WP_001697003.1	csy3	type I F CRISPR-associated protein Csy3	25.21553023	-1.94069456	0.17370327	-6.81057593	9.52E-02	2.43E-01	10.61439373
ABUW_RS16220	ABUW_3743	N2_CP008706.1	3798476	3799287	-	WP_000970831.1	znuB	zinc ABC transporter permease subunit ZnuB	674.2731084	-1.95848392	0.15562056	-7.60344852	2.88E-04	8.54E-04	10.06854215
ABUW_RS1789	ABUW_3678	N2_CP008706.1	373636	3737026	-	WP_000736404.1		heteromeric transposase endonuclease subunit TnsA	663.4275564	-1.987306736	0.25040821	-4.741484799	2.10E-06	3.94E-06	5.044503778
ABUW_RS14535	ABUW_2993	N2_CP008706.1	3012642	3012559	-	WP_000624780.1		hypothetical protein	95.37577849	-1.950754908	0.309456826	-3.847887038	0.00019141	0.00019471	3.717896995
ABUW_RS06700	ABUW_5373	N2_CP008706.1	1886848	188845	-	WP_00187820.1	thiS	sulfur carrier protein ThiS	575.6828887	-1.919262753	0.9186844	-7.367718048	1.74E-03	4.80E-03	12.30898302
ABUW_RS04765	ABUW_5972	N2_CP008706.1	682999	683484	-	WP_001855338.1		YaaYQc family protein	782.8635866	-1.92038993	0.90836382	-7.41096413	1.20E-03	3.42E-03	12.46597389
ABUW_RS1795	ABUW_3634	N2_CP008706.1	3592340	359589	+	WP_000381990.1		monovalent cation/H ⁺ antiporter subunit A	65.13576647	-1.930497338	0.92105639	-7.361887827	1.8E-03	5.12E-03	12.29073004
ABUW_RS10725	ABUW_5635	N2_CP008706.1	637574	638434	-	WP_000129258.1		patatin family protein	960.087583	-1.933457232	0.144909734	-8.235866565	1.78E-06	5.93E-06	5.22694531
ABUW_RS17245	ABUW_3544	N2_CP008706.1	3604014	3604090	-			IRNA-Met	935.294708	-1.94560194	0.302807078	-3.944954493	7.98E-05	0.00010245	3.88523894
ABUW_RS1935	ABUW_5688	N2_CP008706.1	3556966	3558146	-	WP_001266005.1		low temperature requirement protein A	729.4335375	-1.96551252	0.138297597	-8.65270495	5.03E-06	1.79E-07	16.7474907
ABUW_RS07660	ABUW_5658	N2_CP008706.1	556202	557037	-	WP_001875059.1	pmcC	peptide chain release factor(N)-glutamine methyltransferase	554.8787616	-1.989894379	0.9045982	-7.477489451	7.55E-04	2.19E-03	12.6595588
ABUW_RS20800	ABUW_2018	N2_CP008706.1	2009189	2009362	-	WP_000367599.1		hypothetical protein	16.8376993	-1.200947602	0.262896688	-4.569100395	4.82E-06	8.87E-06	1.05207038
ABUW_RS1995	ABUW_2255	N2_CP008706.1	22476	224108	-	WP_001183207.1		PfD domain-containing protein	353.9500428	-1.202079601	0.175876472	-6.834794813	8.2E-02	2.10E-01	10.6777801
ABUW_RS01460	ABUW_5297	N2_CP008706.1	13733	13708	+	WP_000218510.1		hypothetical protein	183.848468	-1.204461785	0.108357756	-1.11660283	1.05E-28	2.72124643	
ABUW_RS1960	ABUW_3286	N2_CP008706.1	331676	331926	+	WP_00186901.1	neB	nickel resistance MFS transporter NeB	253.7252387	-1.204788195	0.95709091	-6.5601648	7.46E-04	1.73E-09	8.761953897
ABUW_RS1665	ABUW_3828	N2_CP008706.1	3866639	3867471	+	WP_000216752.1	ghQRS	RNA glutamyl-Q(34) synthetase GluQRS	334.02173706	-1.20851187	0.21006459	-5.72600933	1.03E-08	2.24E-08	7.64975962
ABUW_RS03880	ABUW_5747	N2_CP008706.1	747339	748100	-	WP_024432496.1		helic_hmm-helic domain-containing protein	828.339515	-1.209785818	0.12905905	-9.373686384	7.00E-21	2.82E-20	19.84975089
ABUW_RS02960	ABUW_5602	N2_CP008706.1	602437	602483	-	WP_00190065.1		hypothetical protein	915.954442	-1.21020031	0.105437995	-1.14773611	1.70E-30	1.04E-29	28.29699589
ABUW_RS18785	ABUW_3858	N2_CP008706.1	3925954	3926574	-	WP_00188627.1		TerR/AcrI family transcriptional regulator	386.9665303	-1.21100023	0.155748646	-7.77727659	7.4E-05	2.27E-04	15.6439714
ABUW_RS18285	ABUW_2641	N2_CP008706.1	2639194	2639793	-	WP_000385988.1		YqZ family protein	321.9073385	-1.218882066	0.10614062	-6.924853202	4.36E-02	1.14E-01	10.94309515
ABUW_RS00725	ABUW_5146	N2_CP008706.1	105572	10669	+	WP_000123435.1	adp	aliphospho-muamylomethylphosphate beta-N-acetylglucosaminidase	902.390056	-1.224128194	0.12014102	-10.9222622	2.16E-24	1.03E-23	22.98782878
ABUW_RS19300	ABUW_4055	N2_CP008707.1	3741	34544	-	WP_025464697.1	aph(P ⁺)-b	antimicrobial cyclodextrin phosphotransferase APH(P ⁺)-b	857.8827749	-1.224774491	0.443379201	-2.76236343	0.005738456	0.007888175	9.20324363
ABUW_RS16225	ABUW_2308	N2_CP008706.1	2293182	2293394	-	WP_000309993.1		hypothetical protein	101.693497	-1.227184598	0.282032332	-4.349619024	1.37E-05	2.39E-05	4.623423043
ABUW_RS17195	ABUW_2424	N2_CP008706.1	241721	241180	-	WP_001064712.1		amino acid ABC transporter permease	61.13199628	-1.228868222	0.353332025	-3.477948609	0.000703033	3.117456979	
ABUW_RS18635	ABUW_3422	N2_CP008706.1	3468808	3469963	+	WP_00105518.1		DUF4105 domain-containing protein	2120.405216	-1.229324389	0.11810845	-10.40846411	2.27E-25	1.12E-24	20.73598798
ABUW_RS02440	ABUW_5497	N2_CP008706.1	507980	508819	+	WP_000167234.1		symmetrical bis(N ⁺ -nucleosyl) leishaphosphatase	3176.931275	-1.231405818	0.17891932	-7.91402254	7.83E-03	2.10E-02	11.6716204
ABUW_RS17250	ABUW_3545	N2_CP008706.1	3604180	3604256	-			IRNA-5	184.45452	-1.234039381	0.130425008	-3.937445255	8.24E-05	0.000104225	7.687516687
ABUW_RS19625	ABUW_2247	N2_CP008706.1	2235455	2236188	-	WP_00117527.1	ung	uracil-DNA glycosylase	36.9217704	-1.235722821	0.10250335	-10.97290045	4.8E-28	2.67E-27	26.57348874
ABUW_RS19880	ABUW_3290	N2_CP008706.1	332831	3323753	-	WP_00102192.1	thiS	threonine-IPNA ligase	22343.62419	-1.239608891	0.956197618	-7.484770699	7.17E-04	1.26E-04	12.6840265
ABUW_RS01915	ABUW_5390	N2_CP008706.1	414680	415081	+	WP_000487022.1		NUDIX domain-containing protein	857.003485	-1.239869656	0.10444607	-8.295239468	1.08E-06	3.65E-06	16.43707714
ABUW_RS03545	ABUW_5089	N2_CP008706.1	105988	107238	+	WP_000841022.1	csy1	type I F CRISPR-associated protein Csy1	2363.289366	-1.240007832	0.13881977	-9.402986367	5.30E-21	2.15E-20	10.66756164
ABUW_RS03560	ABUW_5723	N2_CP008706.1	728645	729262	+	WP_000406996.1	thrH	nal phosphoenzyme phosphatase/homoserine phosphotransferase	960.005949	-1.240225827	0.98333081	-6.656015233	2.8E-01	1.67E-01	10.7676722
ABUW_RS03055	ABUW_5629	N2_CP008706.1	633022	633045	+	WP_00088042.1	secA	peptidyl transferase subunit SecA	8746.689094	-1.24216246	0.12842158	-9.67251098	3.95E-22	1.70E-21	20.76955661
ABUW_RS18585	ABUW_3267	N2_CP008706.1	329687	3297508	-	WP_000462729.1		hypothetical protein	663.7457977	-1.242677479	0.259469364	-7.89303298	1.67E-06	3.10E-06	5.05445662
ABUW_RS16400	ABUW_2916	N2_CP008706.1	2925190	2927394	-	WP_000044166.1		TonB-dependent siderophore receptor	861.1762005	-1.24300273	0.549599846	-2.261950433	0.02378009	0.030629452	15.0686073
ABUW_RS07575	ABUW_5552	N2_CP008706.1	535898	537889	-	WP_000367186.1	cyoB	cytochrome c ubiquinol oxidase subunit I	175014.9556	-1.244668421	0.288387341	-4.317510966	1.58E-05	2.73E-05	4.560337333
ABUW_RS03770	ABUW_5769	N2_CP008706.1	57183	739253	+	WP_000205884.1		RakV/TipV domain-containing protein	958.454889	-1.246880908	0.148263481	-8.48850511	4.15E-07	1.42E-06	16.8477186
ABUW_RS04885	ABUW_5996	N2_CP008706.1	607986	608884	-	WP_000224630.1	tolQ	protein TolQ	3025.860983	-1.254730324	0.21216606	-5.91445993	3.33E-09	7.44E-09	8.128427064
ABUW_RS105105	ABUW_5249	N2_CP008706.1	426643	429149	-	WP_000159337.1		site-specific integrase	41.6342284	-1.255327394	0.274433127	-4.742166051	1.78E-06	8.62E-06	5.064492734
ABUW_RS10105	ABUW_2681	N2_CP008706.1	2671900	2672229	-	WP_00181083.1		IRNA-1	212.3053802	-1.255856724	0.18191624	-6.90349319	5.07E-02	1.32E-01	10.8794207
iRNA20	no	no	no	no	no	no	no	no	55.3701283	-1.256553637	0.295183011	-4.256863303	2.07E-05	3.54E-05	4.504996738
ABUW_RS10500	ABUW_3100	N2_CP008706.1	312446	312426	+	WP_000526665.1		aspartate 1-decarboxylase	30.1939918	-1.257752396	0.1737804	-7.24015391	4.48E-03	1.24E-02	11.09057631
ABUW_RS17750	ABUW_3645	N2_CP008706.1	3706377	3707477	-	WP_000586912.1	lpfF	LPB export ABC transporter permease LpfF	3756.955225	-1.259261331	0.19753631	-3.374840541	1.83E-04	4.34E-04	9.34625927
ABUW_RS1975	ABUW_2257	N2_CP008706.1	2242421	2243182	-	WP_000608692.1	kdsB	3-decay-memo-oculobactone cytidyltransferase	2396.503528	-1.260571895	0.0910124	-8.85072534	1.29E-42	4.189849209	
ABUW_RS03015	ABUW_5613	N2_CP008706.1	61447	614860	-	WP_00122019.1		glycophosphatidylphosphatidyltransferase	1084.957649	-1.260616285	0.125655627	-10.28523512	8.2E-25	3.99E-24	23.3990271
ABUW_RS19900	ABUW_2242	N2_CP008706.1	2238039	2232512	-	WP_00040309.1	ipsA	30S ribosomal protein S1	206336.9575	-1.261080489	0.16191552	-7.788858171	6.71E-05	2.06E-04	15.68613278
ABUW_RS05045	ABUW_828	N2_CP008706.1	830991	834040	-	WP_00094833.1		acyl-CoA thioesterase	453.736543	-1.265191338	0.97912926	-6.392363357	1.63E-06	3.89E-06	9.40050399
ABUW_RS03240	ABUW_5067	N2_CP008706.1	5177094	5179036	-	WP_000631742.1		deoxyribosyldeoxythio-phase	315.7829636	-1.265791869	0.21054587	-5.57492438	4.4E-08	9.22E-08	7.033260679
ABUW_RS09960	ABUW_2051	N2_CP008706.1	2030304	2030324	+	WP_000794351.1		hypothetical protein	978.8090979	-1.266341927	0.493017967	-2.56855518	0.016212335	0.019738895	1.86236416
ABUW_RS05020	ABUW_823	N2_CP008706.1	834302	835102	+	WP_001105859.1	mltG	endolytic transglycosylase M							

ABUW_RS05535	ABUW_101	NZ_CP008706.1	162314	163344	+	WP_000507050.1		peptidoglycan DD-metalloendopeptidase family protein	1098.6179.8	-13.9006832	0.208039454	-6.34047828	2.295-10	5.40E-10	9.267066024
ABUW_RS05070	ABUW_033	NZ_CP008706.1	044307	045329	+	WP_0019855.8.1	era	GTase Era	7341.3348.9	-13.91691946	0.843020355	-8.03208506	9.58E-16	3.07E-15	14.5286162
ABUW_RS0580	ABUW_3817	NZ_CP008706.1	3881050	3882720	-	WP_00004511.1	pgi	glucose-6-phosphate isomerase	8868.76084	-13.9883224	0.137022953	-9.63219819	5.85E-22	2.50E-21	20.60209999
ABUW_RS03905	ABUW_0797	NZ_CP008706.1	774915	775298	+	WP_000275052.1		hydropoietic protein	860.183675	-13.92080727	0.59751591	-8.26716585	1.37E-16	4.59E-16	6.33819731
ABUW_RS04650	ABUW_0548	NZ_CP008706.1	955624	956598	+	WP_000505644.1	genX	EP- <i>P</i> -lytine aminocyclase GenX	75127107305	-132.9330875	0.129708804	-9.18107948	2.40E-24	1.15E-23	22.3393021
ABUW_RS02885	ABUW_0567	NZ_CP008706.1	586563	586589	+	WP_001646506.1		branched-chain amino acid transaminase	8093.378342	-132.6797636	0.133198716	-9.56073389	2.25E-23	1.04E-22	21.98286666
ABUW_RS0770	ABUW_3248	NZ_CP008706.1	3278235	3279624	-	WP_00153727.1	hisD	histidinol dehydrogenase	4674.178727	-132.6923893	0.122428449	-8.83836233	2.25E-27	1.23E-26	25.1909449
ABUW_RS05089	ABUW_030	NZ_CP008706.1	043558	044071	+	WP_00098510.1	recO	DNA repair protein RecO	884.4678057	-132.6228083	0.173860059	-7.639638996	2.18E-14	6.49E-14	13.1877553
ABUW_RS1105	ABUW_2289	NZ_CP008706.1	2278707	2277792	+	WP_000204682.1	tmaA	tRNA (uridine[24]-C5)-methyltransferase TmaA	181.12959	-133.8028644	0.62412742	-8.731483554	2.51E-18	9.09E-18	17.04143612
ABUW_RS0814	ABUW_1671	NZ_CP008706.1	1663430	1664419	+	WP_000149843.1	tal	transaldolase	4363.726706	-133.9665836	0.2014851	-6.621816565	3.55E-11	8.75E-11	10.05799195
ABUW_RS0160	ABUW_0235	NZ_CP008706.1	254146	254745	+	WP_000458293.1		LydE family translocator	186.5974979	-133.3681915	0.257026308	-5.188890301	2.12E-17	4.22E-17	6.374687549
ABUW_RS0800	ABUW_2638	NZ_CP008706.1	2638807	2637475	+	WP_00186837.1		O-methyltransferase	184.568333	-133.9305658	0.141844898	-9.404184973	5.24E-21	2.15E-20	19.678204
ABUW_RS0255	ABUW_4047	NZ_CP008706.1	27538	28038	-	WP_000376623.1		GNA1 family N-acetyltransferase	814.7079071	-133.46178146	0.25024639	-5.33345615	9.64E-08	1.97E-07	6.705533774
ABUW_RS07935	ABUW_826	NZ_CP008706.1	822178	822537	+	WP_00120084.1		5-carboxymethyl-2-hydroxymuconate Delta-isomerase	465.8750387	-136.724658	0.145541067	-9.184518705	4.13E-20	1.60E-19	18.79588002
ABUW_RS0216	ABUW_2723	NZ_CP008706.1	2708818	2718383	+	WP_000868807.1	ahpF	alkylhydroperoxide reductase subunit F	3128.128869	-133.822682	0.296637223	-4.510324667	6.44E-06	1.15E-05	4.9390216
ABUW_RS00720	ABUW_0345	NZ_CP008706.1	959390	960334	+	WP_001265491.1	gshB	glutathione synthase	114.1209668	-134.0202093	0.93162857	-8.218923717	2.09E-16	6.19E-16	15.1600295
ABUW_RS07550	ABUW_3605	NZ_CP008706.1	3663543	3664172	+	WP_000219967.1		FH4 domain-containing protein	2103.186051	-134.0238003	0.15000368	-8.881608563	6.59E-19	2.44E-18	17.51261017
ABUW_RS07430	ABUW_3581	NZ_CP008706.1	3635374	3641293	+	WP_001294933.1	hspG	molecular chaperone HspG	5586.864606	-134.4978708	0.333233478	-4.031712386	5.54E-05	9.16E-05	4.03816426
ABUW_RS05250	ABUW_081	NZ_CP008706.1	903655	904331	+	WP_001277183.1		hydropoietic protein	181.7128939	-134.6730929	0.234604372	-5.736184346	9.68E-09	2.18E-08	17.67171545
ABUW_RS02040	ABUW_0618	NZ_CP008706.1	619721	620233	+	WP_001039542.1		DUF1643 domain-containing protein	980.7946771	-134.6885878	0.179726059	-7.488542624	6.59E-14	2.02E-13	12.69464963
ABUW_RS01000	ABUW_0205	NZ_CP008706.1	283997	283495	+	WP_001038084.1		hydropoietic protein	774.4736635	-134.6949247	0.182246861	-7.390759583	1.44E-10	4.15E-10	12.3816519
ABUW_RS02320	ABUW_0047	NZ_CP008706.1	54563	55103	+	WP_000857011.1		DNA-3'-methyladenine glycosylase I	278.1901954	-134.4934594	0.94410185	-6.940715503	3.90E-12	1.02E-11	10.9193983
ABUW_RS02905	ABUW_0591	NZ_CP008706.1	589347	590111	+	WP_001033815.1		glycoyltransferase family 2 protein	571.9132936	-133.9956408	0.128892608	-10.6445417	1.81E-26	9.43E-26	25.0254831
ABUW_RS05860	ABUW_0234	NZ_CP008706.1	1334463	1335269	-	WP_000608308.1	tpcC	indole-3-glycerol phosphate synthase TpcC	1867.184731	-135.1817042	0.147580346	-9.155062919	5.41E-20	2.08E-19	18.68193667
ABUW_RS05075	ABUW_0334	NZ_CP008706.1	945148	945348	+	WP_001985517.1		NF031034 RNA transferase	1673.609057	-132.9232327	0.190917366	-7.08328608	14.1E-12	3.78E-12	11.4225802
ABUW_RS07560	ABUW_0449	NZ_CP008706.1	1635405	1635933	+	WP_000916319.1	cyoE	prothomex IX farnesyltransferase	16407.49179	-132.9271631	0.212725058	-6.360198556	2.01E-10	4.77E-10	9.321481621
ABUW_RS05040	ABUW_0227	NZ_CP008706.1	1038194	1039070	+	WP_000842416.1		Do family serine endopeptidase	6454.739462	-135.373818	0.233230954	-5.804275956	6.44E-09	1.42E-08	7.84711956
ABUW_RS09745	ABUW_2006	NZ_CP008706.1	2002482	2002700	+	WP_001093107.1		phage coat protein	180.3457965	-135.571471	0.229806725	-5.899369167	3.65E-09	8.10E-09	8.889909454
ABUW_RS02020	ABUW_4046	NZ_CP008707.1	26577	27569	+	WP_001381892.1		TnR family NTP-binding protein	580.7819101	-136.058108	0.248948963	-5.447210058	5.15E-08	1.07E-07	6.97061622
ABUW_RS06045	ABUW_3303	NZ_CP008706.1	3337670	3337161	+	WP_000810073.1	rntD	23S rRNA (succ[6]939)-C15)-methyltransferase RntD	2977.710105	-135.693377	0.134045655	-10.7136919	4.63E-24	2.16E-23	22.65955589
ABUW_RS03340	ABUW_0784	NZ_CP008706.1	767488	767566	+	WP_0005001830.1		hydropoietic protein	30.4210436	-136.0663036	0.349130055	-3.886387936	0.00101743	3.74021954	
ABUW_RS07460	ABUW_0528	NZ_CP008706.1	611779	611474	+	WP_001005190.1		ABC transporter permease	2875.540059	-135.941838	0.17616616	-7.684786546	1.03E-14	4.59E-14	13.3381971
ABUW_RS0830	ABUW_2845	NZ_CP008706.1	2859234	2859941	+	WP_000916363.1		BCN domain-containing protein	3342.165228	-136.2546167	0.176201042	-7.732891168	1.05E-14	3.98E-14	13.49175288
ABUW_RS1050	ABUW_2334	NZ_CP008706.1	231720	231974	+	WP_001265503.1		glutathione S-transferase	32.1617447	-136.4016042	0.17751969	-7.683739425	1.55E-14	4.62E-14	13.3553802
ABUW_RS1475	ABUW_3390	NZ_CP008706.1	343104	3432722	+	WP_001077202.1		NADP-dependent glyceraldehyde 3-phosphate dehydrogenase	7930.803663	-136.6575952	0.176688708	-7.743705642	1.04E-14	3.15E-14	13.01869485
ABUW_RS04155	no	NZ_CP008706.1	829266	829565	+	WP_000667116.1		hydropoietic protein	248.6545498	-136.9005392	0.212959464	-4.61817746	1.38E-10	3.29E-10	9.482804102
sRNA10	no	no	no	no	no	no	no	no	7.596469144	-136.6726628	0.803709179	-1.701895251	0.088906329	0.10717653	9.668520224
ABUW_RS00735	ABUW_0348	NZ_CP008706.1	831367	841093	+	WP_000063665.1		D-alanine-D-alanine ligase	6865.225733	-136.8212275	0.180663689	-7.573061933	3.65E-14	1.07E-13	12.97061822
ABUW_RS03360	ABUW_0900	NZ_CP008706.1	1071238	1018922	+	WP_001216684.1	csy2	type I F-3CRBP-anchored protein Csy2	2687.563553	-136.88818968	0.15974044	-10.0810206	6.70E-24	3.14E-23	22.50307035
ABUW_RS03865	ABUW_0788	NZ_CP008706.1	769640	769858	+	WP_001277691.1		hydropoietic protein	186.3579141	-137.871839	0.263723184	-5.201946882	1.97E-07	3.95E-07	6.403402904
ABUW_RS05570	ABUW_1038	NZ_CP008706.1	116197	1163305	+	WP_000217737.1		EA domain-containing protein	3168.7544	-137.9240708	0.14920344	-10.201803295	3.52E-20	1.37E-19	18.86321943
ABUW_RS0055	ABUW_2070	NZ_CP008706.1	2055492	2051403	+	WP_000548467.1	pgqB	pyrimidoquinoline quinone biosynthesis protein PgqB	1188.533888	-137.334709	0.17832197	-7.101306773	1.34E-14	4.05E-14	13.39254498
ABUW_RS0950	ABUW_3892	NZ_CP008706.1	3960342	3960707	+	WP_001256728.1			390.3394552	-137.4263066	0.234001917	-5.872818116	4.28E-09	9.50E-09	8.022271936
ABUW_RS07490	ABUW_0334	NZ_CP008706.1	630409	632151	+	WP_001003277.1		zinc-ribon and DUF3246 domain-containing protein	1915.950553	-137.6200065	0.28859696	-6.68049636	1.25E-26	6.55E-26	25.1837587
ABUW_RS01895	ABUW_0342	NZ_CP008706.1	364687	365107	+	WP_000180306.1		endonuclease	110.1829436	-137.7422284	0.95459049	-7.047138936	1.62E-12	4.85E-12	11.13428626
ABUW_RS1790	ABUW_3810	NZ_CP008706.1	367163	3672230	+	WP_000897420.1		uroporphyrinogen-III synthase	582.3965972	-137.7648543	0.189956903	-7.252426848	4.09E-13	1.15E-12	11.94692166
ABUW_RS0360	ABUW_3163	NZ_CP008706.1	3198051	3198944	+	WP_000806837.1		cold shock domain-containing protein	1272.654885	-137.80172091	0.184704077	-7.088562865	1.36E-12	3.64E-12	11.13889862
sRNA35	no	no	no	no	no	no	no	no	126.2491262	-138.4326051	0.264919178	-5.225583956	1.74E-07	3.49E-07	6.451714573
ABUW_RS05460	ABUW_1116	NZ_CP008706.1	1136487	11378176	+	WP_001505723.1	patC	phosphate ABC transporter permease subunit PatC	468.5948287	-138.4459366	0.247345129	-5.99277768	2.18E-08	4.65E-08	7.332547107
ABUW_RS14790	ABUW_3048	NZ_CP008706.1	3074477	3075199	+	WP_001216673.1	minC	septum site-determining protein MinC	9556.020293	-138.6973307	0.132691862	-10.44457904	1.55E-25	7.75E-25	24.106983
ABUW_RS1450	ABUW_2997	NZ_CP008706.1	3016267	3019437	+	WP_000405665.1		DEAD/DEAH-box helicase family protein	5084.608077	-138.7557645	0.124241477	-11.68232307	5.63E-29	3.39E-28	27.4898003
ABUW_RS1205	ABUW_3102	NZ_CP008706.1	3156396	3156148	+	WP_000362827.1		biotin-(acyl)-CoA-carboxylase ligase	1129.429257	-139.1949675	0.13249168	-9.40738834	8.88E-26	4.47E-25	24.34960248
ABUW_RS0650	ABUW_3831	NZ_CP008706.1	3889331	3889491	+	WP_000872585.1		polysaccharide biosynthesis/export family protein	14588.7284	-139.9330408	0.148436264	-9.375333053	6.90E-21	2.78E-20	19.5595552
ABUW_RS17335	ABUW_3562	NZ_CP008706.1	3618004	3620193	+	WP_000925020.1		FUSC family protein	756.4748807	-139.9084192	0.229272907	-6.078095919	1.23E-09	2.82E-09	5.547510892
ABUW_RS0585	ABUW_1378	NZ_CP008706.1	2160189	2160789	+	WP_00056973.1		acetyltransferase	9119.420303	-139.8419563	0.156419941	-2.471830376	0.0144985	0.01478482	17.48243989
ABUW_RS0665	ABUW_3834	NZ_CP008706.1	3902322	3903544	+	WP_0003010403.1	FKBP_1	type peptidyl prolyl cis-trans isomerase	3188.6460895	-139.6666335	0.13307852	-8.48020695	1.07E-25	5.37E-25	21.70207571
ABUW_RS0635	ABUW_2807	NZ_CP008706.1	2805563	2807098	+	WP_000691971.1		FAD-binding oxidoreductase	833.7944111	-139.8434007	0.265426925	-5.25058449	1.46E-07	2.99E-07	6.52433810
ABUW_RS0355	ABUW_2751	NZ_CP008706.1	274186	2742432	+	WP_000495834.1	mshB	thymine nucleoside H							

ABUW_RS01890	ABUW_0385	N2_CP008706.1	41196	41876	+	WP_000842362.1	outer membrane lipid asymmetry maintenance protein Msd	4549.31454	-1.464340159	0.154253547	-9.493072824	2.245E-21	9.266E-21	20.03338901
ABUW_RS02900	ABUW_0590	N2_CP008706.1	58895	58930	+	WP_000898966.1	polychaetide deacetylase family protein	568.091744	-1.466440619	0.145056477	-11.77802676	5.07E-32	3.25E-31	30.4881864
ABUW_RS0250	ABUW_0255	N2_CP008706.1	26746	26890	+	WP_000595344.1	acetyl-CoA hydrolase/transferase family protein	9966.206566	-1.468049683	0.319665958	-6.035996744	3.55E-06	6.49E-06	5.97755303
ABUW_RS0395	ABUW_0724	N2_CP008706.1	72789	722340	+	WP_001081037.1	hydropothelial protein	477.554849	-1.46865911	0.248007646	-5.921892292	3.9E-09	7.02E-09	6.84720006
ABUW_RS0180	ABUW_0241	N2_CP008706.1	25879	259679	+	WP_00019180.1	homoserine kinase	9592.207024	-1.468991735	0.165537042	-8.820339193	1.9E-18	4.9E-18	17.37776598
ABUW_RS9635	no	N2_CP008706.1	930381	9331471	+	WP_085840648.1	IS4 family transposase ISAb1	9121.645012	-1.472919075	0.213999193	-8.90219378	5.0E-12	1.33E-11	10.8764836
ABUW_RS03475	ABUW_0796	N2_CP008706.1	71793	71928	+	WP_000816951.1	threonine aminase-lyase	8004.432457	-1.471891673	0.19728016	-0.757699923	5.45E-27	2.91E-26	25.53610701
ABUW_RS07718	ABUW_0679	N2_CP008706.1	657343	657780	+	WP_000993407.1	2- amino-4- hydroxy-6- hydroxymethylthiohydropentidine diphosphok	779.552183	-1.477600848	0.133318365	-11.08325056	15.1E-28	8.57E-28	27.06701978
ABUW_RS09750	ABUW_2007	N2_CP008706.1	2002712	2020056	-	WP_000367699.1	hydropothelial protein	95.6806405	-1.479196933	0.214726279	-5.383939603	7.29E-08	1.00E-07	6.823608741
ABUW_RS16350	ABUW_3161	N2_CP008706.1	318719	3188026	+	WP_001042992.1	ggC	748.4555461	-1.47964042	0.212633831	-6.958619239	3.44E-12	9.01E-12	11.04527521
ABUW_RS16455	ABUW_3386	N2_CP008706.1	3425871	3426890	+	WP_000578593.1	beta-N- acetylhexosaminidase	549.255882	-1.482200167	0.186228903	-10.8801612	1.43E-27	7.84E-27	26.10665934
ABUW_RS03670	ABUW_0745	N2_CP008706.1	744709	746976	+	WP_000005162.1	N-6 DNA methylase	4542.627258	-1.4832829347	0.194160245	-7.638355333	2.23E-14	6.64E-14	13.17793192
ABUW_RS16240	ABUW_3747	N2_CP008706.1	3803233	3805023	+	WP_001090284.1	arginine-- tRNA ligase	5864.716431	-1.483104648	0.107556571	-10.788229918	3.00E-43	3.03E-42	4.151855737
ABUW_RS03835	ABUW_0783	N2_CP008706.1	76718	767484	+	WP_000524483.1	hydropothelial protein	36.90226788	-1.491402872	0.35513159	-4.199579011	2.67E-05	4.53E-05	4.343901798
ABUW_RS04995	ABUW_0108	N2_CP008706.1	129513	1303097	-	WP_0010488111.1	cysW	95.9065251	-1.4933288146	0.222556074	-6.697678703	2.0E-11	5.28E-11	10.77276608
ABUW_RS18730	ABUW_3847	N2_CP008706.1	3915656	3919369	+	WP_000807599.1	lona13-demethylubiquinone 3-O- methylubiquinase/2- octaprenyl-6- hydrox	1287.155924	-1.4935833338	0.203708663	-7.331957898	2.27E-19	6.35E-19	12.19722627
ABUW_RS04800	ABUW_0979	N2_CP008706.1	99191	992000	+	WP_0001910711.1	alpha/beta hydrolase	2624.615581	-1.496555491	0.154078278	-9.127959298	2.66E-22	1.95E-21	20.93930216
ABUW_RS03675	ABUW_0748	N2_CP008706.1	74719	747324	-	WP_000370455.1	hydropothelial protein	333.9494267	-1.496520049	0.13617637	-11.0058142	3.55E-28	1.99E-27	26.70114992
ABUW_RS18865	ABUW_2235	N2_CP008706.1	2224254	2225396	+	WP_000993387.1	cell division protein ZapE	5597.54974	-1.501942193	0.148992169	-9.137894	3.75E-34	1.79E-33	22.74714697
ABUW_RS02105	ABUW_0631	N2_CP008706.1	633698	634098	-	WP_000446411.1	MKS family MFS transporter	2634.822198	-1.502399163	0.15901508	-9.444016685	3.52E-21	1.44E-20	19.84183751
ABUW_RS11020	ABUW_2286	N2_CP008706.1	2271859	2272147	-	WP_001014233.1	Lsp_Kin/Clgand binding domain-- containing protein	212.5627709	-1.503863895	0.20187867	-7.474558887	7.79E-14	2.24E-13	12.64975198
ABUW_RS07720	ABUW_0581	N2_CP008706.1	668840	669749	+	WP_000891022.1	kdpA	956.6843097	-1.505521687	0.216962915	-6.939017429	3.95E-12	1.03E-11	10.76276278
ABUW_RS11605	ABUW_2365	N2_CP008706.1	2352488	2354053	+	WP_000886809.1	ahpF	11671.96534	-1.508412723	0.204060262	-7.392018693	1.45E-13	4.1E-13	12.38615918
ABUW_RS19875	ABUW_3897	N2_CP008706.1	3864832	3865359	+	WP_000621480.1	hxt	2927.398254	-1.509263899	0.172517786	-8.7484153931	2.16E-18	7.85E-18	19.510304
ABUW_RS19885	no	N2_CP008706.1	674650	675740	+	WP_085840648.1	IS4 family transposase ISAb1	463.7116897	-1.510742228	0.24981335	-6.050015861	1.45E-09	3.30E-09	4.84848606
ABUW_RS16320	ABUW_2266	N2_CP008706.1	2250165	2251168	+	WP_001096103.1	phosphotransferase	821188.384	-1.511818067	0.162798877	-9.89281081	4.47E-23	2.02E-22	21.69464863
ABUW_RS08945	ABUW_2028	N2_CP008706.1	2016435	2016563	-	WP_001093107.1	phage coat protein	179.810743	-1.512446097	0.25807914	-6.0098159	1.84E-09	4.9E-09	8.378823718
ABUW_RS18550	ABUW_2648	N2_CP008706.1	2646817	2647356	-	WP_000179337.1	HAD-1A family hydrolase	1691.552471	-1.513354065	0.178097778	-8.497214107	1.94E-17	6.73E-17	16.7198494
ABUW_RS18295	ABUW_3758	N2_CP008706.1	381991	3819412	+	WP_000421542.1	DcdA family protein	12827.60480	-1.5144227	0.140670333	-10.75878784	5.39E-27	2.89E-26	25.53919216
ABUW_RS16595	ABUW_2383	N2_CP008706.1	2370150	2371034	+	WP_000472481.1	hydropothelial protein	175.8018632	-1.515055806	0.19479192	-7.774693167	7.55E-15	2.31E-14	13.6838082
ABUW_RS16505	ABUW_3311	N2_CP008706.1	332765	3333325	+	WP_001075712.1	DUF177 domain-- containing protein	61200.7249	-1.516505668	0.218227421	-6.54943194	3.67E-12	9.60E-12	11.0274577
ABUW_RS04745	ABUW_082	N2_CP008706.1	819475	8195240	+	WP_001077595.1	histidine phosphorylase family protein	677.3377208	-1.517381692	0.154623567	-0.109431956	1.0E-33	3.77E-33	32.67145745
ABUW_RS1070	ABUW_3009	N2_CP008706.1	3555321	3555902	+	WP_000865305.1	gapG	1542.303807	-1.518162443	0.146430195	-0.37772601	3.03E-25	1.54E-24	23.81247928
ABUW_RS11440	ABUW_2352	N2_CP008706.1	2334699	2335128	+	WP_00191103.1	dapC	9170.854349	-1.519633465	0.11380701	-13.3527245	1.9E-40	1.04E-39	38.96296666
ABUW_RS05050	ABUW_0030	N2_CP008706.1	3196	36491	-	WP_000073454.1	pyrimidine permease	752.0950583	-1.519759189	0.200653582	-7.57404811	3.62E-14	1.06E-13	10.97499161
ABUW_RS03965	ABUW_0810	N2_CP008706.1	785559	789101	+	WP_001019703.1	hydropothelial protein	738.1219905	-1.521069139	0.269940376	-5.633493965	1.77E-08	3.79E-08	7.42106079
ABUW_RS16045	ABUW_2160	N2_CP008706.1	2175766	2176230	-	WP_000186516.1	Cys- tRNA(Pro) deacylase	329.024071	-1.524402644	0.19448261	-9.560484806	1.17E-21	4.92E-21	20.3080349
ABUW_RS03565	ABUW_0097	N2_CP008706.1	111810	1110771	+	WP_001041805.1	thiamine phosphate synthase	617.131998	-1.525991025	0.144981183	-10.52544363	6.60E-26	3.35E-25	34.7495519
ABUW_RS05050	ABUW_1026	N2_CP008706.1	148468	1494013	+	WP_001010719.1	gamma carboxyl anhydride family protein	927.0749455	-1.527822561	0.128794461	-11.86248335	1.85E-32	1.2E-31	20.91721663
ABUW_RS18440	ABUW_2148	N2_CP008706.1	2132222	2133551	+	WP_001024697.1	YbaB/Elc family nucleoid-associated protein	2580.891171	-1.52788386	0.16937252	-9.02073054	1.87E-19	7.09E-19	16.9435376
ABUW_RS18195	ABUW_2924	N2_CP008706.1	2934229	2935563	+	WP_000859908.1	D- serine aminocyclase	372.3887111	-1.528586379	0.168603079	-9.637810226	5.54E-22	2.38E-21	20.24321204
ABUW_RS02565	ABUW_0522	N2_CP008706.1	530749	532620	+	WP_001043524.1	5-thioindole(3,4)-methyltransferase MsmOFA/2- dependent 5- carboxymethyl	1598.72618	-1.528881652	0.127504422	-11.99081003	3.97E-33	2.67E-32	31.57348874
ABUW_RS19760	ABUW_3629	N2_CP008706.1	3687222	3688718	+	WP_000607680.1	flwW	2618.674001	-1.529186641	0.200176216	-7.639202461	2.16E-14	6.50E-14	11.9870864
ABUW_RS04280	ABUW_0872	N2_CP008706.1	812214	815054	+	WP_00184466.1	2- oxoglutarate dehydrogenase E1 component	54226.3156	-1.532995951	0.26193897	-5.83951691	5.24E-09	1.9E-08	7.35554201
ABUW_RS18915	ABUW_2345	N2_CP008706.1	2332824	2334327	+	WP_001997711.1	ladA	8234.640347	-1.530223661	0.199887509	-0.753377727	2.89E-37	2.33E-36	38.63264498
ABUW_RS17495	ABUW_3049	N2_CP008706.1	3075270	3076082	+	WP_001074362.1	minD	19000.91287	-1.531969307	0.161973607	-10.13207541	3.98E-24	1.88E-23	22.7235382
ABUW_RS17800	ABUW_3655	N2_CP008706.1	3715718	3718556	+	WP_000780326.1	glnK	3489.939907	-1.532105883	0.18791078	-7.744933747	9.56E-15	2.91E-14	15.53610701
ABUW_RS01860	ABUW_0337	N2_CP008706.1	358322	359551	+	WP_000709118.1	ITF5 transporter	4481333756	-1.5325959707	0.42167361	-6.038973953	0.000272772	0.000244487	3.372150660
ABUW_RS17595	ABUW_3614	N2_CP008706.1	3672235	3673162	+	WP_031444408.1	hemC	923.302193	-1.53338843	0.18221681	-8.41232567	3.92E-17	1.34E-16	16.8728952
ABUW_RS18200	ABUW_2486	N2_CP008706.1	2482159	2482881	-	WP_001043431.1	UTRA domain-- containing protein	329.023048	-1.535542947	0.17102842	-8.541703066	3.83E-19	1.44E-18	17.8437631
ABUW_RS01055	ABUW_0031	N2_CP008706.1	38742	39476	+	WP_000250576.1	ppo	7088.517614	-1.539419227	0.243667914	-6.317660791	2.66E-10	6.24E-10	9.24084541
ABUW_RS18270	ABUW_3349	N2_CP008706.1	3348466	33485308	+	WP_001054081.1	hydropothelial protein	348.1452396	-1.541185109	0.189316783	-8.10714034	3.93E-16	1.29E-15	18.9484929
ABUW_RS18445	ABUW_3180	N2_CP008706.1	3207190	3210809	+	WP_001085884.1	bfnS	9898.999019	-1.541935364	0.186387298	-8.27274951	13.1E-16	4.39E-16	35.3575348
ABUW_RS18495	ABUW_2363	N2_CP008706.1	2349370	2350311	+	WP_001090738.1	sensor/histidine kinase BfnS	4816.07673	-1.542210685	0.156669209	-9.906869131	3.88E-23	1.76E-22	21.57448733
ABUW_RS05990	ABUW_0531	N2_CP008706.1	163763	165520	+	WP_001020910.1	ladA	494.724398	-1.543546862	0.179738106	-5.88832195	8.82E-18	3.1E-17	16.50723661
ABUW_RS16055	ABUW_0034	N2_CP008706.1	40420	41930	+	WP_001050643.1	efflux/RND transporter/periplasmic adaptor subunit	6267.816798	-1.545597472	0.23159803	-6.67525088	2.47E-11	6.1E-11	12.0215033
ABUW_RS08875	ABUW_3024	N2_CP008706.1	319883	320371	+	WP_001845335.1	hydropothelial protein	6328.296387	-1.549000975	0.162991936	-9.503549458	2.03E-21	8.4E-21	20.075204
ABUW_RS18785	ABUW_3452	N2_CP008706.1	3498829	3499993	+	WP_000128078.1	hydropothelial protein	7514.18991	-1.550002398	0.12784617	-0.12467324	7.82E-34	5.44E-33	32.2644011
ABUW_RS18675	ABUW_3836	N2_CP008706.1	3903833	3905385	+	WP_01056805.1	msuI	945.239932	-1.550770633	0.174192291	-8.9031631	5.43E-19	2.02E-18	17.

ABUW_RS03075	ABUW_0625	NZ_CP008706.1	626535	627605	+	WP_00200186.1		SPOR domain-containing protein	24.96.995078	-1627047654	0.129349.109	-12.57873.01	2.765-.36	2.105-.35	34.67778071
ABUW_RS02029	ABUW_0043	NZ_CP008706.1	50718	51620	+	WP_000843074.1		lyfR family transcriptional regulator	455.1460253	-1632767872	0.180.88.12	-1.82964.65	1.096-.43	1.172-.42	41.76447.05
ABUW_RS04146	ABUW_0845	NZ_CP008706.1	825355	825981	-	WP_001986352.1		phosphatase PAP2 family protein	54.0.906078	-1632229424	0.93247.10	-9.9995.9034	1.555-.23	7.85-.23	22.45006.98
ABUW_RS04145	ABUW_2969	NZ_CP008706.1	286249	2864271	+	WP_000243371.1		BCCT family transporter	7253.254778	-1633230.87	0.3366.0078	-0.48.994329	1.225-.06	2.31-.06	5.06368.002
ABUW_RS04890	ABUW_0997	NZ_CP008706.1	908708	909195	-	WP_001273591.1	yhgC	tol-pal-system-associated acyl-CoA thioesterase	17.07.351791	-163331.091	0.2176.46927	-7.506797421	6.065-.14	1.777-.13	12.73203.073
ABUW_RS0500	ABUW_3992	NZ_CP008706.1	3697997	3699352	-	WP_000556127.1	memE	uridine-5-carboxymethylcarbamoyl synthase GTPase	9.11539662	-1634907854	0.33440.0559	-12.94442.33	4.815-.34	3.405-.33	32.46852.938
ABUW_RS0920	ABUW_3896	NZ_CP008706.1	395493	3954665	-	WP_000994663.1	puE	5-[carboxymethylcarbamoyl]ribonucleotide mutase	2690.694069	-163520.956	0.172.03587	-9.500204028	2.095-.21	8.875-.21	20.08.9609
ABUW_RS0725	ABUW_3848	NZ_CP008706.1	3948859	3949176	-	WP_000737570.1		thiol:disulfide interchange protein DsbA/DsbL	7985.88479	-1635334079	0.240834.436	-6.7902834.14	1.02E-.11	2.84E-.11	10.54688.06
ABUW_RS0960	ABUW_2874	NZ_CP008706.1	2882871	2884.884	-	WP_000895449.1		membrane protein	3855.525956	-163577635	0.81978342	-8.993794072	2.395-.19	9.03E-.19	8.0443.025
ABUW_RS0650	ABUW_0317	NZ_CP008706.1	339222	343076	+	WP_000768943.1		VWA domain-containing protein	3920.51119	-1638797646	0.65068284	-10.5672421	4.235-.26	2.07E-.25	24.66354027
ABUW_RS10775	ABUW_2420	NZ_CP008706.1	2407492	2408358	-	WP_002009987.1		cysteine ABC transporter substrate-binding protein	349.4307749	-1639144446	0.61993361	-10.1859205	4.575-.24	2.95E-.23	22.66554625
ABUW_RS0630	ABUW_3421	NZ_CP008706.1	3468384	3468993	+	WP_000312548.1		dihydrofolate reductase	1024.604444	-16409.17631	0.21395717	-7.689552777	1.48E-.14	4.43E-.14	13.35359627
ABUW_RS0530	ABUW_3199	NZ_CP008706.1	3228003	3228875	-	WP_0005728.9		LyfR family transcriptional regulator	136.048703	-1642022.54	0.27183044	-6.040109387	1.545-.09	3.50E-.09	8.45593.956
ABUW_RS02925	ABUW_0595	NZ_CP008706.1	593061	594.88	+	WP_000598629.1	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	1070.862239	-1642907606	0.95822372	-8.84.0279935	9.46E-.19	3.48E-.19	17.45842076
ABUW_RS07655	ABUW_567	NZ_CP008706.1	555114	555202	+	WP_000648007.1	prfA	peptide chain release factor 1	943.94872	-1642918753	0.91862687	-9.05874731	1.325-.19	5.03E-.19	8.29843201
ABUW_RS0930	ABUW_3280	NZ_CP008706.1	3310652	3319033	+	WP_000703078.1	pheT	phenylalanine--tRNA ligase subunit beta	9180.61946	-1644249325	0.97171806	-9.835692049	7.905-.23	3.53E-.22	2145225259
ABUW_RS02445	ABUW_0498	NZ_CP008706.1	508862	509305	-	WP_00054366.1		DUF2147 domain-containing protein	977.7706001	-16445.9805	0.127.6785	-9.5262009.1	17.8E-.21	7.90E-.21	20.14874.05
ABUW_RS04180	ABUW_0852	NZ_CP008706.1	832220	833491	+	WP_00066842.1	serS	serine--tRNA ligase	4697.708007	-16459.981	0.20193262	-8.17304003	3.01E-.15	9.90E-.15	10.64354481
ABUW_RS05500	ABUW_104	NZ_CP008706.1	194722	1947555	+	WP_00187604.1	mmrA	RNA 3'-terminal nucleoside triphosphate synthase MmrA	2729.99985	-164695.96	0.90506632	-9.198044486	7.535-.20	2.89E-.19	9.530912.9
ABUW_RS03010	ABUW_0903	NZ_CP008706.1	6979	67956	+	WP_00175073.1		hlye ac/sodium symporter family protein	568.9669359	-164693.031	0.89595999	-8.69357675	3.34E-.19	1.37E-.19	16.86327943
ABUW_RS05515	ABUW_1027	NZ_CP008706.1	1149110	1150261	-	WP_000187255.1	macC	D-alanyl-D-alanine:carboxypeptidase PBPS6	2881057605	-1647527524	0.98746421	-8.728649421	2.58E-.19	9.30E-.19	17.0315.0705
ABUW_RS05065	ABUW_0332	NZ_CP008706.1	943403	944095	+	WP_000160699.1	dsuC	ribonuclease II	2696.635988	-1650454865	0.9893242	-8.760690399	1.94E-.19	7.05E-.19	17.518.908
ABUW_RS01385	ABUW_0282	NZ_CP008706.1	299961	299993	+	WP_000842465.1	ftsL	cell division protein FtsL	617.0405847	-1651020727	0.156958379	-10.52075548	6.935-.26	3.51E-.25	24.45460288
ABUW_RS0385	no	NZ_CP008706.1	76878	769238	+	WP_000393744.1		hydropathetic protein	126.463478	-1653728869	0.29.02893	-5.682352.96	1.33E-.08	2.88E-.08	7.546069752
ABUW_RS0730	ABUW_3441	NZ_CP008706.1	348500	348649	+	WP_000368721.1		hydropathetic protein	1037.996844	-1654664.91	0.154057734	-10.74054592	6.57E-.27	3.48E-.26	25.45842076
ABUW_RS0560	ABUW_2173	NZ_CP008706.1	254803	215402	-	WP_000103942.1		histidine phosphatase family protein	200.6379682	-1657138239	0.2246.06204	-7.354060238	2.555-.13	7.90E-.13	12.4874.05
ABUW_RS02930	ABUW_895	NZ_CP008706.1	896236	896805	-	WP_0001037.8		TerR(AcR) family transcriptional regulator	616.595987	-1658830201	0.33710097	-4.920708029	8.82E-.07	1.65E-.06	5.7829.9056
ABUW_RS03035	ABUW_0617	NZ_CP008706.1	61842	6187.11	+	WP_000372732.1	tpbB	tyrosine phosphatase subunit beta	4653.874.94	-1658438396	0.2076032.8	-7.9933173.8	1.31E-.15	4.8E-.15	34.7882372
ABUW_RS0955	ABUW_3893	NZ_CP008706.1	3960729	396189	+	WP_000823196.1		glutathionylglutamine synthase family protein	344.646072	-1659728678	0.23963.937	-6.50590645	4.32E-.12	1.0E-.11	10.94692.056
ABUW_RS01005	ABUW_0266	NZ_CP008706.1	283550	284695	-	WP_000153036.1		TcC family protein	359.0277373	-166204.1761	0.245689392	-6.759956311	1.38E-.11	3.47E-.11	10.50467053
ABUW_RS0985	ABUW_2259	NZ_CP008706.1	2244205	2245932	-	WP_001070729.1	msbA	Igpd A export permease/ATP-binding protein MbsA	5249.734235	-166307.647	0.14064464	-11.8651084	1.60E-.32	1.8E-.31	30.9281799
ABUW_RS09140	ABUW_0287	NZ_CP008706.1	305929	305261	+	WP_000189598.1		hydropathetic al protein	874.7863573	-16632.9738	0.29236903	-10.96776993	1.86E-.38	1.62E-.37	36.819.641
ABUW_RS01915	ABUW_2719	NZ_CP008706.1	2706678	2710729	+	WP_000052794.1	ahpC	peroxiredoxin	5516.4.8056	-1663945341	0.247200876	-6.73114662	1.68E-.11	4.22E-.11	10.37468735
ABUW_RS0745	ABUW_3644	NZ_CP008706.1	3705307	3706377	+	WP_00088.004.1	lpgS	LPS export ABC transporter permease LptG	17.2.31678	-1672554627	0.21963494	-7.88449.939	2.32E-.15	9.08E-.15	10.0419.614
ABUW_RS01180	ABUW_2488	NZ_CP008706.1	248413	2485228	+	WP_001039492.1	poIR	TerR(AcR) family transcriptional regulator PoIR	224.0974986	-167265.972	0.9778728	-8.457675967	2.73E-.17	9.40E-.17	10.626872.0
ABUW_RS07570	ABUW_3609	NZ_CP008706.1	366443	3668769	+	WP_00080.927.1		H NS histone family protein	80.14.859494	-1673396551	0.22697.97	-7.37.87477	1.09E-.13	4.77E-.13	12.32148.02
ABUW_RS00515	ABUW_3305	NZ_CP008706.1	3338002	33389.9	-	WP_000072604.1	cysM	cysteine synthase CysM	1062.487223	-1678375583	0.299.0749	-7.63.95751	2.31E-.14	6.88E-.14	12.9124.96
ABUW_RS0655	ABUW_3832	NZ_CP008706.1	389496	3899924	+	WP_00159772.1		low molecular-weight phosphotyrosine protein phosphatase	2947.9.0356	-167949379	0.1979836	-12.0368735	3.01E-.33	2.04E-.32	31.69036983
ABUW_RS07245	ABUW_486	NZ_CP008706.1	473140	473778	+	WP_000509096.1		TerR(AcR) family transcriptional regulator	44.50382304	-1679534268	1.99902634	-1.399729761	0.916942258	0.188.98574	0.725452906
ABUW_RS01465	ABUW_0298	NZ_CP008706.1	1.9069	322544	+	WP_00189947.1	gmb	glutamate synthase large subunit	13107.44394	-1682464903	0.26.94057	-6.423782961	1.33E-.10	3.9E-.10	9.48626937
ABUW_RS0690	ABUW_3491	NZ_CP008706.1	354064	3540796	+	WP_000046492.1		HspJ type I effector protein	917.7.65219	-1682735958	0.20351084	-8.268576953	6.96E-.16	5.43E-.16	10.3439.018
ABUW_RS04465	ABUW_0910	NZ_CP008706.1	903722	905053	-	WP_00198641.1		MFS transporter	3451342625	-168475.055	0.237369745	-7.097582532	1.27E-.12	3.42E-.12	11.646597389
ABUW_RS02445	ABUW_0050	NZ_CP008706.1	55993	57027	-	WP_00118586.1	nutY	ADG-specific adenine glycosylase	600.73.9532	-16849405	0.17409725	-9.633229396	5.79E-.22	2.48E-.21	20.00544832
ABUW_RS01965	ABUW_0278	NZ_CP008706.1	219.93	29701	-	WP_000864822.1		glutamate--tRNA ligase	3986.287.89	-168603.9297	0.132509645	-12.72389054	4.36E-.37	3.37E-.36	35.4723701
ABUW_RS0965	ABUW_3895	NZ_CP008706.1	396292	39648.97	+	WP_000952288.1	guaD	guanine deaminase	1360.433936	-168667.0396	0.9467.678	-8.684.61994	4.56E-.16	1.62E-.16	16.79044499
ABUW_RS04315	ABUW_0881	NZ_CP008706.1	882.04	883147	+	WP_000072941.1	tpbB	tyrosinase--RNA ligase	4321.733557	-169143692	0.91925526	-8.492852351	2.02E-.17	6.99E-.17	16.5552282
ABUW_RS07310	ABUW_3557	NZ_CP008706.1	361919	361958	+	WP_00095425.1	recN	DNA repair protein RecN	22.17.870703	-16927.6225	0.159076929	-12.4394064	1.60E-.35	1.9E-.34	33.9217699
ABUW_RS02580	ABUW_0525	NZ_CP008706.1	533465	534079	+	WP_000645707.1		separation protein hsp2	1089.803304	-1695480248	0.1057.016	-12.49334998	8.92E-.36	6.07E-.35	34.216811
ABUW_RS01315	ABUW_2707	NZ_CP008706.1	2688875	269148	+	WP_000377525.1		copper-translocating P-type ATPase	1657.206891	-1696834958	0.236928273	-7.16.908663	7.96E-.13	2.9E-.12	11.60554625
ABUW_RS0575	ABUW_3410	NZ_CP008706.1	34575.2	3458387	+	WP_00196409.1		hydropathetic protein	473.8246607	-1697034228	0.64342065	-12.32736274	5.30E-.25	2.59E-.24	23.5887024
ABUW_RS01910	ABUW_0267	NZ_CP008706.1	284668	286.85	+	WP_001275655.1		efflux RND transporter/periplasmic adaptor subunit	447.2851277	-1697638331	0.17.958097	-9.893527897	4.44E-.23	2.01E-.22	21.69689034
ABUW_RS08630	ABUW_0772	NZ_CP008706.1	769886	772744	+	WP_000808358.1	ptpP	phosphoenolpyruvate--protein phosphatase	936.868398	-1708982529	0.1799.744	-9.4956970.14	2.19E-.21	9.04E-.21	20.04383.07
ABUW_RS05175	ABUW_0504	NZ_CP008706.1	963176	964309	+	WP_000573844.1		glutamate 5-kinase	9463.86901	-1709262694	0.97498703	-8.56455.907	4.95E-.18	1.76E-.17	16.75448733
ABUW_RS07940	ABUW_3685	NZ_CP008706.1	3742344	3744.980	+	WP_000990004.1		OpdO family outer membrane porin	6457.852532	-1710214754	0.233494973	-7.32441988	2.40E-.13	6.70E-.13	12.73932.02
ABUW_RS07585	ABUW_3612	NZ_CP008706.1	36709.9	3671454	-	WP_001230221.1		hydropathetic protein	9005.922334	-1710558258	0.11533988	-15.070.0906	2.55E-.51	3.51E-.50	49.45460288
ABUW_RS05255	ABUW_0282	NZ_CP008706.1	1043043	10430557	+	WP_00086102.1		hydropathetic protein	2051786042	-1710335291	0.2416407	-7.097496506	1.27E-.12	3.42E-.12	10.94697389
ABUW_RS02770	no	NZ_CP008706.1	563924	564586	-			ATP-binding protein	4696.163082	-171266253	0.219896794	-8.006957426	1.8E-.15	3.76E-.15	14.24162.16
ABUW_RS08035	ABUW_646	NZ_CP008706.1	840874	843.944	-	WP_0005270.15		TorB-dependent receptor	2039.817431	-1710957928	0.37667525	-4.5033204.0	5.		

ABUW_RS14200	ABUW_2925	N2_CP008706.1	2935728	2937359	-	WP_01087641.1	inorganic phosphate transporter	8412.527363	-1.81489066	0.170770254	-0.6276752	2.225e-26	1.155e-25	24.9383024
ABUW_RS04765	ABUW_800	N2_CP008706.1	1929209	195008	-	WP_000083236.1	TonB-dependent siderophore receptor	957.479374	-1.81065918	0.266889771	-6.80479544	1.025e-11	2.595e-11	9.58670024
ABUW_RS1895	ABUW_3478	N2_CP008706.1	3524967	3528299	+	WP_000027305.1	RaeReg family ribonuclease	18383.0286	-1.81628751	0.218386282	-8.432699311	3.385e-17	1.161e-16	15.95054401
ABUW_RS1906	ABUW_924	N2_CP008706.1	183848	140231	+	WP_000095974.1	DNA topoisomerase I subunit B	2496.763635	-1.818539505	0.93806106	-11.81077945	1.235e-28	7.036e-28	27.93044627
ABUW_RS5885	ABUW_3271	N2_CP008706.1	3304238	3304787	-	WP_000501883.1	YggJ family protein	2555.557548	-1.819873799	0.1200249	-5.13873007	8.996e-52	1.265e-50	49.89606245
ABUW_RS0850	ABUW_972	N2_CP008706.1	90661	91958	+	WP_01028416.1	WS (RNA [guanylyl-WSs, NGS]) methyltransferase	870.474966	-1.822069463	0.130575439	-0.95415566	2.875e-44	3.18e-43	42.50723961
ABUW_RS1775	ABUW_3045	N2_CP008706.1	3071969	3072122	-	WP_01002415.1	CmaA family protein	37602.89175	-1.825317414	0.239420459	-7.62389998	2.455e-14	7.305e-14	81.0867774
ABUW_RS04395	ABUW_0699	N2_CP008706.1	893229	893865	-	WP_000193853.1	DOMON-like domain-containing protein	886.3264542	-1.826007692	0.172889091	-0.5739609	3.945e-26	2.025e-25	24.69484863
ABUW_RS1605	ABUW_182	N2_CP008706.1	263161	2165479	-	WP_000419597.1	TonB-dependent receptor	783.270953	-1.826598843	0.340148388	-5.370005882	1.875e-08	1.625e-07	6.790484985
ABUW_RS1635	ABUW_170	N2_CP008706.1	3195608	3196150	-	WP_000276693.1	NADH-quinone oxidoreductase subunit NuoL	12274.49772	-1.827288868	0.276647416	-6.60518147	3.975e-11	9.775e-11	80.010544
ABUW_RS0050	ABUW_103	N2_CP008706.1	114543	116394	+	WP_000011219.1	phosphatidylethanolamine decarboxylase	1809.174178	-1.827360911	0.163358099	-11.8622783	4.765e-29	2.785e-28	27.55599552
ABUW_RS1770	ABUW_3637	N2_CP008706.1	3696263	3697402	+	WP_000063593.1	threonine synthase	13469.92852	-1.828716279	0.197452608	-9.261540243	2.025e-20	7.845e-20	91.001795
ABUW_RS1850	ABUW_3811	N2_CP008706.1	3872632	3874338	-	WP_01183019.1	dsf	1286.21284	-1.829294887	0.260433765	-7.02403184	2.165e-12	5.78e-12	1124336389
ABUW_RS1854	ABUW_3810	N2_CP008706.1	3871969	3872583	+	WP_000486251.1	aspartate/lysine/isomalic aminotransferase	8779.917376	-1.829753452	0.185060207	-9.887341448	4.725e-23	2.135e-22	21.6718204
ABUW_RS1770	ABUW_3641	N2_CP008706.1	3701009	3702430	+	WP_000840548.1	sigma-54-dependent Fis family transcriptional regulator	2381.890296	-1.830105651	0.2273662	-8.049395927	8.325e-16	2.875e-15	14.57348874
ABUW_RS1630	ABUW_3189	N2_CP008706.1	3195090	3195608	-	WP_0102578792.1	NADH-quinone oxidoreductase subunit J	1911.80451	-1.831933786	0.2614751	-7.00626193	2.455e-12	6.485e-12	11.89176748
ABUW_RS1870	ABUW_3250	N2_CP008706.1	3202313	3218569	-	WP_000357156.1	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	9301.652407	-1.832403486	0.173256351	-0.57625582	3.845e-26	1.985e-25	24.70333481
ABUW_RS1415	ABUW_0288	N2_CP008706.1	306254	307058	+	WP_01095041.1	methyltransferase domain-containing protein	1953.00014	-1.83459153	0.14164642	-0.91735592	2.025e-38	1.645e-37	36.75195165
ABUW_RS1450	ABUW_0295	N2_CP008706.1	315037	315066	+	WP_000643712.1	shikimate kinase ArkK	859.921992	-1.835340672	0.105436002	-0.54707102	8.155e-42	7.855e-41	40.9151034
ABUW_RS0945	ABUW_037	N2_CP008706.1	830161	830646	+	WP_000192520.1	DUF3465 domain-containing protein	3313995099	-1.837199055	0.2107797	-6.82444173	4.625e-16	1.655e-17	46.79251806
ABUW_RS1840	ABUW_3727	N2_CP008706.1	3785438	3786652	+	WP_000372838.1	MFS transporter	378.4103434	-1.838737108	0.10161278	-11.38847726	4.235e-30	2.585e-29	28.58839229
ABUW_RS1870	ABUW_3046	N2_CP008706.1	3072267	3073293	+	WP_000100566.1	acyltransferase	1489.824782	-1.841362373	0.190686952	-6.65537025	4.665e-22	2.075e-21	20.69680394
ABUW_RS07495	ABUW_1635	N2_CP008706.1	821565	822170	-	WP_000871703.1	50S ribosomal protein L1 methyltransferase	2958.381955	-1.842855755	0.141762079	-0.99963832	1.235e-38	1.015e-37	36.99567163
sRNA6	no	no	no	no	no	no	no	258.7882435	-1.843326117	0.130416588	-0.060610321	1.366e-09	3.101e-09	8.508838308
ABUW_RS1675	ABUW_3630	N2_CP008706.1	3688743	3690089	-	WP_0001008240.1	UDP-N-acetylmannosyl-L-alanine-D-glutamate ligase	1003.643463	-1.843397252	0.188257148	-9.29801586	1.435e-20	5.705e-20	91.24410514
ABUW_RS1840	ABUW_3869	N2_CP008706.1	3938248	3938323	-	WP_000000000.1	RNA- Ala	3588.094969	-1.843905287	0.270995721	-6.18424058	9.485e-12	4.425e-11	60.718463
ABUW_RS0205	ABUW_0025	N2_CP008706.1	28664	29626	-	WP_000091200.1	methionyl-tRNA formyltransferase	1185.210208	-1.844001064	0.122757017	-5.02555321	5.305e-51	7.975e-50	49.14448804
ABUW_RS03970	ABUW_0811	N2_CP008706.1	390797	789573	+	WP_000091112.1	hypothetical protein	1370.38869	-1.845623475	0.236038468	-7.81963912	5.325e-15	1.645e-14	13.78519515
ABUW_RS1445	ABUW_0646	N2_CP008706.1	826166	828326	-	WP_000547891.1	site-specific recombinase	214.750179	-1.850419526	0.134262236	-13.78214652	3.275e-43	3.295e-42	41.4828041
ABUW_RS0345	ABUW_0694	N2_CP008706.1	688755	688830	-	WP_000000000.1	RNA- Val	84.8079502	-1.855919193	0.278592555	-6.66147267	2.715e-11	6.78e-11	10.17327748
ABUW_RS1670	ABUW_3710	N2_CP008706.1	3772479	3772554	-	WP_000000000.1	RNA- Ala	3600.446472	-1.856262005	0.274288373	-6.76156289	13.5e-11	3.305e-11	10.48148006
ABUW_RS02630	ABUW_0635	N2_CP008706.1	643416	544443	-	WP_010121101.1	hypothetical protein	578.085979	-1.85711191	0.20855473	-8.90754716	5.225e-19	1.945e-19	17.7102827
ABUW_RS0180	ABUW_0277	N2_CP008706.1	295660	295105	-	WP_000000000.1	RNA- Ala	415.4313033	-1.859373752	0.236894998	-7.848918321	4.205e-15	1.305e-14	13.88605665
ABUW_RS1970	ABUW_2876	N2_CP008706.1	2885001	2887019	+	WP_000089154.1	penicillin-binding protein 2	977.5536938	-1.861449998	0.17548846	-0.5850591	3.485e-26	1.795e-25	24.74714697
ABUW_RS1610	ABUW_0327	N2_CP008706.1	349537	350313	+	WP_000552222.1	TSBP family transporter	490.371832	-1.863690448	0.167237999	-11.14394131	7.675e-29	4.435e-28	27.35359527
ABUW_RS14795	ABUW_0878	N2_CP008706.1	900166	919172	+	WP_01028615.1	signal peptide peptidase SppA	5972.536788	-1.866033983	0.173768731	-0.73861975	6.705e-27	3.555e-26	25.44971865
ABUW_RS1680	ABUW_3256	N2_CP008706.1	3287705	3287780	-	WP_000000000.1	RNA- Ala	3602.73212	-1.867518775	0.271066108	-6.88191528	5.915e-12	1.535e-11	10.8153087
ABUW_RS04790	ABUW_0877	N2_CP008706.1	889036	990019	-	WP_01085534.1	lysophospholipid acyltransferase family protein	2134.011004	-1.868370919	0.176008497	-0.5622767	4.515e-26	2.315e-25	24.63888862
ABUW_RS0825	ABUW_0711	N2_CP008706.1	768024	1769871	+	WP_01062813.1	pKb	559.591454	-1.871363688	0.18202252	-0.2845551	8.545e-25	4.145e-24	23.61939601
ABUW_RS0705	ABUW_0142	N2_CP008706.1	155897	165547	-	WP_000210300.1	corbinin phosphohydroxyltransferase	111.926369	-1.872035414	0.179452584	-0.52028793	6.975e-26	3.525e-25	24.45345734
ABUW_RS16025	ABUW_3299	N2_CP008706.1	333108	333178	+	WP_01020011.1	ComEA family DNA-binding protein	356.6664925	-1.873128082	0.17964917	-0.52526331	6.615e-26	3.355e-25	24.47495519
ABUW_RS0135	ABUW_0232	N2_CP008706.1	250338	252215	+	WP_01181864.1	potassium transporter Kup	413.108655	-1.877894422	0.153107789	-0.26517892	1.395e-34	1.005e-33	33
ABUW_RS1670	ABUW_3710	N2_CP008706.1	3726197	3726965	+	WP_000051464.1	helicase-helic transcriptional regulator	492.0673339	-1.882306888	0.333585342	-5.642654663	1.675e-08	3.605e-08	7.443697149
ABUW_RS1705	ABUW_3235	N2_CP008706.1	3263930	3264121	-	WP_000511711.1	class I SAM-dependent methyltransferase	784.9682544	-1.884318008	0.237773358	-7.82475713	2.295e-15	7.165e-15	14.16508968
ABUW_RS0498	ABUW_0062	N2_CP008706.1	914220	918053	+	WP_000471070.1	phosphoribosylphosphorylcholine synthase	20234.41058	-1.886590463	0.171963775	-0.17068276	5.256e-28	2.945e-27	26.5335287
ABUW_RS0135	ABUW_0209	N2_CP008706.1	235219	236046	+	WP_000645099.1	class I SAM-dependent methyltransferase	1920.28502	-1.888907504	0.187052282	-11.2046328	1.395e-29	8.305e-29	28.08092191
ABUW_RS0845	ABUW_0151	N2_CP008706.1	189372	190664	+	WP_000224849.1	3-deoxy-D-manno-olichonic acid transferase	1177.024757	-1.895210732	0.25605366	-5.08861468	1.925e-51	2.665e-50	19.5160288
ABUW_RS02625	ABUW_0514	N2_CP008706.1	525402	525855	-	WP_000779317.1	hypothetical protein	823.446781	-1.896710175	0.190276567	-9.96819382	2.105e-23	9.665e-23	22.01593287
ABUW_RS1645	ABUW_3830	N2_CP008706.1	3896761	3898035	-	WP_01185107.1	tvB	6243.82637	-1.898491646	0.183471853	-0.34759022	4.295e-25	2.105e-24	23.37776071
ABUW_RS0695	ABUW_0172	N2_CP008706.1	1587849	1588034	-	WP_010154366.1	thiazole synthase	2784.109684	-1.898514031	0.16777223	-0.855835061	7.955e-38	6.385e-37	38.1951932
ABUW_RS0835	ABUW_0169	N2_CP008706.1	187814	188196	+	WP_000350419.1	helicase-helic transcriptional regulator	8068.883356	-1.900589304	0.19407601	-9.957281002	2.345e-23	1.075e-22	21.97061622
ABUW_RS02575	ABUW_0624	N2_CP008706.1	633108	533430	-	WP_01161877.1	hypothetical protein	856.703004	-1.907275437	0.184822511	-0.8177245	1.345e-37	1.065e-36	39.57469414
ABUW_RS07105	ABUW_1458	N2_CP008706.1	1450199	1450283	-	WP_000000000.1	RNA- Leu	315.7478288	-1.910100114	0.174319323	-0.402766907	5.655e-05	9.335e-05	4.03018158
ABUW_RS1670	ABUW_3710	N2_CP008706.1	3488910	3490020	-	WP_000323471.1	ATP-binding cassette domain-containing protein	2122.505855	-1.91118108	0.14143972	-10.5405191	9.025e-42	8.675e-41	40.0198369
ABUW_RS0900	ABUW_0508	N2_CP008706.1	418788	424097	-	WP_010211911.1	chitinase lyase	430.2366287	-1.915921721	0.177819936	-0.75787624	5.445e-27	2.915e-26	25.53819701
ABUW_RS0495	ABUW_0744	N2_CP008706.1	747174	7473259	+	WP_000104523.1	3-hydroxyacyl-ACP dehydratase FabZ	9307.396071	-1.915037305	0.154024016	-0.43338682	1.725e-35	1.275e-34	33.89619628
ABUW_RS04400	ABUW_0897	N2_CP008706.1	893880	894203	-	WP_000729551.1	yHbY	3358.065965	-1.92131081	0.194478056	-10.28718459	2.835e-45	2.945e-45	44.53195287
ABUW_RS1885	ABUW_3882	N2_CP008706.1	3923661	3932498	+	WP_010281046.1	tsE	2145.148933	-1.923358286	0.15432291	-0.7011083	5.835e-37	4.485e-36	35.34872199
ABUW_RS1920	ABUW_2246	N2_CP008706.1	2234334	2325458	-	WP_010839368.1	enoyl-CoA hydratase/isomerase family protein	7394.673035	-1.923781037	0.142671483	-0.48399322	1.945e-41	1.	

ABUW_RS1680	ABUW_Z380	NZ_CP008706.1	2366997	2367666	-	WP_00102666.1	tauC	taurine ABC transporter permease TauC	527.3526298	-0.022506468	0.307567733	-6.575808354	4.84E-11	1.9E-0	9.928187993
ABUW_RS03450	ABUW_Z42	NZ_CP008706.1	94385	942269	+	WP_00100751.1		ribose-phosphate pyrophosphokinase	1677.014582	-0.022645228	0.637382056	-3.78070687	0.001482586	0.00214431	2.66807176
ABUW_RS0300	ABUW_Z481	NZ_CP008706.1	3530664	3530739	+			IRNA-Lys	506.165311	-0.025773611	0.445227583	-4.549973287	5.37E-06	9.64E-06	5.05922666
ABUW_RS0650	ABUW_Z197	NZ_CP008706.1	91872	93320	+	WP_001034707.1		LysM/peptidoglycan-binding domain-containing protein	1346.931672	-0.025781906	0.272781833	-7.425399893	1.92E-9	3.22E-13	12.4021410
ABUW_RS0510	ABUW_Z397	NZ_CP008706.1	3441852	3443378	+	WP_000207467.1		fumarate hydratase	8764.720097	-0.027231033	0.188796583	-9.73765781	6.77E-27	3.58E-26	25.4461697
ABUW_RS04190	ABUW_Z654	NZ_CP008706.1	835009	835482	+	WP_00058222.0		IRNA (p-tyrosine[34]-2'-O-methyltransferase	988.8236745	-0.029040473	0.923627796	-3.31721033	1.84E-40	1.66E-39	38.77989191
ABUW_RS0330	ABUW_Z311	NZ_CP008706.1	234494	33513	-	WP_000018937.1	gmk	guanylate kinase	2869.207226	-0.036215992	0.89328416	-0.78023098	2.1E-37	1.66E-36	35.77989191
ABUW_RS0650	ABUW_Z425	NZ_CP008706.1	3471050	3471870	-	WP_00101864.1		Moda/TuO/EdB protein channel family protein	4560.680571	-0.036603702	0.348245728	-5.84818004	4.97E-09	1.0E-08	7.95807318
ABUW_RS0225	ABUW_Z725	NZ_CP008706.1	270566	271877	-	WP_00078142.1		glutathione S-transferase N-terminal domain-containing protein	213.1894348	-0.037373247	0.29716802	-5.272766143	1.81E-20	7.1E-20	9.5006698
ABUW_RS0705	ABUW_Z502	NZ_CP008706.1	3549066	3550178	+	WP_000400008.1		electron transfer flavoprotein-ubiquinone oxidoreductase	10857.30397	-0.038284587	0.93628867	-9.51689799	7.30E-26	3.68E-25	24.3416216
ABUW_RS1405	ABUW_Z967	NZ_CP008706.1	2979839	2980453	-	WP_000254582.1		MacC family protein	806.2335839	-0.03909581	0.80836249	-11.27592405	1.73E-29	1.02E-28	27.9939983
ABUW_RS1405	ABUW_Z986	NZ_CP008706.1	2904183	2905011	-	WP_000140408.1	cydD	sulfate adenylyltransferase subunit CydD	7626.503791	-0.039816716	0.212795448	-9.585766795	9.1E-22	3.88E-21	20.4118827
ABUW_RS0880	ABUW_Z0383	NZ_CP008706.1	409602	410420	+	WP_002155889.1		ABC transporter ATP-binding protein	5190.231617	-0.041243687	0.89630577	-9.76431723	5.07E-27	2.72E-26	25.5654311
ABUW_RS1045	ABUW_Z271	NZ_CP008706.1	2256682	2257869	-	WP_00101093.1		phosphoglycerate kinase	4507.690302	-0.046256175	0.75188522	-11.63404603	2.77E-31	1.74E-30	29.57945075
ABUW_RS04455	ABUW_Z0908	NZ_CP008706.1	902493	903161	+	WP_001278001.1		methyltransferase	1172.794836	-0.048407683	0.93388359	-0.5374791	4.68E-36	3.55E-35	34.4477185
ABUW_RS0665	ABUW_Z066	NZ_CP008706.1	1304747	1302723	-	WP_000082052.1		bifunctional prephenate dehydrogenase[3-phosphoshikimate 1-carboxy]ylidng efflux RND transporter periplasmic adaptor subunit Adt	4200.558492	-0.050070875	0.15869887	-0.91800783	3.56E-38	2.89E-37	36.53916216
ABUW_RS04135	ABUW_Z844	NZ_CP008706.1	824800	825330	+	WP_000866589.1	adel	luliding rffX RND transporter periplasmic adaptor subunit Adt	9018.95611	-0.05033453	0.93845242	-9.57717236	3.80E-26	1.96E-25	24.70774393
ABUW_RS07116	ABUW_Z460	NZ_CP008706.1	1450439	1450523	-			IRNA-Lau	793.7242603	-0.054957727	0.421934538	-4.870323571	1.1E-06	2.1E-06	6.576710745
ABUW_RS0540	ABUW_Z098	NZ_CP008706.1	912436	912412	+	WP_001273422.1	gPyY	S05 ribosomal protein L35	8014.32645	-0.06080991	0.26420625	-7.80004479	6.1E-5	1.90E-4	9.712464
ABUW_RS07250	ABUW_Z547	NZ_CP008706.1	3054440	3054769	-	WP_000555570.1	seCG	prephenyl transferase subunit SeCG	3223.024936	-0.063186662	0.222469891	-0.274010281	1.75E-20	7.08E-20	9.4995674
ABUW_RS01090	ABUW_Z0283	NZ_CP008706.1	300005	301837	+	WP_000227940.1	htl	penicillin-binding protein PBP3	3060.08107	-0.063829568	0.170059958	-0.121058937	8.62E-34	4.77E-33	32.324982
ABUW_RS07795	ABUW_Z696	NZ_CP008706.1	292937	293416	-	WP_000214361.1		MFS transporter	495.306794	-0.067084349	0.21000994	-9.70416603	2.89E-22	1.25E-21	20.90309999
ABUW_RS00100	ABUW_Z0002	NZ_CP008706.1	1590	2738	+	WP_001237350.1		DNA polymerase beta subunit beta	10387.10526	-0.067498861	0.13818954	-14.95880407	1.36E-50	1.81E-49	48.74221463
ABUW_RS0195	ABUW_Z3885	NZ_CP008706.1	3593202	3594143	+	WP_000361794.1		5-carboxymethylimidazole ribonucleotide synthase	4707.399784	-0.070394714	0.20142276	-9.28260671	8.41E-25	4.08E-24	23.3893384
ABUW_RS0565	ABUW_Z014	NZ_CP008706.1	162882	172589	+	WP_000082281.1		glutamate -cysteine ligase	2675.536810	-0.074147047	0.123488261	-16.7963094	2.60E-63	5.66E-62	61.24718357
ABUW_RS04300	ABUW_Z0876	NZ_CP008706.1	859075	859965	+	WP_000114637.1	sucD	succinate-CoA ligase subunit alpha	49629.37226	-0.074748610	0.227310559	-9.12754163	7.03E-20	2.70E-19	85.86862624
ABUW_RS05960	ABUW_Z020	NZ_CP008706.1	1257404	1259784	-	WP_000342684.1		RNP-dependent malic enzyme	28718.8283	-0.076439238	0.157923627	-10.14837606	1.74E-39	1.49E-38	37.6268173
ABUW_RS04475	ABUW_Z740	NZ_CP008706.1	173229	1735884	+	WP_000992588.1	rsfP	NADP metallopeptidease RsfP	6377.830777	-0.080235266	0.12386394	-9.7336149	1231E-55	2.01E-54	63.69860394
ABUW_RS0625	ABUW_Z480	NZ_CP008706.1	3535666	3536041	-			IRNA-Lys	1074.255812	-0.080243833	0.45393194	-4.582728942	4.59E-06	8.30E-06	6.580921908
ABUW_RS07030	ABUW_Z501	NZ_CP008706.1	3542668	3545879	-	WP_000246028.1		DUF1855 domain-containing protein	1007.778379	-0.083808869	0.17232417	-0.09333758	1.1E-33	7.93E-33	32.1007261
ABUW_RS0535	ABUW_Z568	NZ_CP008706.1	2877568	2878677	-	WP_000696025.1		MEtA and DUF4377 domain-containing protein	93392.94382	-0.083724884	0.245353187	-10.8927097	17.1E-9	5.95E-17	92.5545303
ABUW_RS05910	ABUW_Z653	NZ_CP008706.1	961840	963180	+	WP_001215949.1	cgIA	Oxy family GTPase CgIA	8810.94131	-0.089622949	0.90096236	-11.02401872	2.93E-28	1.64E-27	26.78516697
ABUW_RS0430	ABUW_Z177	NZ_CP008706.1	3204292	3204843	+	WP_001274552.1	rdhC	NADH-quinone oxidoreductase subunit A	5871537667	-0.090725824	0.257105162	-8.10605975	3.62E-16	1.1E-16	14.92443304
ABUW_RS05880	ABUW_Z024	NZ_CP008706.1	1424291	1424875	-	WP_000925669.1		aminocycloheptanamide:iminoacid synthase component I	1340.84241	-0.091707325	0.111070532	-8.86324476	4.23E-29	9.31E-28	77.03193032
ABUW_RS07250	ABUW_Z487	NZ_CP008706.1	147362	147498	+	WP_000790164.1	csuAB	Csu fibrinogen binding subunit CsuAB	1918.820395	-0.098919327	1.251962009	-1.677097349	NA	NA	17.03193032
ABUW_RS02635	ABUW_Z0536	NZ_CP008706.1	544597	545034	+	WP_001107136.1	quaA	QuaQ3(4) S-adenosylmethionine:riboosyltransferase-isomerase	1256.058592	-0.11435189	0.96671901	-0.6185001	1.20E-26	6.25E-26	25.2041998
ABUW_RS0335	ABUW_Z747	NZ_CP008706.1	273018	2737143	+	WP_001188820.1	gap	type I(gharaldehyde)-3-phosphate dehydrogenase	452.5436768	-0.120285576	0.16436203	-11.93936243	1.88E-37	1.49E-36	35.6268173
ABUW_RS01570	ABUW_Z019	NZ_CP008706.1	343566	343991	+	WP_000788336.1		prelin-type N-terminal cleavage/methylation domain-containing p	305.5426716	-0.120384967	0.96750163	-0.61877787	17.1E-36	1.30E-35	34.8860565
ABUW_RS060	ABUW_Z895	NZ_CP008706.1	2902539	2904162	-	WP_000104945.1	cyuN	sulfate adenylyltransferase subunit CyuN	7728.310994	-0.120408508	0.12834433	-0.18817403	3.59E-34	2.55E-33	32.59345982
ABUW_RS07700	ABUW_Z635	NZ_CP008706.1	3693846	3694661	-	WP_000011168.1		DacC family protein	2029.563285	-0.125023601	0.152762904	-13.78096568	3.32E-43	3.33E-42	41.47755577
ABUW_RS0685	ABUW_Z107	NZ_CP008706.1	1301934	13010550	-	WP_001278711.1	acpP	acyl carrier protein	47087.30325	-0.125974476	0.16193352	-0.09882751	3.34E-39	2.83E-38	34.58421056
ABUW_RS0645	ABUW_Z073	NZ_CP008707.1	42964	42983	-	WP_00066685.1		hypothetical protein	158.774934	-0.124555554	0.388074364	-5.448068077	5.09E-08	1.06E-07	6.974694105
ABUW_RS04445	ABUW_Z090	NZ_CP008706.1	920310	933874	+	WP_000185855.1	ghnK	hydroxycinnamyl dihydroxyphenylglyoxylamine-1-phosphate N	161.8148832	-0.12458487	0.179049049	-11.800736341	3.58E-32	2.3E-31	30.63638002
ABUW_RS05150	ABUW_Z049	NZ_CP008706.1	1057584	1058531	+	WP_001293637.1	radD	SamA family transporter RadD	5913.050576	-0.124587139	0.174270176	-0.12191916	6.55E-34	4.60E-33	32.3373421
ABUW_RS02390	ABUW_Z099	NZ_CP008706.1	83622	84341	-	WP_000917863.1	puC	phosphoribosylaminoimidazole succinocarboxamide synthase	1832.81424	-0.126109497	0.92585168	-0.04187901	1.01E-38	8.32E-38	37.07987667
ABUW_RS0430	ABUW_Z185	NZ_CP008706.1	3844462	3847892	-	WP_001078999.1		amino acid permease	1884.638101	-0.1263239	0.223491873	-9.488949653	2.83E-21	1.1E-20	19.93552401
ABUW_RS00770	ABUW_Z055	NZ_CP008706.1	170215	172392	+	WP_000896433.1	acE	gamma-glutamyl transferase (acyl-transfering), homodimeric typ	41950.8742	-0.126182247	0.238176107	-8.86152444	7.89E-19	2.92E-18	17.53461716
ABUW_RS0405	ABUW_Z172	NZ_CP008706.1	391789	391973	-	WP_000100957.1	nuoG	NADH-quinone oxidoreductase subunit NuoG	6006.78942	-0.12690534	0.293212377	-7.259917343	4.62E-13	1.28E-12	11.89270003
ABUW_RS0380	ABUW_Z167	NZ_CP008706.1	192898	194785	-	WP_000121157.1	nuoL	NADH-quinone oxidoreductase subunit L	34396.29329	-0.12101451	0.257062162	-8.28982829	1.0E-16	3.8E-16	6.14907502
ABUW_RS04000	ABUW_Z0817	NZ_CP008706.1	792535	793890	-	WP_000240084.1		amino acid permease	6941547382	-0.124500654	0.154838996	-5.75425731	6.42E-56	1.08E-54	63.96657624
ABUW_RS0325	ABUW_Z745	NZ_CP008706.1	273192	273451	-	WP_000517792.1		adenylosuccinate synthase	30642.30006	-0.126481927	0.93589386	-10.0592311	5.63E-39	4.7E-38	37.32697900
ABUW_RS0625	ABUW_Z219	NZ_CP008706.1	3250675	3250750	-			IRNA-Lys	7252.01828	-0.12649621	0.326404865	-6.543736025	6.00E-11	1.46E-10	9.835647144
ABUW_RS08216	ABUW_Z687	NZ_CP008706.1	1882531	1883565	+	WP_001166920.1	muB	UDP-N-acetylmuramate dehydrogenase	1265.344704	-0.124148484	0.12181692	-0.67718268	6.29E-70	1.75E-68	67.75696195
ABUW_RS06410	ABUW_Z14	NZ_CP008706.1	125596	1256119	+	WP_000722151.1		DUF4468 domain-containing protein	3641.237914	-0.12424251	0.23545542	-9.252661438	2.1E-20	8.60E-20	9.0655055
ABUW_RS04270	ABUW_Z0870	NZ_CP008706.1	849083	850918	+	WP_000500957.1		succinate dehydrogenase subunit subunit	5.01813197	-0.124766466	0.224195956	-9.12753191	1.04E-21	4.40E-21	20.35654372
ABUW_RS04700	ABUW_Z0558	NZ_CP008706.1	965658	967107	+	WP_000644180.1		electron transfer flavoprotein subunit beta/Fla family protein	24391.33267	-0.124800587	0.16029945	-11.91891888	9.32E-33	3.129971484	
ABUW_RS16175	ABUW_Z339	NZ_CP008706.1	2347358	2343825	+	WP_000956445.1		type I transaminase	71550.164452	-0.12602359	0.269231122	-7.98418016	1.41E-15	4.48E-15	14.3487299
ABUW_RS00120	ABUW_Z024	NZ_CP008706.1	27363	28667	-	WP_000084730.1	rsnB	RS IRNA (guanine[527]-N(7)-methyltransferase RsnB	1773.498863	-0.121030491	0.1556426				

ABUW_RS18780	ABUW_3670	N2_CP008706.1	3726897	3727940	+	WP_000068656.1	ansB	ACR3 family anisette efflux transporter	1108.843662	-2.254953561	0.307243964	-7.339293281	2.16E-18	6.02E-11	12.2040351
ABUW_RS18405	ABUW_3376	N2_CP008706.1	344258	344550	-	WP_000095254.1	hisS	histidine--rRNA ligase	7952.91316	-2.255293383	0.82293535	-0.89655585	6.65E-44	6.87E-43	42.9034326
ABUW_RS03945	ABUW_819	N2_CP008706.1	917528	917839	+	WP_00146232.1		hypothetical protein	272.6789663	-2.255495697	0.32350012	-6.78343423	1.97E-11	2.97E-11	5.92724355
ABUW_RS920	ABUW_3479	N2_CP008706.1	3528492	3530333	+	WP_000084319.1		long-chain-acyl-CoA synthetase	1109.346738	-2.25707881	0.205883038	-0.929696	5.76E-28	3.16E-27	26.6026032
ABUW_RS1060	ABUW_2176	N2_CP008706.1	2109053	2109161	-	WP_000771849.1		NAD(P)-dependent oxidoreductase	294.940725	-2.257180647	0.2452444	-9.203800966	3.44E-20	1.34E-19	18.1728952
ABUW_RS1525	ABUW_3600	N2_CP008706.1	3660780	3660855	-			RNA--Gly	3504.760186	-2.262884795	0.283786679	-7.875804787	15.1E-15	4.79E-15	14.39686349
ABUW_RS0895	ABUW_2140	N2_CP008706.1	164228	164578	-	WP_000919165.1		arsenate reductase	1033.452954	-2.266939381	0.22108889	-8.243327725	1.27E-24	6.91E-24	23.21024858
ABUW_RS1785	ABUW_3667	N2_CP008706.1	3725997	3726031	+	WP_001275666.1	arsC	arsenate reductase (glutaredoxin)	443.2054857	-2.269731728	0.16080165	-14.1610225	3.07E-45	3.32E-44	43.47886192
ABUW_RS1810	ABUW_0350	N2_CP008706.1	37678	372789	+	WP_001281792.1		GlutLeu/Pha1 dehydrogenase	50154.86083	-2.285371181	0.20354255	-11.5275795	2.97E-29	1.75E-28	27.755696195
ABUW_RS9995	ABUW_3494	N2_CP008706.1	3542358	3543563	-	WP_001284664.1		TIGR03862 family flavoprotein	345.0468804	-2.290567872	0.168175238	-0.6202565	3.04E-42	2.99E-41	40.52432881
ABUW_RS1060	ABUW_2274	N2_CP008706.1	2259015	2260178	+	WP_000133515.1		cupin domain-containing protein	1520.873493	-2.301617082	0.175771593	-0.09184028	3.67E-39	3.10E-38	37.50863831
ABUW_RS18700	ABUW_3841	N2_CP008706.1	390111	3910827	-	WP_001217232.1	iph	rbonuclease PH	4069.859881	-2.303193075	0.15508571	-14.80554987	6.90E-50	8.80E-49	48.05551733
ABUW_RS18285	ABUW_2643	N2_CP008706.1	2641074	264325	-	WP_000988402.1		type I secretion system permease/ATPase	5868.684779	-2.306592735	0.209174877	-11.02710219	2.83E-28	1.95E-27	26.78960228
ABUW_RS05085	ABUW_8336	N2_CP008706.1	846085	846810	+	WP_000729408.1	pdjK	pyridoxal-P--phosphate synthase	2201247449	-2.306849697	0.150758038	-5.30190666	7.45E-53	1.08E-51	50.96567624
ABUW_RS04205	ABUW_0857	N2_CP008706.1	836329	838014	-	WP_000183443.1		APC family permease	2091838522	-2.310722989	0.193742715	-11.93708364	7.58E-33	5.03E-32	31.29343201
ABUW_RS06100	ABUW_048	N2_CP008706.1	8289200	8290155	-	WP_000128669.1		ABC transporter/ATP-binding protein	902.9774036	-2.319077794	0.244361789	-9.46509999	2.83E-21	1.20E-20	9.80281975
ABUW_RS06505	ABUW_9333	N2_CP008706.1	9344007	9342060	+	WP_000457893.1		serine hydroxymethyltransferase	8066.1059	-2.31848406	0.184658941	-2.53580273	4.76E-36	3.59E-35	34.44905555
ABUW_RS18470	ABUW_2155	N2_CP008706.1	2158211	2158435	+	WP_000826151.1		hypothetical protein	910.573221	-2.321260331	0.270556818	-8.56089434	1.05E-17	3.91E-17	16.40732324
ABUW_RS16455	ABUW_3020	N2_CP008706.1	3045841	3046992	-	WP_000128703.1		EmvA/EmrK family multidrug efflux transporter periplasmic adaptor	1010.020231	-2.320163399	0.286959189	-8.092763626	5.83E-16	1.89E-15	14.723582
ABUW_RS0516	ABUW_2774	N2_CP008706.1	720871	721785	-	WP_000107699.1	gatC	Asp--RNA(Glu)/Glu--RNA(Gln)amidotransferase subunit GtaC	1794.461668	-2.321953465	0.167622419	-8.55252376	1.23E-43	1.0E-42	41.80962545
ABUW_RS03520	ABUW_0175	N2_CP008706.1	721919	722359	+	WP_000601079.1		rod shape-determining protein	10323.50671	-2.322494335	0.256779849	-10.04690777	1.50E-19	5.70E-19	18.244102514
ABUW_RS15475	ABUW_3590	N2_CP008706.1	3651275	3655363	-	WP_000083999.1	rpOB	DNA-directed RNA polymerase subunit beta	150085.9078	-2.322794823	0.19309677	-2.03460291	2.34E-33	1.69E-32	31.79860288
ABUW_RS01305	ABUW_0172	N2_CP008706.1	178770	179339	-	WP_000179650.1	gatB	Asp--RNA(Asn)/Glu--RNA(Gln)amidotransferase subunit GtaB	6890.18704	-2.32352181	0.259603095	-8.950285505	3.55E-19	1.33E-18	17.87614836
ABUW_RS02225	ABUW_0453	N2_CP008706.1	465765	466406	+	WP_000085782.1		lumarilac/acetate hydrolase family protein	257125978	-2.32550082	0.147756574	-5.73908632	8.16E-56	1.36E-54	83.86646199
ABUW_RS04045	ABUW_0089	N2_CP008706.1	100659	102497	-	WP_000334179.1	gmsD	glutamine--fructose-6-phosphate transaminase (isomerizing)	21687.44232	-2.325808804	0.15778451	-5.3236145	5.32E-53	7.79E-52	11.9046254
ABUW_RS17000	ABUW_3495	N2_CP008706.1	3543563	3544191	-	WP_000130756.1		SAM-dependent methyltransferase	440.0235929	-2.326593416	0.209527667	-11.9339142	1.20E-28	6.87E-28	27.39034261
ABUW_RS03020	ABUW_0614	N2_CP008706.1	614933	615511	-	WP_000509973.1		cob(lytic acid α -D-ribose adenosyltransferase	3113051336	-2.326867281	0.19966503	-11.65385488	2.19E-31	1.38E-30	29.88010991
ABUW_RS18185	ABUW_2279	N2_CP008706.1	2264199	2264715	+	WP_000204031.1		DUF0258 domain-containing protein	546.2726127	-2.331661592	0.254261943	-9.170312978	4.72E-20	1.82E-19	31.79860288
ABUW_RS1845	ABUW_2154	N2_CP008706.1	2137658	2138032	-	WP_000480035.1		cell envelope integral protein TolA	641.028225	-2.332027307	0.262279905	-8.89204959	6.00E-19	2.23E-18	17.65169514
ABUW_RS17635	ABUW_3602	N2_CP008706.1	3661033	3661108	-			RNA--Thr	4673.477763	-2.33377096	0.270296002	-8.63303503	5.93E-18	2.15E-17	16.77710771
ABUW_RS04265	ABUW_0869	N2_CP008706.1	848705	849070	+	WP_000633672.1	sdhD	oxalate dehydrogenase, hydrophilic membrane anchor protein	16154.74351	-2.336444256	0.218995458	-9.76752428	4.91E-27	2.64E-26	25.57836907
ABUW_RS03900	ABUW_0795	N2_CP008706.1	774559	774882	+	WP_000623931.1		DUF4236 domain-containing protein	2711098949	-2.34186323	0.281864792	-8.942167557	3.83E-19	1.43E-18	17.84686396
ABUW_RS04290	ABUW_0874	N2_CP008706.1	896310	897146	+	WP_000082610.1	lpdA	dihydrolipoyl dehydrogenase	63526.36558	-2.342647521	0.249604462	-9.385439274	6.27E-21	2.53E-20	19.59887948
ABUW_RS05975	ABUW_0223	N2_CP008706.1	630336	6304472	-	WP_000167013.1	metF	methyltetrahydrofolate reductase [NAD(P)H]	4056.028744	-2.347839748	0.21184258	-11.0710272	9.84E-29	5.66E-28	27.24783537
ABUW_RS14255	ABUW_2936	N2_CP008706.1	2959001	2959123	-	WP_000085671.1		glutamine	2796.73827	-2.353328235	0.184671755	-11.2902543	2.49E-46	2.79E-45	44.55456392
ABUW_RS17560	ABUW_3607	N2_CP008706.1	3666531	3667367	-	WP_000170031.1		general secretion pathway protein	1368.70002	-2.354448506	0.162880061	-11.40073636	1.62E-53	2.42E-52	51.618463
ABUW_RS18160	ABUW_3230	N2_CP008706.1	3258903	3259724	-	WP_000126423.1		HAD family hydrolase	913.920868	-2.355901073	0.148650002	-5.84864674	1.44E-56	2.44E-55	94.026107
ABUW_RS18185	ABUW_2842	N2_CP008706.1	2855958	2857601	+	WP_001029231.1		hypothetical protein	974.662033	-2.35787633	0.260785586	-11.74325508	7.65E-32	4.88E-31	30.3116018
ABUW_RS17000	ABUW_3535	N2_CP008706.1	3595186	3595554	-			Na ⁺ /H ⁺ antiporter subunit C	473.7636035	-2.358597059	0.269009961	-8.767694294	1.82E-18	6.64E-18	17.1737183
ABUW_RS17615	ABUW_3618	N2_CP008706.1	3676627	3676896	+	WP_000089996.1		oxidative damage protection protein	797.0002336	-2.36140193	0.117482505	-20.9003404	7.37E-90	4.79E-88	37.81966449
ABUW_RS18710	ABUW_0381	N2_CP008706.1	407351	409198	+	WP_000047395.1		DEAD/DEAHbox helicase	81860.12305	-2.367108746	0.402565709	-5.88012515	4.19E-09	9.11E-09	8.00448263
ABUW_RS18120	ABUW_2307	N2_CP008706.1	2292146	2293105	+	WP_000175360.1	bioB	biotin synthase BioB	17918.82802	-2.36716109	0.138738301	-7.0564897	3.10E-65	7.37E-64	63.925251
ABUW_RS01300	ABUW_0208	N2_CP008706.1	213395	2135214	+	WP_000350212.1		FAD-dependent oxidoreductase	19581484475	-2.370242597	0.190089551	-14.8048972	1.36E-49	1.72E-48	47.76447195
ABUW_RS04315	ABUW_0088	N2_CP008706.1	98390	99990	+	WP_001697141.1		hypothetical protein	3027.300806	-2.370389597	0.194873865	-2.9375834	4.85E-34	3.43E-33	32.46597389
ABUW_RS04900	ABUW_0397	N2_CP008706.1	92336	923476	+	WP_000065579.1		co--chaperone GroES	6377.100597	-2.372166635	0.2556146	-9.280006045	1.69E-20	6.78E-20	19.13277148
ABUW_RS12785	ABUW_2635	N2_CP008706.1	2634617	2635147	+	WP_085920803.1		GNA1 family N-acetyltransferase	865.166934	-2.377702698	0.205732186	-11.55727105	6.78E-31	4.16E-30	29.37882372
ABUW_RS19340	ABUW_2869	N2_CP008706.1	2878733	2880136	-	WP_000172206.1	gdhA	NAD(P)-specific glutamate dehydrogenase	2190.254068	-2.379198846	0.16310259	-2.9191054	1.37E-38	1.12E-37	36.95078196
ABUW_RS04780	ABUW_0875	N2_CP008706.1	885879	886565	+	WP_000049406.1	bioA	lipoprotein-releasing ABC transporter ATP-binding protein LcdA	3163.781643	-2.383973267	0.178625559	-0.34620464	1.25E-40	1.03E-39	38.94692156
ABUW_RS05070	ABUW_0116	N2_CP008706.1	127874	128389	+	WP_001400411.1		disulfide bond formation protein B	864.3564077	-2.387386711	0.17660373	-5.81932647	1.22E-41	1.17E-40	43.931914
ABUW_RS08210	ABUW_0886	N2_CP008706.1	882508	882511	+	WP_000388070.1		low molecular weight phosphotyrosine protein phosphatase	6000.224796	-2.389403708	0.16245951	-11.832116	1.91E-39	5.98E-39	38.01863449
ABUW_RS18625	ABUW_2599	N2_CP008706.1	2599493	25992524	+	WP_000172061.1		hypothetical protein	970.9782277	-2.389999781	0.21669796	-11.02919255	2.76E-28	1.95E-27	26.8068754
ABUW_RS05055	ABUW_8330	N2_CP008706.1	842206	843033	+	WP_000344900.1	lspB	signalpeptidase I	3767.815048	-2.391978856	0.14215558	-6.82443243	1.62E-63	6.14E12943	
ABUW_RS04040	ABUW_0081	N2_CP008706.1	88198	89118	+	WP_001161898.1	hutG	formimidylglutamine	38118671758	-2.39197951	0.318312577	-7.514651736	5.71E-14	1.67E-13	12.7772833
ABUW_RS05090	ABUW_8337	N2_CP008706.1	846817	847461	+	WP_000095056.1		RNA--[m(2)G(m)A]-hydroxylase	9663.334553	-2.392330813	0.100671491	-8.30840416	7.14E-75	2.50E-73	72.60209561
ABUW_RS07780	ABUW_893	N2_CP008706.1	858486	859125	+	WP_000888596.1		bifunctional acylate hydratase 2--methylcrotonate dehydratase	40018.50532	-2.394619568	0.196938991	-2.1091915	5.03E-34	3.81E-33	32.4424281
ABUW_RS17530	ABUW_3601	N2_CP008706.1	3660903	3660978	-			RNA--Tyr	19336.97438	-2.395961604	0.32457287	-7.453435402	9.00E-14	6.23E-13	92.5019071
ABUW_RS01995	ABUW_0284	N2_CP008706.1	30941	303340	+	WP_000218541.1		UDP-N-acetylmannosyl-1-allyl-D-glutamine--2,6-diaminopyridine	2275.390368	-2.403802917	0.198469239	-11.8430234	1.15E-45	1.25E-44	43.30308999
ABUW_RS19320	ABUW_3278	N2_CP008706.1	331828	332188	+	WP_000097689.1		hypothetical protein	2						

ABUW_RS030365	ABUW_0643	NZ_CP008706.1	648874	650517	+	WP_000281964.1		nitrite/sulfite reductase	3884.623421	-2.53105803	0.24477059	-0.34177744	4.5665-25	2.236-24	23.651895	W
ABUW_RS1080	ABUW_2278	NZ_CP008706.1	2263495	2264175	+	WP_00118632.1		DUF1275 domain-containing protein	983.878519	-2.53590963	0.89410827	-0.38862724	7.056-41	6.536-40	39.8500882	W
ABUW_RS1105	ABUW_2283	NZ_CP008706.1	2268551	2268925	+	WP_00191343.1	gcvH	glycine cleavage system protein GcvH	864.4170354	-2.53876579	0.81869685	-0.04528116	3.486-51	4.786-50	49.3205721	W
ABUW_RS0325	ABUW_0615	NZ_CP008706.1	61607	617469	+	WP_000045364.1		ToxR-dependent receptor	5184.832693	-2.538856468	0.10227167	-0.1052206	2.906-73	9.346-72	71.0219631	W
ABUW_RS1310	ABUW_3357	NZ_CP008706.1	3394252	3395976	-	WP_000422094.1		acetylactate synthase 3 large subunit	126.14.23542	-2.54316106	0.17598432	-0.45336591	2.388-47	2.726-46	45.654311	W
ABUW_RS0530	ABUW_3096	NZ_CP008706.1	3121955	3123229	+			rRNA-Gln	175.4021486	-2.551034703	0.290071656	-0.796240255	14.16-18	6.576-18	97.2665046	W
ABUW_RS06416	ABUW_015	NZ_CP008706.1	026106	026141	+	WP_000186804.1		hypothetical protein	79196519703	-2.554808979	0.26183724	-0.781884344	1.356-22	5.946-22	21.2621056	W
ABUW_RS1975	ABUW_3692	NZ_CP008706.1	375101	3752245	-	WP_000097792.1		timorin: intracellular cation channel family protein	80110978912	-2.555021878	0.237646477	-0.73218878	5.796-27	3.096-26	25.5100452	W
ABUW_RS1068	ABUW_2167	NZ_CP008706.1	2183588	2185453	-	WP_000443421.1		SuA-N terminal domain-containing protein	6601226423	-2.55778346	0.154367544	-0.03572382	8.836-81	8.826-79	78.4193664	W
ABUW_RS0346	ABUW_0703	NZ_CP008706.1	708354	708557	-	WP_0002016643.1		hypothetical protein	1509.167046	-2.567044039	0.280889662	-0.10897658	6.306-20	2.436-19	8.61439373	W
ABUW_RS01005	ABUW_0203	NZ_CP008706.1	227864	229166	+	WP_000369968.1	gabT	4-aminobutyrate--2-oxoglutarate transaminase	1012.526494	-2.586551084	0.36812155	-0.72653111	2.126-12	5.616-12	11.2510374	W
ABUW_RS05530	ABUW_130	NZ_CP008706.1	115432	1152199	+	WP_001023216.1	surE	5'/3'-nucleotidase SurE	823.5952353	-2.587695051	0.194500165	-0.30433342	2.816-40	1.966-39	38.70774393	W
ABUW_RS00575	ABUW_0116	NZ_CP008706.1	028551	013860	+	WP_000898344.1		type V secretion system tip protein VtgG	3080.660732	-2.592922971	0.232635963	-0.114583892	7.506-29	4.346-28	27.36251027	W
ABUW_RS02645	ABUW_0538	NZ_CP008706.1	546080	547147	+	WP_001787855.1		site-specific integrase	814.1673932	-2.595458734	0.195052025	-0.30968949	2.036-40	1.836-39	38.73754891	W
ABUW_RS1644	ABUW_2808	NZ_CP008706.1	2807155	2808510	+	WP_071543522.1		amino acid permease	1298.801933	-2.604454542	0.17886181	-0.56105845	4.956-48	5.906-47	46.22914779	W
ABUW_RS1600	ABUW_3821	NZ_CP008706.1	3887000	3888175	-	WP_000935236.1		DegT/OxyR/VfrY1595 amonotransferase family protein	90058.69027	-2.604972293	0.92562851	-0.17474835	2.296-65	5.426-64	63.26600071	W
ABUW_RS1610	ABUW_3417	NZ_CP008706.1	345750	3465568	+	WP_000595085.1		polyploid protein glycosyl transferase	1692.16671	-2.605758451	0.293193361	-0.88781822	6.236-19	2.316-18	17.63383802	W
ABUW_RS1590	ABUW_3819	NZ_CP008706.1	3846907	3848472	-	WP_000591427.1	galU	UTP--glucose-1-phosphate uridylyltransferase GalU	7967.34234	-2.606505703	0.150496654	-0.97487558	9.116-49	5.656-47	86.24795105	W
ABUW_RS1380	ABUW_2962	NZ_CP008706.1	2972325	2973765	+	WP_000185269.1		YaeJ-family protein	614.5604164	-2.607401188	0.241038654	-0.809194787	3.096-27	1.675-26	25.77723533	W
ABUW_RS03825	ABUW_0791	NZ_CP008706.1	765364	765119	+	WP_001787444.1		hypothetical protein	99.8070954	-2.616020004	0.292224073	-0.302159409	4.186-19	1.556-18	17.8665754	W
ABUW_RS1045	ABUW_2592	NZ_CP008706.1	2899260	2901167	+	WP_000966799.1		CtMfH-family transporter	3737.767202	-2.611087497	0.194439344	-0.43024227	4.026-41	3.766-40	39.42481216	W
ABUW_RS01825	ABUW_0668	NZ_CP008706.1	660383	662010	-	WP_001189538.1		benzoate/H ⁺ symporter BenE-family transporter	328.650121	-2.611654743	0.245800679	-0.10246482	2.296-26	1.916-25	28.24421216	W
ABUW_RS1425	ABUW_1376	NZ_CP008706.1	1303808	1304285	-	WP_000878003.1		NADH-quinone oxidoreductase subunit B	8071178895	-2.612440042	0.28943347	-0.028854327	1.736-19	6.596-19	8.181149	W
ABUW_RS17225	ABUW_3540	NZ_CP008706.1	3588641	3599042	-	WP_000897046.1		ribosome, cytosolic factor A	14401.45414	-2.613015937	0.19990608	-0.106764877	5.040-39	4.226-38	37.37468755	W
ABUW_RS00995	ABUW_0201	NZ_CP008706.1	224705	226147	+	WP_000180767.1		amino acid permease	1792.061029	-2.617647833	0.326712891	-0.009190217	1.166-15	3.696-15	14.43291763	W
ABUW_RS17440	ABUW_3583	NZ_CP008706.1	3641934	3642165	+	WP_000472947.1		outer membrane beta-barrel protein	17177.0116	-2.61825993	0.475568771	-0.50553372	3.686-08	7.736-08	1.71820506	W
ABUW_RS08620	ABUW_0770	NZ_CP008706.1	167219	1768937	-	WP_001824601.1		PTS transporter subunit IIC	1053.336865	-2.622364383	0.167492323	-0.65662431	2.996-55	4.846-54	53.1916464	W
ABUW_RS08460	ABUW_0737	NZ_CP008706.1	173454	1735206	+	WP_000122222.1	uppB	di-trans, poly-cis-decayenyl-1-transferase	3100.332732	-2.623448224	0.178166925	-0.74266463	4.486-49	5.536-48	47.25271487	W
ABUW_RS02250	ABUW_0458	NZ_CP008706.1	470499	471074	+	WP_000543071.1		xanthine phosphoribosyltransferase	2287.203375	-2.61821436	0.20519567	-0.82200688	1.236-37	9.836-37	36.00744468	W
ABUW_RS1665	ABUW_3838	NZ_CP008706.1	3906589	3907144	+	WP_000202926.1		carboxylating nicotinate-nucleotide diphosphorylase	957.7337611	-2.641070391	0.237705476	-0.11068384	1.116-28	6.386-28	27.1951932	W
ABUW_RS16105	ABUW_3297	NZ_CP008706.1	3329241	3329723	-	WP_000216216.1	tskX	ino-4-hydroxy-D-xylose, hypoxanthine/guanthine diphosphokinase	749.0634299	-2.640765051	0.16100072	-0.53975456	3.306-57	5.856-56	55.33284101	W
ABUW_RS17265	ABUW_3548	NZ_CP008706.1	3604782	3605676	+	WP_000189311.1		l-hydroxy-glucose isomerase	3180.553632	-2.648602928	0.21610965	-0.20565305	14.716-34	1.065-33	32.07149419	W
ABUW_RS1555	ABUW_3812	NZ_CP008706.1	3874665	3875816	-	WP_000587286.1	ldd	FMN-dependent L-lactate dehydrogenase LldD	2830.650457	-2.650558987	0.342556058	-0.737572719	10.16-14	3.086-14	15.1194428	W
ABUW_RS09610	ABUW_0176	NZ_CP008706.1	168616	168110	+	WP_000045119.1	adeC	drug efflux RND transporter outer membrane channel subunit A	419.19653	-2.661024545	0.178017224	-0.189500858	3.556-50	4.606-49	48.33732427	W
ABUW_RS12850	ABUW_2650	NZ_CP008706.1	2648551	2649972	+	WP_00182272.1		cytosine--rRNA ligase	81987.478586	-2.664940884	0.138476746	-0.24468108	1.566-82	7.786-81	80.1092004	W
ABUW_RS1145	ABUW_2910	NZ_CP008706.1	2922149	2922763	-	WP_001191892.1		carbonic anhydrase	14123.18559	-2.666022785	0.170635321	-0.61826611	5.476-55	8.646-54	53.06348826	W
ABUW_RS15955	ABUW_2873	NZ_CP008706.1	2882131	2882784	+	WP_001202044.1	adk	adenylate kinase	10126.67971	-2.667706918	0.164027802	-0.26411434	1.776-59	3.426-58	47.46591789	W
ABUW_RS15410	ABUW_1373	NZ_CP008706.1	1359885	1320116	+	WP_001091086.1	nuoF	NADH-quinone oxidoreductase subunit NuoF	22232.86764	-2.673429597	0.320631933	-0.10451076	5.046-16	1.646-15	14.78516615	W
ABUW_RS1595	ABUW_3820	NZ_CP008706.1	3884884	3886858	-	WP_000721144.1		polycyclic carbonyl biosynthesis protein	25116.74524	-2.676824866	0.121069178	-0.221097802	2.566-08	3.316-06	10.5480172	W
ABUW_RS17205	ABUW_3536	NZ_CP008706.1	3595554	3597365	+	WP_000459267.1		monovalent cation/H ⁺ antiporter subunit D	2672.823597	-2.677990888	0.226321037	-0.1183804705	2.486-32	1.626-31	30.79044499	W
ABUW_RS03590	ABUW_0729	NZ_CP008706.1	735553	736371	+	WP_000426935.1		unidentifiable-diphosphate phosphatase	3173.796915	-2.681021048	0.188661623	-0.12123896	7.686-46	4.866-45	44.07262964	W
ABUW_RS05155	ABUW_050	NZ_CP008706.1	0558748	061005	-	WP_000031228.1		glyoxaldehyde-3-phosphate dehydrogenase	47029.24808	-2.682204376	0.180121442	-0.181910887	3.776-50	4.866-49	48.43133673	W
ABUW_RS05810	ABUW_190	NZ_CP008706.1	1222429	1232322	+	WP_000209397.1		uroporphyrinogen decarboxylase	2208.172454	-2.703787252	0.199538826	-0.94751975	2.016-64	6.626-63	62.63315062	W
ABUW_RS17375	ABUW_3570	NZ_CP008706.1	3627409	3628323	-	WP_000588991.1	lpxO	lipid A hydroxylase LpxO	4794.465865	-2.704155538	0.211961968	-0.75709219	2.826-37	2.216-36	35.05560773	W
ABUW_RS0285	ABUW_0262	NZ_CP008706.1	279723	281084	+	WP_000190021.1	etiA	energy-dependent transaminyl-thiote protein EtiA	27429.05219	-2.708601455	0.179858462	-0.04851249	3.336-51	4.826-50	49.8309296	W
ABUW_RS04970	ABUW_010	NZ_CP008706.1	1024711	1025421	-	WP_000167724.1	queE	7-carboxy-7'-deazaguanine synthase QueE	5361.255039	-2.72708808	0.206058256	-0.23453929	5.546-40	4.916-39	38.30819151	W
ABUW_RS1420	ABUW_1375	NZ_CP008706.1	1301736	1303523	-	WP_000852160.1	nuoC	NADH-quinone oxidoreductase subunit C	25803.6877	-2.73071481	0.261929004	-0.168916246	3.466-22	1.496-21	10.8269173	W
ABUW_RS10380	ABUW_2106	NZ_CP008706.1	2129212	2124003	-	WP_000918444.1	arcC	chiotamate synthase	3097.526888	-2.739974709	0.19188546	-0.25419883	2.386-46	2.686-45	44.57180521	W
ABUW_RS08465	ABUW_0738	NZ_CP008706.1	1735206	1736300	+	WP_000893489.1		phosphatidate cytidyltransferase	5468.341054	-2.741800586	0.167424667	-0.16239068	1.926-48	2.326-47	46.46345102	W
ABUW_RS14860	ABUW_3062	NZ_CP008706.1	3088882	3090352	-	WP_001183055.1	psgG	30S ribosomal protein S7	66711.1624	-2.742428362	0.20908143	-0.10709112	4.836-39	4.066-38	37.39147397	W
ABUW_RS1705	ABUW_2820	NZ_CP008706.1	2824869	2825750	-	WP_000732866.1		hypothetical protein	3284.280267	-2.746950297	0.130667535	-0.210204621	4.266-98	3.656-96	95.43770714	W
ABUW_RS05980	ABUW_0214	NZ_CP008706.1	064544	065826	-	WP_000994842.1	rep	adenosylhomocysteine	101414.91652	-2.75644887	0.190207501	-0.148809353	1.446-47	1.666-46	45.77899191	W
ABUW_RS14770	ABUW_3043	NZ_CP008706.1	3065326	3071725	+	WP_000930305.1		DNA helicase Rep	2860.885424	-2.761747373	0.178104102	-0.5003455	3.146-54	4.836-53	52.1905287	W
ABUW_RS17270	ABUW_3549	NZ_CP008706.1	3605867	3607179	+	WP_001214987.1	piB	type IV-A plus assembly ATPase PiB	1038.801225	-2.765514188	0.211924258	-0.1034423	3.166-39	2.676-38	37.57348174	W
ABUW_RS16640	ABUW_3829	NZ_CP008706.1	3895917	3896747	-	WP_000832516.1	wecB	UDP-N-acetylglucosamine-2-epimerase (non-hydrolyzing)	25336.66454	-2.776804507	0.1256122	-0.221061954	2.766-08	3.476-06	50.4598705	W
ABUW_RS16416	ABUW_3124	NZ_CP008706.1	3201913	3201722	-	WP_000979142.1	nuoE	NADH-quinone oxidoreductase subunit NuoE								

ABUW_RS0780	ABUW_597	N2_CP008706.1	694365	694793	+	WP_002028338.1		membrane protein	676.4302409	-2.99031061	0.2323006	-0.87256548	6.42E-38	5.17E-37	36.26850946
ABUW_RS1730	ABUW_3541	N2_CP008706.1	3599042	3601741	-	WP_000130326.1	infB	translation initiation factor IF-2	102708.377	-2.99255149	0.98584713	-5.06210867	2.87E-51	3.95E-50	49.4034029
ABUW_RS0705	ABUW_1452	N2_CP008706.1	9444	9444369	-	WP_001106722.1	rpsJ	30S ribosomal protein S21	30163.00103	-2.996196437	0.158318268	-9.92464194	7.15E-80	3.03E-78	77.51855737
ABUW_RS0080	ABUW_5016	N2_CP008706.1	9888	9904	+			RNA-1e	95562.46857	-2.999664125	0.342973086	-8.740602735	2.21E-18	8.01E-18	17.00963748
ABUW_RS0235	ABUW_5475	N2_CP008706.1	487759	487835	+			RNA-1e	61548.9179	-3.002019534	0.343830683	-8.731955503	5.25E-18	9.1E-18	17.00441862
ABUW_RS1610	ABUW_3206	N2_CP008706.1	332836	3329195	-	WP_000624763.1	panB	3-methyl-2-oxobutanate dehydrogenyltransferase	3305.91019	-3.007163243	0.17849189	-8.84787098	1.09E-63	2.48E-62	6.116054332
ABUW_RS0550	ABUW_2316	N2_CP008706.1	337394	338395	+	WP_000079187.1		PfIII family protein	353.5946306	-3.0169815075	0.27390041	-0.99299223	4.10E-28	2.30E-27	26.33827179
ABUW_RS04975	ABUW_1614	N2_CP008706.1	625050	626231	-	WP_000080867.1	dapD	4,5-tetrahydroxy-2,6-dicarboxylate N-succinyltransferase	17006.86161	-3.023682758	0.18494272	-8.3491951	4.41E-60	8.58E-59	58.06651771
ABUW_RS1470	ABUW_3031	N2_CP008706.1	3058862	3059889	+	WP_000355491.1		type IV plus hecycling molality protein PflT	604.5924693	-3.024727751	0.299093463	-11.67427273	1.73E-31	1.09E-30	29.9625735
ABUW_RS1720	ABUW_3537	N2_CP008706.1	3597368	3597895	+	WP_001177202.1		Na ⁺ /H ⁺ antiporter subunit E	835.9779905	-3.025563456	0.27812458	-0.87846334	1.46E-27	7.97E-27	26.09854168
ABUW_RS1170	ABUW_2296	N2_CP008706.1	2283653	2284819	+	WP_00109545.1		methionine adenosyltransferase	10122.90254	-3.029732393	0.148636851	-20.38345389	2.35E-92	1.66E-90	89.77899191
ABUW_RS1930	ABUW_2342	N2_CP008706.1	2325711	2326802	+	WP_000506572.1	ychF	redox-regulated ATPase YchF	3186.90602	-3.034780459	0.268544481	-11.30084836	1.30E-29	7.76E-29	28.11018328
ABUW_RS1715	ABUW_3518	N2_CP008706.1	3566252	3568339	-	WP_001885790.1	pnp	polynucleotide nucleotidyltransferase	41203.4912	-3.041188456	0.18240885	-6.17989865	2.10E-62	4.40E-61	60.35654732
ABUW_RS8625	ABUW_3826	N2_CP008706.1	3892006	3893100	-	WP_00100653.1		hypothetical protein	5524.31425	-3.042883381	0.196046632	-5.5212224	2.49E-54	3.86E-53	52.4134127
ABUW_RS02625	ABUW_5034	N2_CP008706.1	542759	543328	-	WP_001004716.1		LenA family protein	187.512676	-3.049645834	0.195167677	-5.6305784	4.51E-55	7.81E-54	53.13875556
ABUW_RS1635	ABUW_3221	N2_CP008706.1	3250917	3250993	-			RNA-1Pro	954.140052	-3.068146041	0.334184562	-9.90992762	4.27E-20	1.65E-19	8.78251906
ABUW_RS02550	ABUW_5519	N2_CP008706.1	529763	529767	-	WP_000083565.1		DUF4442 domain-containing protein	1510.999282	-3.074381999	0.22407766	-8.8586105	7.74E-44	7.98E-43	42.69259361
ABUW_RS1940	ABUW_3590	N2_CP008706.1	3558282	3558578	+	WP_000051038.1		undecylenoyl-phosphatase	367.9452863	-3.075569777	0.21919908	-0.98495389	1.93E-44	2.03E-43	42.69259361
ABUW_RS03355	ABUW_0682	N2_CP008706.1	670335	670555	+	WP_000658992.1		Hsp domain-containing protein	668.112979	-3.075561696	0.20367759	-8.3013883	16.5E-51	2.24E-50	49.64975198
ABUW_RS10375	ABUW_2727	N2_CP008706.1	2714369	2715085	+	WP_000202860.1	tmB	RNA (guanosine[45]-N ⁷)-methyltransferase TmB	806.9630599	-3.076481835	0.263390355	-11.68031917	1.61E-31	1.02E-30	29.91959983
ABUW_RS04545	ABUW_0626	N2_CP008706.1	934661	935466	+	WP_000271049.1	ticA	RNA 2'-thiouridylyl(32') synthetase TicA	3018.347163	-3.086889376	0.17039672	-8.1058891	7.61E-73	2.40E-71	70.61978761
ABUW_RS1610	ABUW_3062	N2_CP008706.1	3105759	3102192	+	WP_000621866.1	ispE	4-(cytidine 5'-diphosphate)-2-C-methyl-D-erythroid kinase	7003.354137	-3.01144058	0.252378641	-0.29004166	1.02E-34	7.42E-34	33.19556969
ABUW_RS0455	ABUW_1736	N2_CP008706.1	1733894	1734448	+	WP_00006428.1	frt	ibosome recycling factor	5586.980737	-3.10277721	0.15553297	-9.9493205	1.52E-88	9.14E-87	86.0390358
ABUW_RS1125	ABUW_2387	N2_CP008706.1	2272722	2276024	+	WP_00104968.1	puA	nitrogenotriphosphate dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase	29744.34279	-3.103841874	0.20100138	-5.44190721	8.59E-54	1.30E-52	53.19556969
ABUW_RS03530	ABUW_5171	N2_CP008706.1	723220	723711	+	WP_001021007.1	mevD	rod shape-determining protein MevD	1216.99917	-3.104749183	0.258721208	-0.00035699	3.54E-33	2.38E-32	31.62342304
ABUW_RS01005	ABUW_0246	N2_CP008706.1	262407	263108	-	WP_000055338.1	hlaA	5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide	3287.81921	-3.108844274	0.178984171	-7.36841071	1.43E-67	3.65E-66	56.45377474
ABUW_RS10375	ABUW_2755	N2_CP008706.1	2744837	2745156	+	WP_000729880.1		NCSD family peptidase	1074.321945	-3.10984401	0.19269677	-6.1853932	1.37E-58	2.55E-57	52.60340882
ABUW_RS02610	ABUW_5598	N2_CP008706.1	529706	5299127	+	WP_000024256.1		hypothetical protein	1014.058063	-3.11002951	0.223243075	-0.93683968	3.78E-44	3.94E-43	46.94507794
ABUW_RS1475	ABUW_3065	N2_CP008706.1	3029709	3030938	+	WP_000083270.1		beta-ketoacyl-ACP synthase II	44223.62446	-3.117450073	0.18572763	-6.83536062	1.34E-63	3.04E-62	61.51712542
ABUW_RS17240	ABUW_3543	N2_CP008706.1	3603274	3603798	-	WP_000777730.1	rmpP	ibosome maturation factor RmpP	10056.9193	-3.126079406	0.244893038	-0.80605765	1.52E-37	1.20E-36	52.69289575
ABUW_RS04810	ABUW_0981	N2_CP008706.1	92691	93761	-	WP_000071984.1	purM	phosphoribosylformyltransferase cyclo-ligase	17016.62391	-3.12723365	0.19651162	-6.81967213	1.75E-63	3.86E-62	61.4118827
ABUW_RS1620	ABUW_3238	N2_CP008706.1	3250594	3250870	+			RNA-1Pro	682.580712	-3.128367835	0.398448739	-7.876440619	3.37E-16	1.04E-14	13.82966616
ABUW_RS18135	ABUW_2269	N2_CP008706.1	2255156	2256193	-	WP_0011740111		fructose-bisphosphate aldolase class II	18551.2851	-3.139957454	0.174162043	-6.02894248	1.95E-72	3.58E-71	70.44618897
ABUW_RS19540	ABUW_2189	N2_CP008706.1	216091	2160978	+	WP_00011876.1		sulfite exporter TsaD/TsaE family protein	1667.48087	-3.153664408	0.378766917	-3.326140073	3.35E-17	2.82E-16	15.54975089
ABUW_RS19630	ABUW_3827	N2_CP008706.1	3893053	3894136	-	WP_000089825.1		oligosaccharyl transferase family protein	32161.22827	-3.1548975816	0.21921433	-1.88710954	4.00E-50	5.14E-49	48.28903868
ABUW_RS19545	ABUW_3119	N2_CP008706.1	3138825	3139962	+	WP_000054321.1		8-amino-7-oxononanoate synthase	1340.31016	-3.166601816	0.167088321	-8.89407716	1.28E-79	3.30E-78	77.27872410
ABUW_RS00070	ABUW_0014	N2_CP008706.1	6180	67392	+	WP_000333558.1		lysine--RNA ligase	3456.259966	-3.175501516	0.16123505	-6.64553937	6.31E-86	3.44E-84	83.46344156
ABUW_RS1816	ABUW_3722	N2_CP008706.1	3780308	3781962	+	WP_00075285.1		LydM peptidoglycan-binding domain-containing protein	1642.025642	-3.175974662	0.176612229	-7.98275621	2.66E-72	8.08E-71	70.09366496
ABUW_RS07880	ABUW_1614	N2_CP008706.1	607409	607918	-	WP_00009660.1		peptidyl-polysite-trans isomerase	16065.265	-3.198793906	0.22067136	-14.49562794	1.29E-47	1.50E-46	24.45307374
ABUW_RS19345	ABUW_2749	N2_CP008706.1	2740105	2741295	+	WP_001185176.1		aspartate kinase	6566.554875	-3.216484068	0.23218485	-0.82667868	1.76E-43	1.79E-42	41.71474697
ABUW_RS1495	ABUW_3594	N2_CP008706.1	3657608	3658036	-	WP_001744882.1	pKk	SOS ribosomal protein L11	87835.05068	-3.21880029	0.22888546	-1.6523839	1.71E-45	1.86E-44	43.7040706
ABUW_RS19270	ABUW_3145	N2_CP008706.1	317093	317185	+	WP_001169880.1		5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	878.172599	-3.245965547	0.20195336	-6.07284779	3.97E-58	7.20E-57	56.1426675
ABUW_RS19375	ABUW_3097	N2_CP008706.1	323056	323236	+	WP_001133287.1		ribose-phosphate pyrophosphokinase	31431.0057	-3.250725495	0.230454491	-1.1057055	3.50E-45	3.76E-44	43.62442191
ABUW_RS04245	ABUW_0865	N2_CP008706.1	844476	845408	+	WP_00094655.1		ribotransferase-related sulfotransferase	4834.555896	-3.259953262	0.22102184	-11.74263193	3.43E-49	4.25E-48	47.3719107
ABUW_RS17490	ABUW_3593	N2_CP008706.1	3665009	3667004	-	WP_001016984.1	p1A	SOS ribosomal protein L1	247823.1832	-3.26312584	0.21919908	-6.0289824	2.26E-38	1.84E-37	36.73192191
ABUW_RS01830	ABUW_0331	N2_CP008706.1	352908	354140	-	WP_000077814.1	serA	phosphoglycerate dehydrogenase	93382.22402	-3.26312584	0.16689695	-20.78818584	4.48E-96	3.61E-94	93.4244928
ABUW_RS19610	ABUW_3823	N2_CP008706.1	3888917	3889331	+	WP_00019785.1		sugar transferase	719.338186	-3.284400011	0.160934059	-20.4081462	1.41E-92	1.03E-90	89.98782728
ABUW_RS01445	ABUW_0234	N2_CP008706.1	252970	254049	+	WP_001057128.1		DNA/RNA non-specific endonuclease	1821.69022	-3.285081885	0.173830358	-8.89809075	1.91E-79	4.96E-78	73.30451832
ABUW_RS01545	ABUW_0314	N2_CP008706.1	336833	337393	+	WP_002194578.1	p1V	type IV plus modification protein P1V	607.260306	-3.305492447	0.333295352	-9.91607379	3.49E-23	1.59E-22	17.19860288
ABUW_RS03220	ABUW_0654	N2_CP008706.1	61690	660968	-	WP_000070856.1		uracil-xanthine permease	1570.287403	-3.307073703	0.314346984	-0.52041342	6.96E-26	3.52E-25	24.45307374
ABUW_RS01340	ABUW_2748	N2_CP008706.1	2737313	273949	+	WP_00019457.1	alsB	alanine--RNA ligase	9488.16599	-3.316357911	0.199342655	-6.65161854	2.95E-62	6.10E-61	60.21467161
ABUW_RS18450	ABUW_3060	N2_CP008706.1	308280	3087470	-	WP_001029610.1	tuf	elongation factor Tu	23118.7247	-3.324525928	0.2114799	-6.72023929	1.62E-55	1.82E-54	53.73992661
ABUW_RS18175	ABUW_2422	N2_CP008706.1	2409332	2410063	+	WP_001103359.1		amino acid ABC transporter ATP-binding protein	9316.955682	-3.325424267	0.377975477	-7.79789481	1.39E-18	5.10E-18	17.29242882
ABUW_RS02555	ABUW_0520	N2_CP008706.1	529803	5303291	-	WP_001108893.1		YajP family cyclic G-GMP-binding protein	922.4282197	-3.327458002	0.204077824	-6.30484481	9.90E-60	1.77E-58	67.75202673
ABUW_RS02870	ABUW_1898	N2_CP008706.1	1935291	1935746	+	WP_000099412.1	anrQ	type II-5-dehydroquinolate dehydratase	2697.680364	-3.330030392	0.12443384	-26.9760617	2.82E-90	3.76E-87	156.421008
ABUW_RS14945	ABUW_3394	N2_CP008706.1	3433621	3437174	-	WP_000365488.1		phosphogluconate dehydratase	3986.954711	-3.333070628	0.273105556	-0.20321402	2.99E-34	2.33E-32	32.8719304
ABUW_RS19630	ABUW_3825	N2_CP008706.1	3890759	3893212	-	WP_000088417.1		oligosaccharyl repeat unit polymerase	5300.202046	-3.332919191	0.21955855	-6.6928433	1.69E-55	2.75E-54	53.50666731
ABUW_RS10280	ABUW_2732	N2_CP00													

ABUW_RS04440	ABUW_0905	NZ_CP008706.1	901081	901666	-		tRNA-Leu	70.5203518	-3.641950649	0.455009125	-8.00406611	1.2051-6	3.84E-15	9.41656878	
ABUW_RS02095	ABUW_0426	NZ_CP008706.1	44033	442052	+	WP_002000592.1	secY	174538.7486	-3.648370056	0.249747174	-14.60827761	2.49E-48	2.99E-47	46.524281	
ABUW_RS08975	ABUW_844	NZ_CP008706.1	942058	942325	+	WP_00121835.1	hypothetical protein	5222.889643	-3.65826911	0.20200293	-16.8222554	7.16E-74	2.34E-72	71.630784	
ABUW_RS02605	ABUW_0530	NZ_CP008706.1	53095	530660	-	WP_00185897.1	secF	521513325	-3.661342309	0.20825334	-17.58270397	3.34E-69	8.98E-68	67.04672366	
ABUW_RS0300	ABUW_3355	NZ_CP008706.1	339272	3393728	-	WP_00185443.1	ivc	335956.40446	-3.69434292	0.159386	-27.28747569	5.97E-84	2.41E-80	95.619383	
ABUW_RS1565	ABUW_3381	NZ_CP008706.1	236763	2366557	-	WP_00114471.1	ATP-binding cassette domain-containing protein	719.953052	-3.696842313	0.454097943	-18.846681	3.52E-16	1.28E-15	60.3792003	
ABUW_RS02090	ABUW_0425	NZ_CP008706.1	440847	441087	+	WP_00175340.1	piD	81888.07951	-3.708961542	0.264840234	-13.99597274	1.63E-44	1.72E-43	42.76447155	
ABUW_RS02210	ABUW_0429	NZ_CP008706.1	443273	443569	+	WP_00184086.1	piK	59266.30441	-3.7125866	0.278468865	-13.33214252	1.51E-40	1.37E-39	38.86327943	
ABUW_RS0405	ABUW_0286	NZ_CP008706.1	304750	305868	+	WP_000928089.1	phospho-N-acetylmutamyl-pentapeptidyl-transferase	4307.776346	-3.730056262	0.179838776	-20.74112327	1.47E-15	1.17E-13	92.301914	
ABUW_RS1450	ABUW_2976	NZ_CP008706.1	299293	2993527	+	WP_00127033.1	amino acid peptidase	704.2848933	-3.735664114	0.238970391	-15.63241415	4.38E-55	7.00E-54	53.15490196	
ABUW_RS20315	no	NZ_CP008706.1	3311078	3311833	+	WP_001987120.1	hypothetical protein	3856.129539	-3.737100635	0.371025892	-10.0723446	7.32E-24	3.43E-23	22.46470588	
ABUW_RS02155	ABUW_0428	NZ_CP008706.1	442897	443253	+	WP_000090815.1	piM	81939.55891	-3.743760215	0.279844375	-13.37800776	8.10E-41	7.51E-40	59.1423006	
ABUW_RS04160	ABUW_0848	NZ_CP008706.1	829662	829973	+	WP_000271409.1	piU	54542.30376	-3.753476159	0.219689808	-17.0853466	1.19E-65	4.55E-64	63.3419888	
ABUW_RS08450	ABUW_1735	NZ_CP008706.1	1733080	1733808	+	WP_000852257.1	pyH	6480.81924	-3.760491412	0.18775276	-22.28105615	5.64E-100	0.09E-100	67.0414361	
ABUW_RS18165	ABUW_3732	NZ_CP008706.1	3789330	3790744	+	WP_000944481.1	atpD	56884.2032	-3.763289603	0.243362638	-15.4637116	6.10E-54	9.27E-53	52.03292027	
ABUW_RS07200	ABUW_1677	NZ_CP008706.1	1655281	166516	+	WP_000397471.1	gltS	4470.04707	-3.765338601	0.2368493	-15.89751335	6.58E-57	1.14E-55	54.94309155	
ABUW_RS05000	ABUW_1019	NZ_CP008706.1	903084	931227	-	WP_000083117.1	cysT	16.0387869	-3.785556079	0.441937310	-18.57077957	9.73E-18	3.42E-17	66.46597389	
ABUW_RS1710	ABUW_3521	NZ_CP008706.1	262084	262623	+		tRNA-Ser	99.40023687	-3.797118503	0.595664357	-6.37458414	1.63E-10	4.35E-10	9.361516743	
ABUW_RS17485	ABUW_3592	NZ_CP008706.1	366983	366589	-	WP_001196230.1	piU	89899.34162	-3.798580789	0.22846681	-16.62640095	4.49E-62	9.8E-61	60.03715732	
ABUW_RS05490	ABUW_1022	NZ_CP008706.1	114531	114519	-	WP_00093094.1	purB	9530.79776	-3.824575182	0.154248146	-24.79459726	102E-105	3.41E-103	92.4872456	
ABUW_RS01950	ABUW_0405	NZ_CP008706.1	432180	432471	+	WP_000070712.1	piJ	89528.80339	-3.834394814	0.238678404	-10.06510997	4.48E-58	8.10E-57	56.0195198	
ABUW_RS04165	ABUW_0849	NZ_CP008706.1	829992	830249	+	WP_000201832.1	piM	30326.02303	-3.842642352	0.10216174	-18.27943076	1.21E-74	4.16E-73	52.39090667	
ABUW_RS07545	ABUW_046	NZ_CP008706.1	532793	533239	-	WP_000382591.1	piL	105251.3301	-3.8802418	0.248204	-15.63330212	4.32E-55	6.93E-54	53.15926677	
ABUW_RS16540	ABUW_3403	NZ_CP008706.1	348925	345186	+	WP_000052885.1	TonB-dependent siderophore receptor	7747.738344	-3.885777441	0.532224255	-17.30101327	2.86E-13	7.95E-13	64.07960287	
ABUW_RS16790	ABUW_3453	NZ_CP008706.1	350053	350115	+	WP_000967566.1	hypothetical protein	5224.585304	-3.889419542	0.219338004	-17.9286482	7.05E-72	2.09E-70	69.07985371	
ABUW_RS06035	ABUW_0335	NZ_CP008706.1	1273330	1273082	+	WP_001082118.1	piB	102238.1676	-3.900550486	0.220038314	-17.73849678	2.62E-70	7.38E-69	68.0194364	
ABUW_RS18160	ABUW_3118	NZ_CP008706.1	318079	318828	-	WP_000055882.1	bicC	1733.30145	-3.905661566	0.167763878	-23.28072410	6.95E-102	1.47E-107	116.8326827	
ABUW_RS18635	ABUW_3828	NZ_CP008706.1	3894324	3895583	-	WP_000565604.1	wecC	28873.63592	-3.912536993	0.166576662	-24.98799401	8.26E-108	3.33E-115	53.47715558	
ABUW_RS02650	ABUW_0696	NZ_CP008706.1	693467	694487	-	WP_000396481.1	acpC	23673.18733	-3.919507631	0.220736999	-17.75644959	1.54E-70	4.36E-69	68.36051051	
ABUW_RS18170	ABUW_3733	NZ_CP008706.1	3750775	3751444	+	WP_001284971.1	gumA	54667.5716	-3.920070696	0.269471697	-14.54061022	5.87E-48	6.96E-47	64.0793076	
ABUW_RS02155	ABUW_0432	NZ_CP008706.1	445342	445719	+	WP_00121830.1	piQ	87878.97395	-3.921639276	0.255160741	-15.36928939	2.63E-53	3.91E-52	51.60778234	
ABUW_RS16016	ABUW_3093	NZ_CP008706.1	3121591	3121655	+		tRNA-Gln	527.5722379	-3.927938991	0.351017951	-11.9651244	4.71E-29	2.78E-28	57.5595652	
ABUW_RS18160	ABUW_3824	NZ_CP008706.1	3889533	3890744	-	WP_001024267.1	glycoyltransferase family 4 protein	16564.74478	-3.927972295	0.163387675	-24.0408199	104E-127	2.80E-125	92.5552842	
ABUW_RS16020	ABUW_3094	NZ_CP008706.1	3121663	3121677	+		tRNA-Gln	268.3045712	-3.924345434	0.334016015	-11.80318663	3.76E-32	2.42E-31	30.61914643	
ABUW_RS02385	ABUW_0424	NZ_CP008706.1	440667	440643	+	WP_000849088.1	piM	58027.68502	-3.943325175	0.265319856	-14.86247707	5.77E-50	7.39E-49	63.1835556	
ABUW_RS17275	ABUW_3550	NZ_CP008706.1	3607690	3608835	+	WP_000271621.1	type II secretion system F family protein	1140.985159	-3.953824968	0.216102962	-18.29375033	9.28E-75	3.22E-73	72.49214410	
ABUW_RS01950	ABUW_0430	NZ_CP008706.1	345951	346319	+	WP_000041562.1	piS	333588.52231	-3.958400779	0.227584006	-17.33905844	9.31E-68	2.40E-66	65.01978876	
ABUW_RS02115	ABUW_0430	NZ_CP008706.1	443872	444298	+	WP_000152024.1	piD	143627.8764	-3.958580287	0.272470282	-14.53314554	7.47E-48	8.78E-47	46.05605048	
ABUW_RS18165	ABUW_3489	NZ_CP008706.1	2485285	2486881	-	WP_0010162883.1	NAD(P)H-dependent oxidoreductase	443.651626	-3.969619337	0.404821867	-19.804350201	1.08E-22	4.78E-22	71.19664449	
ABUW_RS02150	ABUW_0431	NZ_CP008706.1	444316	445323	+	WP_000186311.1	poA	31729.18397	-3.983544598	0.284748242	-13.98970742	1.80E-44	1.19E-43	62.17896663	
ABUW_RS18005	ABUW_3903	NZ_CP008706.1	3969443	3971003	+	WP_001188090.1	ydcC	33583.20947	-3.991815001	0.21723258	-18.37579298	2.05E-75	7.45E-74	73.0784373	
ABUW_RS02340	ABUW_0598	NZ_CP008706.1	595379	597157	-	WP_000984511.1	aspS	26296.28745	-3.999862531	0.193889537	-20.62950458	1.69E-94	1.15E-92	91.77492163	
ABUW_RS17695	ABUW_3634	NZ_CP008706.1	3697379	3693699	+	WP_000808735.1	xerD	1343.210569	-4.003767877	0.147708479	-27.0587712	8.39E-162	1.69E-168	97.01662155	
ABUW_RS08990	ABUW_0827	NZ_CP008706.1	823187	8241456	+	WP_000781452.1	emo	24287.51903	-4.009495876	0.156695981	-25.58773712	2.09E-144	9.35E-142	110.029184	
ABUW_RS18985	ABUW_0322	NZ_CP008706.1	345093	345743	+	WP_000464595.1	tmd	tRNA [guanine(37)-N1]-methyltransferase Tmd	337.01.8309	-4.031971563	0.195039894	-18.8601862	1.09E-166	1.88E-165	64.7294216
ABUW_RS18990	ABUW_2382	NZ_CP008706.1	2386867	2389707	-	WP_000651495.1	tauA	782.022316	-4.033208798	0.542270792	-17.435968995	1.04E-10	2.97E-10	12.5723535	
ABUW_RS02045	ABUW_0416	NZ_CP008706.1	437279	437847	+	WP_001982034.1	piN	106725.8474	-4.035951952	0.245634997	-16.43068764	1.5E-60	2.28E-59	58.84200516	
ABUW_RS18565	ABUW_3814	NZ_CP008706.1	3875855	3878252	-	WP_0118571963.1	ldpP	5075.973923	-4.076372295	0.351975382	-11.57852936	5.29E-31	3.28E-30	29.48410816	
ABUW_RS18290	ABUW_2319	NZ_CP008706.1	2304179	2304616	+	WP_001161759.1	PACE efflux transporter	486.7408237	-4.08930184	0.538187738	-17.598575495	2.99E-14	8.85E-14	13.05300673	
ABUW_RS02075	ABUW_0422	NZ_CP008706.1	439810	440160	+	WP_0001003184.1	piR	42395.19474	-4.094291106	0.282510022	-14.49234652	1.35E-47	1.57E-46	54.00410035	
ABUW_RS18175	ABUW_0320	NZ_CP008706.1	344108	344389	+	WP_000260334.1	piP	25973.41621	-4.10504224	0.263800252	-15.56117634	1.34E-54	2.09E-53	52.67985371	
ABUW_RS18160	ABUW_3457	NZ_CP008706.1	3504451	3504672	+	WP_001084370.1	infA	5707.830075	-4.114588226	0.22824071	-18.0270448	1.19E-72	3.65E-71	70.43770714	
ABUW_RS18535	ABUW_3402	NZ_CP008706.1	3447176	3448510	+	WP_001188432.1	tlgR	29049.37583	-4.116236365	0.165023449	-24.80858723	7.24E-106	2.65E-103	92.57574541	
ABUW_RS02080	ABUW_0423	NZ_CP008706.1	440193	440660	+	WP_001141925.1	piE	52107.17173	-4.119409232	0.278919316	-14.76391444	2.50E-49	3.10E-48	67.0584541	
ABUW_RS16025	ABUW_3095	NZ_CP008706.1	3121789	3121863	+		tRNA-Gln	98.1736355	-4.12919383	0.381938719	-10.815762	2.96E-27	1.60E-26	25.9588002	
ABUW_RS01440	ABUW_0293	NZ_CP008706.1	121770	121797	+	WP_000695059.1	piL	402.4531648	-4.150676432	0.248502875	-16.64236858	3.44E-62	7.07E-61	60.0500509	
ABUW_RS02425	ABUW_0494	NZ_CP008706.1	505559	505987	-	WP_000854895.1	piM	44506.47449	-4.184598992	0.21741974	-19.03907469	8.09E-81	3.62E-79	78.44291943	
ABUW_RS1165	ABUW_3642	NZ_CP008706.1	368759	369811	-	WP_000868152.1	diU	803.3598108	-4.188557109	0.189967409	-21.83825703	1.01E-105	1.23E-103	92.9100949	
ABUW_RS02050	ABUW_0417	NZ_CP008706.1	437567	437874	+	WP_001026885.1	piU	44858.95409	-4.193036168	0.229857513	-16.08787126	5.71E-73	1.82E-71	70.78992861	
ABUW_RS1430	ABUW_2972	NZ_CP008706.1	2868720	2868378	+	WP_001021934.1	betA	5009.567378	-4.19435564	0.450413594	-19.24562016	2.34E-20	9.16E-20	63.0385463	
ABUW_RS1840	ABU														

ABUW_RS02000	ABUW_0407	NZ_CP008706.1	433179	433781	+	WP_001050255.1	tpdD	50S ribosomal protein L4	190424.3195	-4.793323202	0.332517109	-14.41526788	4.15E-47	4.73E-46	45.32518866
ABUW_RS00635	ABUW_0128	NZ_CP008706.1	432723	433998	-	WP_001167274.1		ion channel protein TssX	2811.272538	-4.85809118	0.240690079	-20.1840109	1.35E-90	9.24E-89	88.03432803
ABUW_RS02025	ABUW_0412	NZ_CP008706.1	435566	436318	+	WP_000529922.1	gpcC	30S ribosomal protein S3	129966.0493	-4.858367017	0.321421905	-15.1623311	1.29E-51	1.79E-50	49.74714697
ABUW_RS02020	ABUW_0411	NZ_CP008706.1	435325	435564	+	WP_001982638.1	gplV	50S ribosomal protein L22	52252.33271	-4.865655952	0.31931533	-15.267531	9.52E-53	1.37E-51	50.86327943
ABUW_RS06040	ABUW_0236	NZ_CP008706.1	1279220	1280095	+	WP_000125378.1		elongation factor Ts	41943.25274	-4.865788508	0.218002517	-22.31978128	2.37E-10	3.99E-108	87.3990271
ABUW_RS02005	ABUW_0408	NZ_CP008706.1	433778	434098	+	WP_001058538.1	gplW	50S ribosomal protein L23	57055.1086	-4.872900265	0.295775353	-16.47500447	5.55E-61	1.11E-59	58.95467702
ABUW_RS01435	ABUW_0292	NZ_CP008706.1	31519	312259	+	WP_000076101.1		type 4a pilus biogenesis protein PiliD	1434.943211	-4.874454962	0.27943226	-17.44413818	3.81E-68	1.00E-66	66
ABUW_RS01495	ABUW_0304	NZ_CP008706.1	327823	328296	+	WP_000993729.1		pilin	11795.64268	-4.887022671	0.336813888	-14.50956402	1.05E-47	1.23E-46	45.81009489
ABUW_RS18190	ABUW_3737	NZ_CP008706.1	3794371	3794616	-	WP_000424060.1	atpE	F0F1ATP synthase subunit C	45828.50365	-4.944683324	0.27170389	-18.19185651	5.34E-74	1.76E-72	71.75448733
ABUW_RS03465	ABUW_0704	NZ_CP008706.1	708980	710455	+	WP_001005337.1		alanine:cation symporter family protein	7592.184518	-4.98100347	0.261476798	-19.04950465	6.63E-61	3.00E-79	78.52287875
ABUW_RS18180	ABUW_3735	NZ_CP008706.1	379333	3793849	-	WP_000818995.1		F0F1ATP synthase subunit delta	50071.63658	-5.136484288	0.28153919	-18.24424862	2.30E-74	7.85E-73	72.1051034
ABUW_RS09600	ABUW_1974	NZ_CP008706.1	1975742	1976932	+	WP_001169096.1	adeA	ultravid efflux RND transporter periplasmic adaptor subunit AdeA	18712.17969	-5.163433666	0.320646643	-16.10318952	2.42E-58	4.44E-57	56.35261703
ABUW_RS05005	ABUW_1620	NZ_CP008706.1	1931308	1931916	-	WP_000140921.1		alpha/beta hydrolase	280.8572397	-5.23726585	0.552304384	-9.482571566	2.48E-21	1.02E-20	19.99199983
ABUW_RS18185	ABUW_3736	NZ_CP008706.1	3793862	3794332	-	WP_001024691.1		F0F1ATP synthase subunit B	36085.43341	-5.239508232	0.293750694	-17.83658163	3.68E-71	1.07E-69	68.87061622
ABUW_RS16350	ABUW_3365	NZ_CP008706.1	3406102	3406095	-	WP_002027450.1		enoyl-ACP reductase	24203.586424	-5.247638925	0.12761154	-24.66446215	2.57E-104	7.98E-132	131.0979971
ABUW_RS14445	ABUW_2975	NZ_CP008706.1	2991309	2992197	+	WP_000698108.1		homocysteine S-methyltransferase family protein	592.732493	-5.56059837	0.307808192	-18.06514096	6.00E-73	1.90E-72	72.0725464
ABUW_RS01290	ABUW_0263	NZ_CP008706.1	281663	282156	+	WP_000721434.1		hypothetical protein	4441.725076	-5.618505649	0.26039315	-21.5227669	9.53E-103	9.37E-101	100.0282604
ABUW_RS00925	ABUW_0187	NZ_CP008706.1	209373	210254	-	WP_000773301.1	omp33-36	porin Omp33-36	43762.53578	-6.050106087	0.33281021	-18.17874868	7.60E-74	2.47E-72	71.60730305
ABUW_RS14740	ABUW_3037	NZ_CP008706.1	3063650	3064105	-	WP_000782976.1		bacteriorhodopsin	7815.817815	-6.801795851	0.328100607	-20.73082371	1.83E-95	1.42E-93	92.84771166

Table S7. RNA-seq data: Absolute and relative expression (NaCl/MEP > 2-fold up)

locus_tag	'old_locus_tag'	chem	start	stop	strand	refseq_id	symbol	name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	-log10
ABUW_RS20160	no	NZ_CP008706.1	1697527	1697621	+			hypothetical protein	15.1972919	4.330269647	1.278991576	3.385690514	0.000709994	0.003341783	2.176021777
ABUW_RS07250	ABUW_1487	NZ_CP008706.1	1474362	1474898	+	WP_000790104.1	csuAB	Cou fibrinial major subunit CsuAB	1918.820395	3.93170839	1.248007321	3.150197019	NA	NA	1.7416111
ABUW_RS07270	ABUW_1491	NZ_CP008706.1	1478869	1479367	+	WP_000603294.1	csuB	Cou fibrinial usher CsuD	970.5711899	3.834296657	1.128767633	3.3968187495	NA	NA	1.7416111
ABUW_RS07275	ABUW_1492	NZ_CP008706.1	1479364	1480383	+	WP_002017500.1	csuE	Cou fibrinial lip address CsuE	294.4313251	3.794839881	1.190900074	3.42193368	NA	NA	1.7416111
ABUW_RS07265	ABUW_1490	NZ_CP008706.1	1476039	1476872	+	WP_001986519.1	csuC	Cou fibrinial biogenesis chaperone CsuC	340.8660512	3.46147659	1.123402286	3.081244033	0.002061376	0.00810063	2.090945418
ABUW_RS01510	ABUW_0307	NZ_CP008706.1	330921	331115	-	WP_000289091.1		bacterioferritin-associated ferredoxin	600.0857499	3.305797807	0.723275719	4.570590986	4.86E-06	4.34E-05	4.362991619
ABUW_RS10640	ABUW_2189	NZ_CP008706.1	2173608	2175392	-	WP_001165890.1		siderophore biosynthesis protein	2465.579795	3.216636551	0.629004643	5.1185184	3.16E-07	3.80E-06	5.420634901
ABUW_RS18405	ABUW_3780	NZ_CP008706.1	3840068	3841195	-	WP_001801766.1		acyl-CoA dehydrogenase family protein	643.9599498	2.905742637	0.330445328	8.79341489	1.45E-18	2.66E-16	15.57561062
ABUW_RS01275	ABUW_0260	NZ_CP008706.1	276984	277874	-	WP_001035486.1		SDR family NAD(P)-dependent oxidoreductase	1479.56875	2.800456816	0.461020001	6.073162751	1.25E-09	2.90E-08	7.5370017
ABUW_RS15320	ABUW_2784	NZ_CP008706.1	2779143	2779532	+	WP_000372413.1		Paal family thioesterase	33.1812634	2.786545359	0.565719609	4.924992189	8.44E-07	8.90E-06	5.050710353
ABUW_RS10070	ABUW_2074	NZ_CP008706.1	2056008	2056409	-	WP_000207886.1		transcriptional repressor	45.75954753	2.771062695	0.864197869	3.206537291	0.001343429	0.005667723	2.246591419
ABUW_RS05760	ABUW_1180	NZ_CP008706.1	1210483	1212111	+	WP_000744369.1	basE	(2,3-dihydroxybenzoyl)adenylate synthase BasE	272.1992465	2.733499505	0.730714618	3.740857835	0.000183393	0.00126238	2.988751909
ABUW_RS05725	ABUW_1173	NZ_CP008706.1	1199938	1200879	+	WP_001070792.1	bauD	ferric acinetobactin ABC transporter permease subunit BauD	55.64408655	2.661903786	0.867899354	3.067056185	0.002161717	0.00841229	2.075058761
ABUW_RS01180	ABUW_0237	NZ_CP008706.1	255242	255931	-	WP_001845866.1	argZ	argininase Z	10712.92277	2.19357665	0.287802738	9.10225654	8.93E-20	2.40E-17	8.19595455
ABUW_RS18400	ABUW_3779	NZ_CP008706.1	3839273	3840046	-	WP_001919691.1		enoyl-CoA hydratase	234.409076	2.472788785	0.327588127	7.548468888	4.40E-14	3.52E-12	11.45394541
ABUW_RS07255	ABUW_1488	NZ_CP008706.1	1474973	1475521	+	WP_000577009.1	csuA	Cou fibrinial biogenesis permease CsuA	288.6416321	2.472237337	1.276935458	1.936043416	0.052862384	0.15417693	0.937652362
ABUW_RS18280	ABUW_3351	NZ_CP008706.1	3387175	3388038	-	WP_000037364.1		hypothetical protein	980.7425242	2.457801155	0.42629493	5.765496414	8.14E-09	1.46E-07	6.8362614
ABUW_RS11940	ABUW_2454	NZ_CP008706.1	2441852	2442655	+	WP_000121729.1		enoyl-CoA hydratase/isomerase family protein	1274.636723	2.452348482	0.323804161	7.536865664	4.81E-14	3.73E-12	11.42829638
sRNA75	no	no	no	no	no	no	no	no	4615842247	2.448524659	0.41812087	5.884166917	4.00E-09	8.27E-08	7.062707941
ABUW_RS07245	ABUW_1486	NZ_CP008706.1	1473140	1473778	-	WP_000590096.1		TetR/CirR family transcriptional regulator	44.50382304	2.424349904	1.160073198	2.089824942	0.036633528	0.08990781	1.065548055
ABUW_RS10635	ABUW_2188	NZ_CP008706.1	2172182	2173615	-	WP_000483876.1		SidA/CuDPvA family monooxygenase	174.867092	2.353616636	0.544542108	4.32220101	1.54E-05	0.00019923	3.92497125
ABUW_RS20145	ABUW_1183	NZ_CP008706.1	1214365	1214520	+	WP_001176111.1		hypothetical protein	44.87573437	2.352664674	0.536247042	4.387277673	1.15E-05	9.27E-05	4.033043791
sRNAs	no	no	no	no	no	no	no	no	3.947129552	2.348898292	1.48424592	1582554725	0.1032299	0.070737619	0.678527932
ABUW_RS10585	ABUW_2178	NZ_CP008706.1	2160169	2160789	-	WP_000956973.1		acetyltransferase	1819.420303	2.328747803	0.562913214	4.169597072	3.52E-05	0.00024875	3.604236728
ABUW_RS06610	ABUW_1055	NZ_CP008706.1	1368163	1368323	-	WP_000993415.1		hemin uptake protein HemP	362.5923692	2.322606301	0.441415346	5.261252318	1.43E-07	1.85E-06	5.733512259
ABUW_RS10080	ABUW_2076	NZ_CP008706.1	2056761	2058421	+	WP_001025794.1		SDR family oxidoreductase	273.1466939	2.298704552	0.6890805	3.335901323	0.000805023	0.003882873	2.410848801
ABUW_RS05730	ABUW_1174	NZ_CP008706.1	1200879	1201826	+	WP_001232385.1	bauC	ferric acinetobactin ABC transporter permease subunit BauC	4176.918332	2.291426154	0.571315274	3.989054669	6.39E-05	0.000418395	3.378415535
ABUW_RS19170	ABUW_2321	NZ_CP008706.1	2826194	2826283	-			rRNA-5er	99.40023687	2.266497363	0.445046881	5.09271827	3.53E-07	4.17E-06	5.93973467
ABUW_RS10630	ABUW_2187	NZ_CP008706.1	2170722	2172181	-	WP_000442383.1		DHA2 family efflux MFS transporter permease subunit	497.7528411	2.252634141	0.460648717	4.89013404	1.01E-06	1.05E-05	4.980315482
ABUW_RS11995	ABUW_2465	NZ_CP008706.1	2457318	2457986	-	WP_000080703.1		3-oxoacyl-CoA transferase subunit A	34.94059084	2.244010128	0.44810936	4.162519069	3.91E-06	3.55E-05	4.449320532
ABUW_RS07260	ABUW_1489	NZ_CP008706.1	1475527	1476045	+	WP_000476475.1	csuB	Cou fibrinial biogenesis permease CsuB	124.0377787	2.240799714	1.1308925806	1.719379194	0.000808111	0.07149842	0.914062702
sRNA44	no	no	no	no	no	no	no	no	4.738178039	2.233626408	1.31872965	1.604763324	0.108549844	0.239384275	0.891621176
ABUW_RS12725	ABUW_2621	NZ_CP008706.1	2618549	2619007	-	WP_001273311.1		hypothetical protein	494.1494428	2.21991769	0.372870511	5.956718271	2.57E-09	5.60E-08	7.251973467
ABUW_RS10075	ABUW_2075	NZ_CP008706.1	2056937	2057578	-	WP_000028856.1		isochromatase family protein	489.7438161	2.218114121	0.58120017	3.95244734	7.74E-05	0.000490814	3.309082701
ABUW_RS14505	ABUW_2987	NZ_CP008706.1	3005847	3006368	-	WP_081032250.1		sigma-70 family RNA polymerase sigma factor	69.92426214	2.196318591	0.458221877	4.79313411	1.04E-06	1.63E-05	4.789033631
sRNA76	no	no	no	no	no	no	no	no	2019.910062	2.194385325	0.298352417	7.355011055	1.91E-13	1.02E-11	10.9201513
ABUW_RS11915	ABUW_2449	NZ_CP008706.1	2435735	2436406	-	WP_001029902.1		class ISAM-dependent methyltransferase	578.580408	2.189823	0.298269253	7.341957091	2.18E-11	1.29E-11	10.89048837
ABUW_RS10515	ABUW_2183	NZ_CP008706.1	2177866	2177912	+	WP_000758239.1		DUF3237 domain-containing protein	23.86190691	2.160404332	0.586237905	3.672020513	0.000286505	0.00526891	2.81891944
ABUW_RS00595	ABUW_1143	NZ_CP008706.1	1189895	1189920	+	WP_000026856.1		YsdD/YX family protein	9.5373680	2.103704085	0.380259798	6.824451648	8.83E-12	3.56E-10	9.40029979
ABUW_RS19395	ABUW_3778	NZ_CP008706.1	3838235	3839260	-	WP_00190933.1		enoyl-CoA hydratase/isomerase family protein	119.23198	2.082105994	0.2438016	5.537414413	1.37E-17	2.2E-15	11.65502331
ABUW_RS05780	ABUW_1184	NZ_CP008706.1	1214513	1214555.1	+	WP_001028155.1	banA	lobacin export ABC transporter permease/ATP-binding subunit	296.3056317	2.161533779	0.383174332	5.42339663	1.56E-08	8.12E-07	8.096402184
ABUW_RS11945	ABUW_2455	NZ_CP008706.1	2442668	2444658	+	WP_000461920.1		acetylpropiolyl(methylcrotonyl)-CoA carboxylase subunit alpha	387.508829	2.080745219	0.293425087	7.091231714	1.33E-12	6.81E-11	10.79805621
ABUW_RS05765	ABUW_1181	NZ_CP008706.1	1212129	1212998	+	WP_001018265.1	basF	lobacin biosynthesis bifunctional isochromatase family/ carrier protein	181.843174	2.072323628	0.14877714	3.370302066	0.000750858	0.003489283	2.427638684
ABUW_RS20485	ABUW_3653	NZ_CP008706.1	1655820	1655993	-	WP_001193332.1		sigma-70 family RNA polymerase sigma factor	37.2054944	2.061952904	0.57432498	4.508556002	6.53E-06	5.67E-05	4.45680386
ABUW_RS05735	ABUW_1175	NZ_CP008706.1	1201923	1202593	+	WP_000562117.1	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	151.0769417	2.053394866	0.568569943	3.611679742	0.000304422	0.00191715	7.792711897
ABUW_RS19255	ABUW_3346	NZ_CP008706.1	3379744	3382500	-	WP_001051980.1	acsA	acetyltransferase AcsA	547.7368484	2.00971272	0.265381298	7.572926073	3.65E-14	3.00E-12	11.52280136
ABUW_RS10720	ABUW_1170	NZ_CP008706.1	1191727	1193907	-	WP_085920665.1	banB	acinetobactin non-ribosomal peptide synthetase subunit BasB	49.7369801	1.956777326	0.275620367	2.955567162	0.00320948	0.0104009	7.943019175
ABUW_RS18555	ABUW_3812	NZ_CP008706.1	3874665	3875816	-	WP_000857286.1	ladP	FMN-dependent L-lactate dehydrogenase LadP	2830.455057	1.98837183	0.319317086	5.863033062	4.54E-09	9.20E-08	7.01631391
ABUW_RS18565	ABUW_3814	NZ_CP008706.1	3876585	3878252	-	WP_01857993.1	isdP	L-lactate permease	5075.973923	1.948484928	0.346410156	5.728591912	1.10E-08	1.78E-07	6.719496598
ABUW_RS19765	ABUW_1912	NZ_CP008706.1	1906447	1906647	+	WP_000462396.1		hypothetical protein	4.998927239	1.977426355	1.082299855	1.822195538	0.068435788	0.19198281	0.847992261
ABUW_RS15330	ABUW_3157	NZ_CP008706.1	313339	315072	+	WP_001001866.1		mechanosensitive ion channel	14.9122788	1.97386017	0.357587601	6.53781671	6.25E-11	2.96E-09	8.885100347
ABUW_RS17430	ABUW_3581	NZ_CP008706.1	3639374	3641293	+	WP_00104903.1	higP	molecular chaperone HigP	558.864606	1.950401326	0.332838454	5.83481958	5.11E-09	9.09E-08	7.000552248
ABUW_RS05800	ABUW_1188	NZ_CP008706.1	1219412	1220581	+	WP_000983826.1	basJ	acinetobactin biosynthesis isochromatase synthase BasJ	175.9262843	1.939220938	0.493478005	3.929700852	8.51E-05	0.00034591	3.917878235
ABUW_RS08045	ABUW_9459	NZ_CP008706.1	945428	9454738	+	WP_000179474.1		hypothetical protein	323.084066	1.93531191	0.328621414	5.921676251	1.91E-05	6.76E-04	7.96941234
ABUW_RS18560	ABUW_3813	NZ_CP008706.1	3875813	3876565	+	WP_001222772.1	isrR	transcriptional regulator IsrR	208.84112	1.92465512	0.329706148	5.837486292	5.30E-09	1.02E-07	6.990720243
ABUW_RS14500	ABUW_2986	NZ_CP008706.1	3004830	3005846	+	WP_001024054.1		FecR domain-containing protein	37.8729969	1.91516019	0.4930537	3.892962386	9.90E-05	0.00068409	3.215804517
ABUW_RS11935	ABUW_2453	NZ_CP008706.1	2440421	2441842	+	WP_00107277.1		methylcrotonyl-CoA carboxylase	190.262352	1.910207761	0.339105481	5.63528281	1.75E-08	2.86E-07	6.543886993
ABUW_RS05745	ABUW_1177	NZ_CP008706.1	1203654	1203952	+	WP_001018286.1	bauA								

ABLU_RS06065	ABLU_1241	NZ_CP008706.1	028739	028391	-	WP_000835608.1		DUF682 domain-containing protein	639.006159	1875994652	0.265524045	7.065253354	160E-12	7.88E-11	10.10320E10
ABLU_RS06115	ABLU_2596	NZ_CP008706.1	2559891	2550541	-	WP_001033088.1		TerR/AcrI family transcriptional regulator	217.933828	1869998204	0.82803286	2.04642949	0.043942074	0.0996306	100.60961
ABLU_RS06850	ABLU_919	NZ_CP008706.1	916397	916397	+	WP_000061668.1		NAD(P)-dependent 2,4-dienoyl-CoA reductase	713.802050	1860604565	0.38522322	5.841063188	5.9E-09	1.00E-07	6.998742895
ABLU_RS16005	ABLU_282	NZ_CP008706.1	2163161	2165479	-	WP_000415997.1		TonB-dependent receptor	783.270963	1843391917	0.336028986	5.427647392	5.7E-08	8.3E-07	6.08833407
ABLU_RS16300	ABLU_3151	NZ_CP008706.1	3174373	3178506	+	WP_000044599.1		TerR/AcrI family transcriptional regulator	795.038323	1817723397	0.295733643	6.564883569	7.02E-10	1.94E-08	7.75944482
ABLU_RS06245	ABLU_933	NZ_CP008706.1	939047	939130	+	WP_000037356.1		Iron-containing edox enzyme family protein	683.608021	181565507	0.204422025	8.97661427	6.88E-09	1.39E-06	15.8763193
ABLU_RS05715	ABLU_189	NZ_CP008706.1	189239	1897206	+	WP_000919246.1	basA	acinetobactin non-ribosomal peptide synthetase subunit BasA	355.4575955	1793709847	0.427258506	4.10814653	2.85E-05	0.000195679	3.708457542
ABLU_RS08645	ABLU_975	NZ_CP008706.1	974456	9747401	-	WP_000049688.1		hypothetical protein	2649.474744	1790523849	0.263841937	6.79302047	1.9E-11	4.2E-10	9.375350965
ABLU_RS17370	ABLU_3569	NZ_CP008706.1	3626706	3627236	-	WP_000295953.1		peptidoglycan hydrolase	95.9792999	1790514913	0.246751445	7.256350251	3.98E-13	2.23E-11	10.65280744
ABLU_RS18550	ABLU_3811	NZ_CP008706.1	3872632	3874338	-	WP_001893016.1	ddl	D-lactate dehydrogenase	1286.212284	1787222497	0.255035292	7.00774579	2.42E-12	1.16E-10	9.940086466
ABLU_RS05770	ABLU_182	NZ_CP008706.1	121816	1214267	+	WP_000063880.1	basG	acinetobactin biosynthesis histidine decarboxylase BasG	94.241077	1781916613	0.454067371	3.923029328	8.74E-05	0.000544522	3.263984437
ABLU_RS02385	ABLU_0486	NZ_CP008706.1	497507	499120	+	WP_000154085.1		acetyl-CoA carboxylase carboxyltransferase subunit	192.7416279	1777887176	0.390236749	4.555919402	5.22E-06	4.63E-05	4.33454853
ABLU_RS08035	ABLU_945	NZ_CP008706.1	946874	943134	-	WP_000527016.1		TonB-dependent receptor	2039.817431	1769720935	0.37531925	4.716339897	2.41E-06	2.27E-05	4.643675542
ABLU_RS18920	ABLU_2450	NZ_CP008706.1	2436477	2438107	-	WP_00183733.1		AMP-binding protein	17617.6243	1730771975	0.318898612	5.481695319	4.72E-08	7.02E-07	6.93945268
ABLU_RS18950	ABLU_2456	NZ_CP008706.1	2444655	2445557	+	WP_001288910.1		hydroxyethylglutaryl-CoA lyase	869.797706	1722957224	0.289969275	5.94861937	2.82E-09	6.07E-08	7.218697568
ABLU_RS18470	ABLU_2358	NZ_CP008706.1	2340767	2342074	+	WP_000819595.1		dicarboxylate/amino acid cation symporter	2310.978507	1721467841	0.365838197	4.704669848	2.54E-06	2.39E-05	4.621652772
ABLU_RS10395	ABLU_2223	NZ_CP008706.1	2307578	2307654	+			RNAse Ia	34.16747999	171494884	0.496743484	5.432583164	0.000555658	0.002733607	2.563263965
ABLU_RS18530	ABLU_3807	NZ_CP008706.1	3864042	3869199	-	WP_000097516.1	pgpC	2-methylerythrate synthase	378.1352569	1710130101	0.274573314	6.235602721	4.50E-10	1.15E-08	7.937449147
sRNA93	no	no	no	no	no	no	no	no	424.999025	1700879339	0.400870021	4.242959807	2.21E-05	0.000165505	3.71898085
ABLU_RS15055	ABLU_2781	NZ_CP008706.1	2778038	2777177	+	WP_001051439.1		acyl-CoA dehydrogenase family protein	65.850032	1696048561	0.344265406	4.930948601	8.9E-07	8.65E-06	5.002008442
ABLU_RS16025	ABLU_2084	NZ_CP008706.1	2049977	2048210	-	WP_000044016.1		hypothetical protein	395.3538908	1695668614	0.743681613	2.280160533	0.022601727	0.058878765	1230041007
ABLU_RS06830	ABLU_0687	NZ_CP008706.1	695949	696052	-	WP_001084261.1		enterocidin A/B family lipoprotein	8296.695798	1684554164	0.31833935	5.295931074	121E-07	1.60E-06	5.796194886
ABLU_RS17460	ABLU_3587	NZ_CP008706.1	3645893	3646429	-	WP_001034851.1		hypothetical protein	928.718039	1682751192	0.306164022	5.492460811	3.88E-08	5.83E-07	6.234106474
ABLU_RS02710	ABLU_0552	NZ_CP008706.1	554968	555162	-	WP_000069051.1		hypothetical protein	62.8789432	168261806	0.36428006	4.617770229	3.88E-06	3.54E-05	4.5215278
ABLU_RS09635	ABLU_1981	NZ_CP008706.1	1986888	1987537	-	WP_000377262.1		hypothetical protein	624.288302	1680269226	0.208736953	8.046997003	8.30E-16	1.0E-13	12.9942446
ABLU_RS09785	ABLU_2015	NZ_CP008706.1	2007127	2007411	+	WP_000050492.1		DUF2523 domain-containing protein	95.52870962	1678312576	0.581849887	2.881792186	0.003879868	0.010723732	1.862572769
ABLU_RS09050	ABLU_859	NZ_CP008706.1	856429	856628	-	WP_000387550.1		hypothetical protein	559.554375	1667763729	0.543799245	3.068873934	0.002163101	0.00842929	2.07508571
ABLU_RS02375	ABLU_0484	NZ_CP008706.1	494759	496564	+	WP_000002862.1		DUF1446 domain-containing protein	270.2034319	1656382873	0.366293901	4.522005053	6.10E-06	5.35E-05	4.271950791
ABLU_RS17270	ABLU_2620	NZ_CP008706.1	2619026	2618454	+	WP_000406271.1		GNA1 family N-acetyltransferase	165.6377502	1646423325	0.2908828	6.974051465	1.42E-08	2.39E-07	6.62120342
ABLU_RS18990	ABLU_2464	NZ_CP008706.1	2456565	2457318	-	WP_000160393.1		3-oxoacid CoA-transferase subunit B	74.4200576	1647133896	0.309033867	5.329942442	9.82E-08	1.33E-06	5.87262583
ABLU_RS14515	ABLU_2889	NZ_CP008706.1	3007563	3008527	+	WP_000050679.1		thymidopyrophosphate synthase family protein	45.66903242	1636341021	0.390512678	4.96353678	2.72E-05	0.000197776	3.703263661
ABLU_RS11950	ABLU_2354	NZ_CP008706.1	2338893	2337738	-	WP_000359319.1		AcrC family transcriptional regulator	652.4444195	1631768401	0.236243687	6.907960296	4.95E-12	2.08E-10	9.682505993
ABLU_RS17635	ABLU_3622	NZ_CP008706.1	3688064	3689945	-	WP_000998520.1		TerR/AcrI family transcriptional regulator	73.45291951	1617990329	0.310713452	5.092608829	3.53E-07	4.17E-08	5.379573467
ABLU_RS04980	ABLU_915	NZ_CP008706.1	920816	9227356	-	WP_000866522.1	carO	ornithine uptake protein CarO type 3	499.458359	1617741669	0.26581944	6.085961042	1.9E-09	2.72E-08	7.564384442
ABLU_RS11955	ABLU_2355	NZ_CP008706.1	2337728	2338213	-	WP_000066035.1		glutathione peroxidase	608.4157007	1614058733	0.256838962	6.284370902	3.29E-10	8.90E-09	6.850550353
sRNA27	no	no	no	no	no	no	no	no	240.087951	160582618	0.274361644	5.852594377	4.83E-09	9.58E-08	7.018428607
ABLU_RS18285	ABLU_3352	NZ_CP008706.1	3388369	3388941	+	WP_000043984.1		TerR/AcrI family transcriptional regulator	492.5532601	1596678859	0.33486473	8.481671995	1.46E-06	1.47E-05	4.833775995
ABLU_RS07145	ABLU_525	NZ_CP008706.1	5150787	5150851	+	WP_000347180.1		dicarboxylate/amino acid cation symporter	271.0146729	1583192641	0.26710943	5.92711983	3.08E-09	6.57E-08	7.162299448
sRNA30	no	no	no	no	no	no	no	no	11.9376102	1574653728	0.903370861	1743086695	0.8818472	0.028454512	0.788200203
ABLU_RS19345	ABLU_4069	NZ_CP008707.1	40921	41416	+	WP_000758691.1		molecular chaperone DnaJ	220.6958265	1572969554	0.435068264	3.61097271	0.000305051	0.01161926	2.75238559
ABLU_RS14240	ABLU_2933	NZ_CP008706.1	2947306	2948451	-	WP_00073756.1		galactose chaperone	4310.777044	1572800467	0.274971652	5.718665931	1.07E-08	1.84E-07	6.738228226
ABLU_RS10055	ABLU_2477	NZ_CP008706.1	2470553	2471770	-	WP_00050111.1		CoA transferase	225.8395161	1568360102	0.214448176	3.701483667	2.60E-10	1.52E-11	10.8192245
ABLU_RS09595	ABLU_1975	NZ_CP008706.1	206489	207181	+	WP_000125655.1		hypothetical protein	96.420462	1568253962	0.282534194	5.506705583	2.85E-08	4.4E-07	6.355577997
ABLU_RS11640	ABLU_2372	NZ_CP008706.1	2358457	2358618	-	WP_000784879.1		DUF1427 family protein	58.86948507	1561284516	0.460077801	3.393521277	0.000690902	0.003266768	2.488185955
sRNA46	no	no	no	no	no	no	no	no	377.831004	1556179106	0.28102642	5.828882686	3.22E-08	4.93E-07	6.308197873
ABLU_RS18930	ABLU_2452	NZ_CP008706.1	2439044	2440216	+	WP_001053639.1		isovaleryl-CoA dehydrogenase	2343.05188	1541893851	0.360597976	4.278212719	1.90E-05	0.000145059	3.838455489
ABLU_RS04500	ABLU_0917	NZ_CP008706.1	923186	923476	+	WP_000065970.1		co-chaperone GroES	93.7010597	1540518889	0.254777093	6.046536106	1.48E-09	3.37E-08	7.472324504
ABLU_RS10325	ABLU_286	NZ_CP008706.1	281781	214810	+	WP_000091760.1		hypothetical protein	94.97048432	1532668071	0.491102577	3.103804948	0.001803547	0.007258921	2.01939384
ABLU_RS00995	ABLU_0201	NZ_CP008706.1	224705	226147	+	WP_000190767.1		amino acid permease	1792.061029	1529204061	0.322376129	4.743359887	2.10E-06	2.0E-05	4.698835033
ABLU_RS01495	ABLU_0304	NZ_CP008706.1	327823	328236	+	WP_000093729.1		pilin	1935.64268	152040512	0.334982075	4.537975687	5.68E-06	5.00E-05	4.30194292
ABLU_RS18835	ABLU_2432	NZ_CP008706.1	2420572	2420808	+	WP_000795916.1		hypothetical protein	217.5339598	151857431	0.303247709	0.910340608	5.43E-07	6.03E-06	5.21693984
ABLU_RS04505	ABLU_0916	NZ_CP008706.1	923535	925199	+	WP_001274623.1	groL	chaperonin GroEL	52679.22472	1518211061	0.300442163	5.053257675	4.34E-07	4.94E-06	3.30979888
ABLU_RS10395	ABLU_280	NZ_CP008706.1	216159	2162782	+	WP_001011556.1		PeptD family -containing protein	714.4884196	151656411	0.30938819	4.898745846	9.65E-07	1.00E-05	4.950216092
ABLU_RS09605	ABLU_0682	NZ_CP008706.1	6858484	6858969	+	WP_000155937.1		anionic, rpo-hydroxylating dihydrogenase subunit beta	714.8232945	1513499585	0.400640055	3.343673886	0.000932524	0.000284559	2.54018164
ABLU_RS05019	ABLU_010	NZ_CP008706.1	1252933	1251340	+	WP_000036596.1		hypothetical protein	1927.004105	1511413789	0.172501701	3.7173056506	17.4E-18	3.05E-16	5.16227913
ABLU_RS05210	ABLU_0450	NZ_CP008706.1	464192	464198	+			RNAse Ang	2063.981742	1509143071	0.468654787	3.218781672	0.00187347	0.005428719	2.260986351
ABLU_RS09490	ABLU_951	NZ_CP008706.1	953288	9533076	+	WP_075847182.1		hypothetical protein	92.77099314	1498829183	0.29318933	5.117146827	3.19E-07	3.82E-06	5.418005595
ABLU_RS06225	ABLU_0276	NZ_CP008706.1	1022204	1022389	+	WP_001078405.1		hypothetical protein	26.1802741	1469548421	0.372363516	4.01052232	5.84E-05	0.000388491	3.410619273
ABLU_RS14245	ABLU_2779	NZ_CP008706.1	2772544	2773995	+	WP_001181903.1		aldehyde dehydrogenase	2253.35107	149488692	0.280465194	5.329961042	9.82E-08	1.33E-06</	

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ABUW_RS01340	ABUW_0273	NZ_CP008706.1	292197	292272	-				irRNA- Glu	1442.86927	1069899451	0.446278408	2.397381869	0.016512736	0.045412842	1.342821918
ABUW_RS01575	ABUW_2795	NZ_CP008706.1	2793499	2793837	-	WP_000671321.1			hypothetical protein	37.7235294	1067799952	0.628739437	1698318713	0.089447825	0.175740483	0.755219146
ABUW_RS02300	ABUW_2530	NZ_CP008706.1	2521848	2522621	-	WP_00156942.1			enoyl-CoA hydratase/isomerase family protein	794.6383576	1067720219	0.538703357	1982019866	0.047477129	0.150682516	0.975996858
ABUW_RS02960	ABUW_3331	NZ_CP008706.1	328562	3293092	+	WP_000750072.1			spore coat protein U domain-containing protein	7973.259285	1064399009	0.42341518	2.153842346	0.11942381	0.034866559	1.957159001
ABUW_RS03590	ABUW_3798	NZ_CP008706.1	2795178	2796641	+	WP_000402089.1			amino acid permease	986.6580092	1063319703	0.358897646	2.962732451	0.03049315	0.01178605	1.051420042
ABUW_RS0415	ABUW_3782	NZ_CP008706.1	3842938	3843828	-	WP_001017291.1	mmB		3-hydroxyisobutyrate dehydrogenase	414.5389476	1062662098	0.487360588	2.180443234	0.029224622	0.07971885	1.142837125
ABUW_RS0470	ABUW_2898	NZ_CP008706.1	2905472	2906919	-	WP_000479778.1			capsule assembly Wz family protein	7378.623707	1062258686	0.97636137	5.374820016	1.677E-08	1.09E-06	5.964309924
ABUW_RS0525	ABUW_3806	NZ_CP008706.1	3865436	3868042	-	WP_001093583.1	acnD		Fe/S-dependent 2-methylisocitrate dehydratase AcnD	4507.353954	1059852399	0.31920368	3.320023737	0.000900098	0.004065577	2.390877717
ABUW_RS10340	ABUW_2332	NZ_CP008706.1	2314843	2315685	-	WP_000100649.1			amino acid ABC transporter permease	1259.253655	1059082738	0.212002392	4.995616916	5.86E-07	6.40E-06	5.93576045
ABUW_RS14785	ABUW_3047	NZ_CP008706.1	3073309	3074355	+	WP_001181647.1			hypothetical protein	884.7788451	1058860333	0.198660291	5.330004931	9.82E-08	1.33E-06	5.875262683
ABUW_RS01820	ABUW_0371	NZ_CP008706.1	394311	395411	+	WP_000111668.1			HPP family protein	462.841785	1054409964	0.186888155	5.588104688	2.30E-08	3.67E-07	6.43504698
ABUW_RS01880	ABUW_2878	NZ_CP008706.1	2887613	2888182	-	WP_001009281.1			HupE/UaeJ family protein	244.4901145	1051519597	0.236895923	4.4384740785	9.05E-06	7.56E-05	4.121604945
ABUW_RS08915	ABUW_3332	NZ_CP008706.1	327946	3285599	+	WP_000121760.1			CoA transferase subunit B	94.29694725	1050678931	0.356019634	2.95182548	0.003165596	0.01821403	1.938494639
ABUW_RS02640	ABUW_0537	NZ_CP008706.1	545816	545952	+				irRNA- Leu	4302.923936	1049630278	0.574424158	1.627273909	0.067658596	0.146003991	0.852002351
ABUW_RS06220	ABUW_0275	NZ_CP008706.1	1301959	1302138	+	WP_000066269.1			hypothetical protein	15.43144567	1047700854	0.444664744	2.356156587	0.01465033	0.049630165	1.034254283
ABUW_RS03605	ABUW_0732	NZ_CP008706.1	738671	739546	+	WP_001095768.1	hchA		protein deglycase HchA	637.2567347	1047219761	0.429385712	4.199197197	2.68E-05	0.00019557	3.709815029
ABUW_RS0480	ABUW_2157	NZ_CP008706.1	2193265	2193690	-	WP_000005121.1			GFA family protein	72.482608	104572956	0.404781998	0.009720209	0.02958779	1.52688179	
ABUW_RS13100	ABUW_2699	NZ_CP008706.1	2684478	2684672	+	WP_000999196.1			exo-deoxyribonuclease V1 small subunit	35.42714579	1043677454	0.439014468	2.377319039	0.017438997	0.047223039	1.325846065
ABUW_RS14910	ABUW_3072	NZ_CP008706.1	3099400	3100356	-	WP_000146428.1			oxidoreductase	290.917417	1042036569	0.17240528	6.085221639	1.16E-09	2.72E-08	1.756858442
ABUW_RS06200	ABUW_0270	NZ_CP008706.1	1299169	1299912	+	WP_000200304.1			replication protein	49.9121657	1039685432	0.348206783	2.985627623	0.00282812	0.010521234	1.077933337
ABUW_RS05350	ABUW_0190	NZ_CP008706.1	1107238	1108122	+	WP_001021568.1	cys2		type I-F CRISPR-associated protein Cys2	2687.563553	1037868541	0.152748802	7.818289339	5.35E-15	6.12E-13	12.218886
ABUW_RS0090	ABUW_2078	NZ_CP008706.1	2058405	2060097	-	WP_000971588.1	modB		poly(ADP-ribose) polymerase subunit	68.94161377	1037520799	0.27057953	5.834404844	0.00012585	0.000745699	1.02580111
ABUW_RS09745	ABUW_2006	NZ_CP008706.1	2002482	2002700	-	WP_001093107.1			phage coat protein	180.3457965	1036885294	0.211650086	4.91070204	9.52E-07	9.93E-06	5.002887677
ABUW_RS0535	ABUW_3808	NZ_CP008706.1	3869266	3870510	-	WP_001118624.1	pppB		methylisocitrate lyase	1442.490576	1034578014	0.277384639	3.729759571	0.000191663	0.01069591	2.170802624
ABUW_RS01665	ABUW_0338	NZ_CP008706.1	355989	361739	-	WP_001061626.1	yccS		TIGR01666 family membrane protein	740.35361	1032977668	0.193687136	5.333228049	9.65E-08	1.33E-06	5.877232983
ABUW_RS03995	ABUW_0816	NZ_CP008706.1	792383	792458	-				irRNA- Arg	6.284937665	1029088028	0.337185939	1.633462029	0.06689931	0.200733811	0.697379904
ABUW_RS13960	ABUW_2458	NZ_CP008706.1	2446555	2450437	+	WP_001017562.1			indolepyruvate ferredoxin oxidoreductase family protein	10779.54997	102892118	0.304026108	3.384318494	0.000715552	0.003354609	2.474358502
ABUW_RS0090	ABUW_3312	NZ_CP008706.1	3346077	3347531	-	WP_000394405.1			NAD(P)H transhydrogenase (NADH-specific) subunit beta	1857.780479	1027385648	0.271820049	3.778263891	0.00017926	0.000000193	3.04566454
ABUW_RS02750	ABUW_2628	NZ_CP008706.1	2624478	2625780	-	WP_000595937.1			MF5 transporter	81.1163458	1026095719	0.30764315	3.335434323	0.000851938	0.003828773	2.140846803
ABUW_RS05590	ABUW_1142	NZ_CP008706.1	1166889	1168985	+	WP_000380475.1			carbon starvation protein A	4232.63448	1026071051	0.323074165	3.175961332	0.001943409	0.006206314	2.077164402
ABUW_RS08395	ABUW_2026	NZ_CP008706.1	2013604	201888	-	WP_000050492.1			DUF2523 domain-containing protein	19.73908256	1020886976	0.534201936	1.91050684	0.055988069	0.20714936	0.918238992
ABUW_RS01915	ABUW_2702	NZ_CP008706.1	2686206	2686535	+	WP_000980435.1			hypothetical protein	90.1267261	1019230301	0.625519303	2.237327064	0.025251877	0.064067893	1.93359561
ABUW_RS0605	ABUW_2801	NZ_CP008706.1	2799502	2799924	+	WP_000368712.1			Lrp/ArcC family transcriptional regulator	211.8438197	1018885419	0.338929818	3.006184065	0.002845488	0.009905828	2.004101999
ABUW_RS04465	ABUW_0190	NZ_CP008706.1	903722	905053	-	WP_001886541.1			MF5 transporter	3451.342625	1016856025	0.236153512	4.305911082	1.66E-05	0.000128357	3.89581574
ABUW_RS00115	ABUW_0023	NZ_CP008706.1	21716	27319	+	WP_001097638.1			methionine/alanine import family NSS transporter small subunit	778.9216626	10146111	0.20716687	5.02828312	4.94E-07	5.51E-06	5.25862196
ABUW_RS05285	ABUW_0176	NZ_CP008706.1	1089934	1090344	-	WP_000696669.1			hypothetical protein	156.2854221	1013421003	0.278575782	3.66411755	0.000248141	0.00145571	2.87199334
ABUW_RS10740	ABUW_2413	NZ_CP008706.1	2395388	2400125	+	WP_001027442.1			SDR family oxidoreductase	68.87157484	1010665529	0.289684968	3.381938411	0.000716763	0.003739408	2.47195361
ABUW_RS02925	ABUW_2863	NZ_CP008706.1	2658192	2658662	-	WP_000600043.1			hypothetical protein	47.134617	1010043852	0.332815172	3.034849181	0.00240656	0.00918147	2.037069961
ABUW_RS01840	ABUW_2787	NZ_CP008706.1	3849865	3850224	-	WP_000071347.1			RidA family protein	10576.61193	1009431877	0.237977749	4.24706996	2.22E-05	0.00018622	3.779572173
ABUW_RS09995	ABUW_2058	NZ_CP008706.1	2038281	2040152	-	WP_000632343.1			hypothetical protein	2580.471187	1008251734	0.291579167	3.457004453	0.000544403	0.002701229	2.5684683
sRNA14	no	no	no	no	no	no	no	no		23.9158784	1004887594	0.560624174	1.792498066	0.073067537	0.149511889	0.82532398
ABUW_RS01365	ABUW_4073	NZ_CP008707.1	42564	42893	-	WP_001066685.1			hypothetical protein	158.7724934	1002566102	0.37056906	2.705117211	0.006823919	0.022172334	1.654190541

Table S8. RNA-seq data: Absolute and relative expression (NaCl/MEP > 2-fold down)

ABUW_RS08185	ABUW_1680	NZ_CP008706.1	1673895	1676045	+	WP_045887671.1			DNA polymerase II subunit gamma/tau	3039.780533	-1.000555097	0.10959883	-9.129249826	6.90E-20	1.99E-17	16.70223539
ABUW_RS03440	ABUW_0699	NZ_CP008706.1	702919	703494	-	WP_000125649.1			SdpJ family protein	3866.899451	-1.00070861	0.13057744	-7.66371947	1.81E-14	1.69E-12	11.77148858
ABUW_RS01360	ABUW_3367	NZ_CP008706.1	3407929	3408495	-	WP_000099436.1	om		oligonucleotidase	2244.009604	-1.002811228	0.13190951	-7.628471527	2.41E-14	2.03E-12	11.69354751
ABUW_RS08610	ABUW_3323	NZ_CP008706.1	3388917	3389531	-	WP_000191785.1			sugar transferase	7109.381886	-1.00576107	0.195522873	-6.304087588	2.89E-10	7.91E-09	8.10195977
ABUW_RS01750	ABUW_2211	NZ_CP008706.1	2198608	2198964	+	WP_000473790.1			hypothetical protein	274.1205317	-1.000049775	0.257147032	-3.912532266	9.14E-05	0.00067421	3.246094327
ABUW_RS04965	ABUW_012	NZ_CP008706.1	1023999	1024670	-	WP_001047780.1	queC		7-cyano-7-deazaguanine synthase QueC	715.1697573	-1.006253193	0.173922728	-5.785633346	7.22E-09	1.31E-07	6.882380201
ABUW_RS04990	ABUW_017	NZ_CP008706.1	1028440	1029501	-	WP_000027499.1			sulfate ABC transporter ATP-binding protein	610.7820234	-1.007212775	0.137618836	-7.319864787	2.50E-13	1.48E-11	10.82956076
ABUW_RS02930	ABUW_0596	NZ_CP008706.1	594190	594963	-	WP_001885908.1			hypothetical protein	1106.355826	-1.007802577	0.259748826	-3.87919659	0.00014494	0.000635004	3.19722339
ABUW_RS08100	ABUW_1662	NZ_CP008706.1	1655414	1655641	+	WP_000774578.1			hypothetical protein	12.026639	-1.008074801	0.164724196	-1.1557494566	0.11953311	0.28977085	0.699001329
ABUW_RS05680	ABUW_3230	NZ_CP008706.1	3258903	3259724	-	WP_000216423.1			HAD family hydrolase	913.120686	-1.008416841	0.14374307	-6.984725769	2.85E-12	1.29E-10	8.89162199
ABUW_RS05170	ABUW_0513	NZ_CP008706.1	1061940	1063160	+	WP_001021949.1	cgIA		Otg family GTPase CgIA	88.1514311	-1.011416772	0.18870669	-5.341078191	9.24E-08	1.28E-06	5.89194712
ABUW_RS03755	ABUW_0765	NZ_CP008706.1	756258	756334	+				irRNA- Arg	3.723196614	-1.019509519	1.117923023	-0.91967549	0.167185801	0.499703459	0.30287844
ABUW_RS04430	ABUW_0903	NZ_CP008706.1	899936	899921	-				irRNA- Leu	26.65423437	-1.024947353	0.575438613	-1.17818465	0.07488557	0.152889225	0.81619161
ABUW_RS09370	ABUW_1624	NZ_CP008706.1	1622491	1623222	+	WP_000883491.1			GntR family transcriptional regulator	1072.836297	-1.024969793	0.199401033	-5.74037855	2.74E-07	3.34E-06	5.476586271
ABUW_RS05995	ABUW_3293	NZ_CP008706.1	3236394	3236963	-	WP_000567533.1			HP1 family phosphoanion protein	1027.167493	-1.026322695	0.18035046	-6.575462948	1.38E-08	2.33E-07	6.632314292
ABUW_RS07830	ABUW_3661	NZ_CP008706.1	3721548	3722837	-	WP_000137809.1			ISL3-like element ES-Psu 2 family transposase	707.6091856	-1.026957836	0.230895523	-4.44718536	8.68E-06	7.30E-05	4.16678796
ABUW_RS04970	ABUW_013	NZ_CP008706.1	1024711	1025421	-	WP_000157274.1	queE		7-cyano-7-deazaguanine synthase QueE	5361.255099	-1.028181375	0.205359754	-5.006357197	5.55E-07	6.12E-06	5.21926892
ABUW_RS20425	ABUW_0650	NZ_CP008706.1	654407	655565	-	WP_000692859.1			hypothetical protein	6450.455749	-1.030305624	0.324808975	-3.170357718	0.00522514	0.000280549	2.201993156
ABUW_RS07715	ABUW_679	NZ_CP008706.1	1657343	1657780	-	WP_000993407.1			2-amino-4-hydroxy-6-hydroxymethylthiopyridine dihydrochloride	712.551283	-1.03087929	0.32778457	-7.763840505	8.24E-15	8.51E-13	12.07018483
ABUW_RS04405	ABUW_297	NZ_CP008706.1	2979839	2980453	-	WP_000254582.1			MacC family protein	806.2355839	-1.037830439	0.17752191	-5.84622784	5.03E-09	9.88E-08	10.0512282
ABUW_RS07720	ABUW_3639	NZ_CP008706.1	3698770	3699405	+	WP_000633799.1			response regulator	3946.078941	-1.038093373	0.16301006	-6.368240993	1.91E-10	5.43E-09	8.26584284
ABUW_RS06800	ABUW_4007	NZ_CP008706.1	41890	5282	+	WP_000109197.1			hypothetical protein	422.042738	-1.040797905	0.352196301	-2.955164218	0.003125027	0.0104649	1.94291809
ABUW_RS07820	ABUW_3659	NZ_CP008706.1	3718660	3721147	+	WP_000482599.1			SuP family inorganic anion transporter	25.4464297	-1.041649926	0.104298355	-5.088960231	3.59E-07	4.22E-06	5.37423156
ABUW_RS07835	ABUW_3663	NZ_CP008706.1	3722859	3723371	-	WP_000021628.1			signal peptidase II	237.543444	-1.041999032	0.322100764	-3.243690041	0.0012771	0.00523199	2.2819045
ABUW_RS10360	ABUW_2272	NZ_CP008706.1	2259015	2260178	+	WP_000133515.1			cupin domain-containing protein	1520.873493	-1.043210212	0.174553829	-5.97645562	2.28E-09	5.05E-08	7.296854249
ABUW_RS02810	ABUW_0574	NZ_CP008706.1	571575	571387	-	WP_000990625.1			phage baseplate assembly protein V	67.2684021	-1.043449964	0.347139728	-3.004421903	0.002660801	0.00959506	0.20215993
ABUW_RS02050	ABUW_0410	NZ_CP008706.1	4317657	4317974	+	WP_001062851.1	npX		S05 ribosomal protein L24	44858.954549	-1.04478689	0.229686279	-1.548740635	5.40E-06	4.78E-05	4.32067855
ABUW_RS02255	ABUW_0440	NZ_CP008706.1	23711	23893	+	WP_000373385.1			pyrin family protein	192.356475	-1.046944378	0.424038085	-2.468894121	0.015493401	0.038379723	1.15408409
ABUW_RS09505	no	NZ_CP008706.1	1655977	1657197	+	WP_000133515.1				8184231451	-1.049412208	0.306863354	-3.420131762	0.000625908	0.003030928	2.52153617
ABUW_RS05245	ABUW_068	NZ_CP008706.1	107911	1079623	+	WP_000203995.1			peptidyl(poly) isomerase	6545.332805	-1.04977694	0.200419933	-5.248570711	1.53E-07	1.92E-09	5.76908890
ABUW_RS02435	ABUW_0496	NZ_CP008706.1	507167	507979	+	WP_000284347.1	romA		IA (adenine (15)-N6)-(adenine (15)-N8)-dimethyltransferase	4622.731277	-1.051603724	0.19201937	-6.490614265	8.55E-11	1.72E-09	6.05664887
ABUW_RS01865	ABUW_0380	NZ_CP008706.1	406111	406941	+	WP_000433616.1			inositol monophosphatase	7645.493775	-1.053851925	0.172644412	-6.10475122	1.03E-09	2.45E-08	7.61012863
ABUW_RS14885	ABUW_3067	NZ_CP008706.1	3045890	3045440	+	WP_000381018.1			pinin family protein	10523.9798	-1.054591872	0.27161245	-3.89403274	0.00133775	0.00078454	3.15384853
ABUW_RS01915	ABUW_0234	NZ_CP008706.1	252970	254049	+	WP_000157281.1			DNA/RNA non-specific endonuclease	898.126892	-1.058465094	0.165938743	-6.378659971	1.79E-10	5.15E-09	8.29203282
ABUW_RS15100	ABUW_3110	NZ_CP008706.1	312505	3132960	-	WP_000290730.1	rpmF		S05 ribosomal protein L32	27950.58697	-1.06119487	0.181277333	-5.853541418	4.81E-09	9.58E-08	7.98426607
ABUW_RS17185	ABUW_3352	NZ_CP008706.1	358917	3595019	+	WP_000665140.1			AAA family ATPase	2004.64178	-1.064723859	0.157297154	-6.722954228	12.7E-11	6.44E-10	1.133226004

ABUW_RS02320	ABUW_0472	N2_CP008706.1	483782	484615	+	WP_000180209.1	psaA	CDP-diacylglycerol--serine C-3-phosphatidyltransferase	1061443959	-1.066895471	0.131774066	-8.097082407	5.63E-16	7.32E-14	13.1557049
ABUW_RS05835	ABUW_1895	N2_CP008706.1	122070	1223618	-	WP_001187843.1	foE	GTP cyclohydrolase FoE	8609.4445	-1.070934964	0.207467985	-5.18269814	2.99E-06	5.52366444	
ABUW_RS17805	ABUW_3556	N2_CP008706.1	378336	378563	+	WP_000084900.1		accessory factor Lbik family protein	259.900431	-1.07824815	0.250436087	-4.3054846	1.67E-05	0.00019358	3.89157373
ABUW_RS19105	ABUW_2081	N2_CP008706.1	206163	2063058	+	WP_000204398.1	antA	anthranilate 1,2-dioxygenase large subunit	63.5334186	-1.08364815	0.380779884	-2.845865975	0.00429003	0.01381428	18.0264884
ABUW_RS01930	ABUW_3131	N2_CP008706.1	334494	335323	+	WP_00015937.1	gnk	guanylate kinase	2869.207226	-1.08476645	0.168779454	-6.83190691	6.38E-12	3.41E-10	9.647225059
ABUW_RS17335	ABUW_3826	N2_CP008706.1	283355	283377	+	WP_001982681.1	mt	ribonuclease T	2362.840551	-1.08522656	0.16164519	-7.425198155	1.0E-13	7.58E-12	11.9203361
ABUW_RS14560	ABUW_2999	N2_CP008706.1	302140	3022097	-	WP_000780844.1		DUF4397 domain-containing protein	570.093373	-1.08912931	0.22931819	-4.770219991	1.84E-06	1.79E-05	4.747974582
ABUW_RS12005	ABUW_2304	N2_CP008706.1	228819	2289464	+	WP_001028328.1	ruvC	crossover/junction endonuclease RuvC	7015422299	-1.089585211	0.145106637	-7.507823766	6.01E-14	4.40E-12	11.35616527
ABUW_RS06180	ABUW_0264	N2_CP008706.1	192705	1927414	-	WP_000418027.1			384.8742103	-1.095221682	0.257847602	-4.247155388	2.16E-05	0.000163059	3.787564557
ABUW_RS08430	ABUW_1731	N2_CP008706.1	1727825	1728478	+	WP_000543879.1	adeN	multidrug efflux transposon/repressor AdeN	1486.450167	-1.097218947	0.234249543	-4.683979026	2.81E-06	2.61E-05	4.583031941
ABUW_RS09960	ABUW_2051	N2_CP008706.1	203034	2030324	+	WP_000794351.1		hypothetical protein	178.8090979	-1.1058833	0.493626057	-2.240324603	0.02506975	0.063726235	1.95681736
sRNA40	no	no	no	no	no	no	no	no	2.421847124	-1.108382259	1.463235001	-0.7574817525	0.448375737	0.586837172	0.231482385
ABUW_RS09700	ABUW_5995	N2_CP008706.1	996037	996243	+	WP_032017215.1		hypothetical protein	559.6643898	-1.108769686	0.276397102	-4.01069812	6.03E-05	0.00039914	3.368187465
ABUW_RS14060	ABUW_2895	N2_CP008706.1	2802539	2904162	+	WP_000194951.1	cysN	sulfate adenylyltransferase subunit CysN	7728.319994	-1.110220886	0.17247599	-6.43712297	1.22E-10	3.66E-09	8.43640543
ABUW_RS00755	ABUW_082	N2_CP008706.1	167724	168626	+	WP_000240700.1		UDP-3-O-acetyl-L-acetylglucosamine deacetylase	2634.371161	-1.110412287	0.121086525	-9.152892021	6.68E-20	1.99E-17	16.70223539
ABUW_RS13145	ABUW_2709	N2_CP008706.1	2691763	2692722	-	WP_000423280.1		Lysyl family transcriptional regulator	327.7681079	-1.110669883	0.257195295	-4.326167333	1.52E-05	0.00018011	3.92807197
ABUW_RS05065	ABUW_1032	N2_CP008706.1	1034303	1044095	+	WP_000160699.1	mc	ribonuclease II	2696.635898	-1.11686004	0.88221751	-5.92843	3.06E-09	6.55E-08	7.183467901
ABUW_RS06405	ABUW_1910	N2_CP008706.1	1925723	1925509	+	WP_000453244.1		hypothetical protein	549.9476711	-1.1206919	0.224032461	-5.003601299	5.63E-07	6.19E-06	5.20014038
ABUW_RS08445	ABUW_1734	N2_CP008706.1	1731865	1732028	+	WP_000856681.1	rmO	30S ribosomal protein S2 methyltransferase RmO	3784.765729	-1.124742629	0.174582223	-6.429478371	1.28E-10	3.82E-09	4.171782096
ABUW_RS03090	ABUW_1629	N2_CP008706.1	1629567	1627401	+	WP_001664591.1		DMT family transporter	16.45953033	-1.124495231	0.48211076	-2.433356528	0.190599614	0.04198736	1.379146569
ABUW_RS17295	ABUW_3554	N2_CP008706.1	361040	3611899	+	WP_001118161.1	rimB	23S rRNA (guanosine(2351)-2'-O)-methyltransferase RimB	866.910679	-1.126413356	0.16101088	-9.983296917	2.88E-12	1.20E-10	9.889162149
ABUW_RS05075	ABUW_1034	N2_CP008706.1	104548	1045348	+	WP_001885517.1		GN0318X family lipoprotein	1073.609057	-1.127351018	0.193989931	-5.90027252	3.58E-09	7.16E-08	7.024336848
ABUW_RS04955	ABUW_1427	N2_CP008706.1	1417603	1418105	+	WP_001188074.1		GNAT family N-acetyltransferase	6.777451437	-1.130022322	0.171097743	-1.571624723	0.114904926	0.21297598	0.67305542
ABUW_RS05440	ABUW_2975	N2_CP008706.1	297039	2992187	+	WP_000160699.1		homocysteine S-methyltransferase family protein	592.732493	-1.130681076	0.262459996	-4.010398077	9.98E-05	0.000366273	3.402102883
ABUW_RS04710	ABUW_0973	N2_CP008706.1	983495	984403	+	WP_001140078.1		EamA family transporter	59117567457	-1.134025166	0.200617333	-1.652677897	1.58E-08	2.63E-07	6.588051274
ABUW_RS12115	ABUW_2510	N2_CP008706.1	250542	2506453	+	WP_000107911.1		hypothetical protein	93.78452307	-1.137186483	1.098507382	-1.035937383	0.300231936	0.043496012	10.36164784
ABUW_RS07445	ABUW_1629	N2_CP008706.1	161471	1616496	+	WP_000161025.1		methionine AdoC transporter ATP-binding protein	5552.750816	-1.138786003	0.184278266	-6.18021713	6.40E-10	1.60E-08	7.795340377
ABUW_RS03100	ABUW_0632	N2_CP008706.1	635103	635174	-	WP_001885920.1		hemolysin HlyB protein	966.9342932	-1.144514214	0.181726157	-6.289816833	3.01E-10	8.21E-09	0.885806337
ABUW_RS05070	ABUW_1033	N2_CP008706.1	1044107	1045129	+	WP_001885518.1	era	GTPase Era	7341.134813	-1.146587574	0.164334395	-6.91771024	3.01E-12	1.32E-10	9.497179882
ABUW_RS02315	ABUW_0471	N2_CP008706.1	482883	483740	+	WP_001109438.1		23S rRNA (adenine(2030)-N6)-methyltransferase RmJ	2941.526004	-1.146663386	0.18891979	-8.904817404	5.34E-10	1.10E-10	16.94070705
ABUW_RS17215	ABUW_3440	N2_CP008706.1	3438328	34384544	+	WP_000024269.1	topA	type I DNA topoisomerase	1445138712	-1.149167705	0.154565563	-7.434021736	1.05E-13	7.34E-12	11.1445509
ABUW_RS02385	ABUW_1902	N2_CP008706.1	1898554	1899244	+	WP_001025253.1		ANTAR domain-containing protein	32.76561499	-1.149759996	0.43185146	-2.68239848	0.00775689	0.02451549	16.16254554
ABUW_RS05565	ABUW_1107	N2_CP008706.1	1180910	1181104	+	WP_001020845.1	pmE	50S ribosomal protein L31	6336.271843	-1.158492104	0.27307438	-4.182034461	3.15E-05	0.000225536	3.646784783
ABUW_RS16420	ABUW_4087	N2_CP008706.1	41307	54286	+	WP_000422638.1	APH(3)	Vitri family aminoglycoside O-phosphotransferase	1897.9928	-1.160018686	0.16845494	-7.320329361	2.47E-13	1.48E-11	16.82566076
ABUW_RS11880	ABUW_2441	N2_CP008706.1	242966	2429717	-	WP_000498474.1			84.522427	-1.16226703	0.483650415	-2.403118888	0.01256104	0.044940682	174717978
ABUW_RS13370	ABUW_2754	N2_CP008706.1	2743727	2744725	+	WP_001077412.1		adenosine deaminase	3552.053443	-1.165484737	0.16144082	-5.941893297	2.82E-09	6.07E-08	7.216897586
ABUW_RS09460	ABUW_1844	N2_CP008706.1	184335	1844602	+	WP_000155108.1		NADH hydrolase	812.1859289	-1.166375761	0.152917595	-3.726743554	0.00019397	0.00719425	2.966807551
ABUW_RS08400	ABUW_1725	N2_CP008706.1	1722653	1723144	+	WP_000149167.1		hypothetical protein	661.232879	-1.167488995	0.20464492	-5.710707664	1.6E-08	1.96E-07	6.707269842
ABUW_RS11020	ABUW_2328	N2_CP008706.1	231623	231693	+	WP_000141054.1		LrpA/Cm family transcriptional regulator	1194.19308	-1.168491463	0.268370872	-4.354017414	1.34E-05	0.000105393	3.978054004
ABUW_RS12675	ABUW_2510	N2_CP008706.1	260356	2603883	+	WP_001838420.1		hypothetical protein	626.620853	-1.17874469	0.22237718	-5.300565392	1.16E-07	1.54E-06	5.16562512
ABUW_RS01960	ABUW_0399	N2_CP008706.1	429193	426869	-	WP_001254461.1		YhaA family ribosome biogenesis GTP-binding protein	987.9190807	-1.183183953	0.136735799	-8.653066411	5.01E-18	8.42E-16	15.07488308
ABUW_RS05280	ABUW_0288	N2_CP008706.1	1007638	1008093	+	WP_001036767.1		hypothetical protein	784.5427729	-1.187165539	0.389184517	-0.30244913	0.002198222	0.008175687	2.057519429
sRNA20	no	no	no	no	no	no	no	no	55.37016283	-1.18429611	0.299170989	-3.992018526	5.55E-05	0.000427186	3.369462041
ABUW_RS02440	ABUW_0497	N2_CP008706.1	507980	508819	+	WP_000187234.1		symmetrical bis(GTP-nucleosyl) tetraphosphatase	3176.013075	-1.197275739	0.17249181	-6.55891567	3.43E-12	1.45E-10	9.837356721
ABUW_RS15970	ABUW_2672	N2_CP008706.1	266873	2669107	-	WP_001004672.1			70.76622331	-1.199178321	0.686570108	-1.746361591	0.080717388	0.92310607	0.798646106
ABUW_RS04395	ABUW_0896	N2_CP008706.1	893329	893865	+	WP_000719363.1		DCMN-like domain-containing protein	886.3264542	-1.199897609	0.17801617	-6.880161048	2.95E-12	1.31E-10	9.884252168
ABUW_RS06940	ABUW_1425	N2_CP008706.1	145603	145823	+	WP_002039465.1			14.26584385	-1.20210163	0.645517492	-1.862115963	0.02687846	0.11819591	0.800355327
ABUW_RS06070	ABUW_042	N2_CP008706.1	128347	1284364	+	WP_001172347.1		septal ring lytic transglycosylase RipA family protein	634.663081	-1.202909467	0.171024148	-7.784182297	1.82E-12	8.71E-11	0.05978807
ABUW_RS15525	ABUW_1198	N2_CP008706.1	1226562	12237638	+	WP_000131055.1		DUF1852 domain-containing protein	3257.508537	-1.216356023	0.416610802	-2.920059601	0.004396974	0.0125335	1.900767621
ABUW_RS10005	ABUW_2243	N2_CP008706.1	2233197	2233303	-	WP_000218021.1	(d)CMP kinase	9883.165651	-1.223123298	0.180053374	-6.609619947	3.85E-11	1.35E-09	8.869698761	
ABUW_RS02100	ABUW_0427	N2_CP008706.1	442673	442789	+	WP_000168707.1	pmJ	50S ribosomal protein L36	9327.935958	-1.224644912	0.228716701	-1.352546209	8.67E-08	1.21E-06	5.91600019
ABUW_RS18005	ABUW_3882	N2_CP008706.1	390667	3951053	+	WP_001885173.1		hypothetical protein	1450.553949	-1.229104647	0.134949491	-3.902545278	9.52E-05	0.000581903	3.229087075
ABUW_RS07555	ABUW_1648	N2_CP008706.1	1633487	1633870	+	WP_001216679.1	psf	30S ribosomal protein S6	4181.034465	-1.232214434	0.24723949	-4.983520025	6.24E-07	6.74E-06	1.51077768
ABUW_RS16520	ABUW_1997	N2_CP008706.1	1995687	1995687	-	WP_000733561.1		methionine synthase	7548.28151	-1.235549049	0.390410758	-3.164741002	0.00162209	0.006187998	2.944635346
ABUW_RS03225	ABUW_0655	N2_CP008706.1	661147	662982	+	WP_001800092.1	topA	translational GTPase TopA	37234.40992	-1.238494179	0.2345387	-3.505091663	1.0E-07	1.54E-06	5.821676186
ABUW_RS06560	ABUW_0403	N2_CP008706.1	405368	4057908	+	WP_000458161.1	yegQ	rRNA 5-hydroxyuridine modification protein YegQ	1610.726209	-1.240194251	0.301412275	-4.114619695	3.88E-05	0.000271342	5.68058056
ABUW_RS06635	ABUW_0860	N2_CP008706.1	873440	873710	+	WP_001916671.1		YacA family protein	1970.630429	-1.241940488	0.21114819	-5.878239997	4.16E-09	8.52E-08	7.069428071
ABUW_RS06290	ABUW_0290	N2_CP008706.1	100858	1009199	+	WP_000435252.1	</								

ABUW_RS16360	ABUW_363	NZ_CP008706.1	318651	318694	-	WP_000806837.1		cold shock domain-containing protein	1272.654885	-1.450947373	0.95185929	-7.433667896	1.00E-13	7.34E-12	11.1344559
ABUW_RS20535	no	NZ_CP008706.1	281299	281548	-			hypothetical protein	324.7326784	-1.456907872	0.37783338	-8.85926995	0.00018294	0.00009249	3.30365596
ABUW_RS19975	no	NZ_CP008706.1	332174	3321825	-	WP_012297364.1	intC	translation initiation factor IF-3	19125.63244	-1.466995879	0.98753919	-7.772022328	7.73E-15	6.9E-15	12.0866592
ABUW_RS19190	ABUW_2718	NZ_CP008706.1	2702466	2706323	-	WP_000931998.1	hspA	ATP-dependent RNA helicase HspA	5359.5757327	-1.469091261	0.202919479	-7.240059892	5.48E-13	2.48E-11	10.0637608
ABUW_RS12785	ABUW_2635	NZ_CP008706.1	2634497	2635147	+	WP_065920603.1		GTP-dependent N-acyltransferase	865.369934	-1.469980221	0.204059927	-7.203669239	5.86E-13	3.06E-11	10.5145046
ABUW_RS10295	ABUW_2119	NZ_CP008706.1	2130370	2103987	+	WP_005023749.1		Earna family transporter	360.079499	-1.486674909	0.259650236	-5.725682865	1.03E-08	1.80E-07	6.75454945
ABUW_RS02270	ABUW_0462	NZ_CP008706.1	473894	474370	+	WP_000730372.1	ybeY	rRNA maturation RNase Y	1478.000886	-1.526732556	0.54687961	-9.869756824	5.63E-23	2.52E-20	9.58952964
ABUW_RS17240	ABUW_3543	NZ_CP008706.1	3603274	3603798	-	WP_000777730.1	rnpP	ribosome maturation factor RnpP	10056.93193	-1.535462846	0.244401563	-6.282541014	3.33E-10	8.95E-09	8.048341059
ABUW_RS01605	ABUW_0306	NZ_CP008706.1	330212	330676	-	WP_000678123.1	bfr	bacterioferritin	5792.399281	-1.539809525	0.430267666	-3.578724698	0.000345275	0.001780603	2.74761271
ABUW_RS06725	ABUW_0378	NZ_CP008706.1	191272	198243	+	WP_000200422.1	rnhB	ATP-dependent RNA helicase RnhB	7114.22188	-1.540258682	0.94259387	-8.357622868	6.40E-17	9.55E-15	14.02002289
ABUW_RS06720	ABUW_0377	NZ_CP008706.1	1909596	139188	+	WP_000126912.1		cold shock protein	35787.8034	-1.541926996	0.258300815	-5.96919719	2.39E-09	5.25E-08	7.79679555
ABUW_RS02770	no	NZ_CP008706.1	563924	564586	+			ATP-binding protein	4696.10362	-1.542125402	0.21946262	-7.208003472	5.68E-13	3.01E-11	10.52143483
ABUW_RS12175	ABUW_2318	NZ_CP008706.1	2302706	2304121	+	WP_000378386.1		cytosine permease	585.107479	-1.563768942	0.279959236	-5.585702282	2.33E-08	3.70E-07	6.432227165
srRNA7	no	no	no	no	no	no	no		1268.47158	-1.568970018	0.412930214	-3.799600912	0.000144929	0.000836562	3.077501991
ABUW_RS19740	ABUW_3685	NZ_CP008706.1	3742844	3744180	+	WP_000910004.1		OppD family outer membrane porin	6457.852532	-1.581706968	0.233545931	-6.772573445	1.27E-11	4.64E-10	9.33323043
ABUW_RS06555	ABUW_0444	NZ_CP008706.1	1356272	1356535	-	WP_01186305.1		YfhI family Fe ⁴⁺ -4S cluster ferredoxin	312.2757823	-1.591840512	0.38713428	-4.11561939	3.93E-05	0.00273486	5.353096555
ABUW_RS1610	ABUW_1322	NZ_CP008706.1	1342445	1343296	+	WP_01964773.1	otsB	trehalase-phosphatase	9339.033208	-1.606616296	0.682894589	-2.352344872	0.09655469	0.05008574	13.00955531
ABUW_RS19300	ABUW_4056	NZ_CP008707.1	33741	34544	+	WP_025464897.1	aph(3'')-b	aminoglycoside O-phosphotransferase APH(3'')-b	587.9827749	-1.60755926	0.445487093	-3.608542836	0.000307922	0.001822044	2.788669625
ABUW_RS05400	ABUW_1104	NZ_CP008706.1	112108	1122778	+	WP_011417890.1		ferredoxin reductase	8687.40143	-1.628060519	0.257333687	-6.45201918	1.0E-10	3.37E-09	8.472512718
ABUW_RS19105	ABUW_2487	NZ_CP008706.1	2483057	2484271	+	WP_000353523.1	pobA	4-hydroxybenzoate 3-monoxygenase	93.80805266	-1.639401727	0.370215008	-4.428258424	9.50E-06	7.88E-05	4.97228929
ABUW_RS10540	ABUW_2469	NZ_CP008706.1	2150091	2150978	+	WP_000101876.1		sulfite exporter TauS/SaF family protein	967.46078	-1.644291371	0.377879459	-4.35106479	1.35E-05	0.000062656	3.973645598
ABUW_RS15515	ABUW_3196	NZ_CP008706.1	3224190	3225401	+	WP_000249482.1		flavin reductase	472.464774	-1.721401382	0.311420508	-5.527873524	3.24E-08	4.93E-07	6.307321898
ABUW_RS07795	ABUW_0596	NZ_CP008706.1	1592937	1594136	+	WP_002014361.1		MFS transporter	495.3096794	-1.759065079	0.21947644	-8.26055196	1.45E-16	2.01E-14	13.09551158
ABUW_RS18945	ABUW_3484	NZ_CP008706.1	3532620	3533774	+	WP_000279705.1	hemW	radical SAM family heme chaperone HemW	2448.018599	-1.762041856	0.319598347	-5.530610573	3.9E-08	4.89E-07	6.31079518
ABUW_RS19495	ABUW_4513	NZ_CP008707.1	63264	63524	+	WP_000876194.1		hypothetical protein	28.90464355	-1.78838335	0.64441437	-2.775211141	0.005518588	0.018599442	1.730500085
ABUW_RS20515	ABUW_2517	NZ_CP008706.1	2508647	2508880	+	WP_01741933.1		hypothetical protein	112.5253485	-1.791431241	0.366970435	-4.881877292	1.05E-06	1.09E-05	4.963904082
ABUW_RS19145	ABUW_2444	NZ_CP008706.1	2400358	2400867	+	WP_000992233.1		rhodanese-like domain-containing protein	29.33491776	-1.79694944	0.406273441	-4.422004943	9.73E-06	8.04E-05	4.094942307
ABUW_RS02775	ABUW_0645	NZ_CP008706.1	1564879	1565020	+	WP_001071815.1		phage tail assembly protein	5204.559927	-1.824128543	0.302869285	-6.022842483	1.7E-09	3.88E-08	1.471210731
ABUW_RS05405	ABUW_1005	NZ_CP008706.1	1127911	1128885	+	WP_001057073.1		acyl-CoA desaturase	19930.02931	-1.837542631	0.27194429	-6.775433368	1.24E-11	4.62E-10	9.35667388
ABUW_RS06710	ABUW_0375	NZ_CP008706.1	1895336	1900202	+	WP_01288359.1	gpoH	RNA polymerase sigma factor RpoH	4537.974202	-1.847993639	0.563737008	-1.719088426	4.35E-32	1.75E-28	27.75671363
ABUW_RS08030	ABUW_0445	NZ_CP008706.1	1840257	1840811	+	WP_01103116.1		Ter/AcrR family transcriptional regulator	113.2415457	-1.849759998	1.009946905	-1.831541826	0.067109711	0.019608951	0.845832037
ABUW_RS19305	ABUW_4057	NZ_CP008707.1	34574	35365	+	WP_001261740.1		ANT(3'') is family aminoglycoside nucleotidyltransferase AadA2	653.4054952	-1.875181535	0.430050496	-4.360375237	1.30E-05	0.000103067	3.986808588
ABUW_RS11675	ABUW_2379	NZ_CP008706.1	2366107	2366988	+	WP_001099252.1	tauD	taurine dioxygenase	573.8570798	-1.897101285	0.232491066	-8.089902698	5.97E-16	7.52E-14	13.2388701
ABUW_RS19295	ABUW_0855	NZ_CP008707.1	32905	33741	+	WP_000448066.1	APH(8)-I family aminoglycoside O-phosphotransferase	480.2357999	-1.898519328	0.44848771	-4.23315798	2.30E-05	0.000172247	3.763847739	
ABUW_RS03960	ABUW_0413	NZ_CP008706.1	790240	790644	+	WP_000854583.1		hypothetical protein	1115.837329	-1.901742862	0.2987384	-6.385997463	1.70E-09	9.44E-09	8.30664149
ABUW_RS19195	ABUW_2424	NZ_CP008706.1	2410721	2411080	+	WP_01014472.1		amino acid ABC transporter permease	1513.979628	-1.96134288	0.358425147	-5.472112923	4.45E-08	6.64E-07	6.78009891
ABUW_RS20240	no	NZ_CP008706.1	2508189	2509305	+	WP_005143592.1		hypothetical protein	198.407152	-1.96524829	0.561473475	-3.500162299	0.000449575	0.002353498	2.262826228
ABUW_RS1845	ABUW_2434	NZ_CP008706.1	2422599	2423002	+	WP_000983536.1		hypothetic al protein	38.63620481	-1.97847899	1574206632	-1.25681011	0.208822386	0.32547598	4.17946201
ABUW_RS20500	no	NZ_CP008706.1	564581	564676	-			GpE family phage tail protein	956.075731	-2.008422211	0.26184661	-7.683779772	1.54E-14	1.52E-12	11.81874644
ABUW_RS03975	ABUW_0812	NZ_CP008706.1	1789693	1790189	+	WP_000107290.1		hypothetical protein	104.000813	-2.033185587	0.278447678	-7.25729047	3.45E-13	1.96E-11	7.0768031
ABUW_RS20205	ABUW_2391	NZ_CP008706.1	2379669	2380163	+	WP_000749814.1		hypothetical protein	256.479899	-2.075672357	0.430877393	-4.81715526	1.46E-06	1.47E-05	4.833962249
ABUW_RS19190	ABUW_2423	NZ_CP008706.1	2410666	2410731	+	WP_000418072.1		amino acid ABC transporter permease	108.884133	-2.09125171	0.461906084	-4.454151589	8.42E-06	7.14E-05	4.00062337
ABUW_RS01660	ABUW_0337	NZ_CP008706.1	158322	1595551	+	WP_000790118		MFS transporter	4481.133756	-2.12141875	0.422242372	-5.002846589	5.65E-07	6.20E-06	5.250754793
ABUW_RS18170	ABUW_2378	NZ_CP008706.1	2365305	2366039	+	WP_000649032.1		aspartate/ glutamate racemase family protein	57.8899143	-2.12477321	0.383693767	-5.50133236	3.77E-08	5.69E-07	6.24505107
srRNA3_untruncated	no	no	no	no	no	no	no		6.596721055	-2.13302506	0.77789758	-2.742909299	0.0060875	0.02009468	1.696918906
ABUW_RS1625	ABUW_2390	NZ_CP008706.1	2378950	2379954	+	WP_000566431.1	cysB	cytochrome d ubiquinol oxidase subunit II	1418.1735	-2.220789863	0.436368641	-5.089251737	3.59E-07	4.22E-06	5.734423166
srRNA22	no	no	no	no	no	no	no		0.40750211	-2.256881443	1.94627014	-1.508338222	0.13467985	0.236255358	6.026618333
ABUW_RS16080	ABUW_3310	NZ_CP008706.1	3344551	3344952	+	WP_00147580.1	rnfS	ribosome silencing factor	10929.26828	-2.262279584	0.241704068	-3.95307841	8.00E-21	2.68E-18	17.57127223
ABUW_RS14740	ABUW_3037	NZ_CP008706.1	3063650	3064105	+	WP_000478297.1		bacteriohemerythrin	7815.817815	-2.277826416	0.322632666	-7.060064645	1.66E-12	8.08E-11	10.92686746
ABUW_RS03965	ABUW_0810	NZ_CP008706.1	1788559	1789101	+	WP_01019703.1		hypothetical protein	738.1219905	-2.285386698	0.273470757	-8.296295231	1.07E-16	1.55E-14	13.81002207
ABUW_RS19785	ABUW_2422	NZ_CP008706.1	2409332	2410063	+	WP_01010359.1		amino acid ABC transporter ATP-binding protein	93.8656982	-2.299537679	0.371879742	-6.168766229	6.16E-15	5.58E-08	7.89919085
ABUW_RS1580	ABUW_2380	NZ_CP008706.1	2366997	2367866	+	WP_001092656.1	tauC	taurine ABC transporter permease TauC	527.3526298	-2.330982607	0.30885809	-7.54709909	4.45E-14	3.52E-12	11.45395437
ABUW_RS02785	ABUW_0687	NZ_CP008706.1	1565819	1566793	+	WP_000963361.1		phage tail sheath protein	162.3937995	-2.353754135	0.345423048	-6.81420097	9.48E-12	3.78E-10	9.422121337
ABUW_RS10350	ABUW_2389	NZ_CP008706.1	2678239	2678463	+	WP_000355030.1		hypothetical protein	226.7599471	-2.355961367	0.46500211	-5.066564122	4.05E-06	4.67E-05	5.32151049
ABUW_RS19620	ABUW_2389	NZ_CP008706.1	2377512	2378957	+	WP_000052002.1		cytochrome ubiquinol oxidase subunit I	2322.982851	-2.393186373	0.398450936	-6.006175815	1.90E-09	4.25E-08	7.37435458
ABUW_RS08725	ABUW_1792	NZ_CP008706.1	1788686	1787285	+	WP_005918945.1	cysO	cys operon YbgC family protein	324.3220714	-2.440089861	0.433110505	-5.633873651	1.76E-08	2.87E-07	6.754471863
ABUW_RS18170	ABUW_2439	NZ_CP008706.1	2428766	2428987	+	WP_000108365.1		hypothetical protein	193.818588	-2.451189006	0.634462375	-3.862222288	0.00012333	0.000076914	3.96496466
ABUW_RS08745	ABUW_1796	NZ_CP008706.1	1790129	1790323	+	WP_000053889.1		hypothetic al protein	1533.909964	-2.466482043	0.416379896	-6.010265283	1.85E-09	4.17E-08	7.739967904

Table S9. RNA-seq data: Absolute and relative expression (LowFe/MEP > 2-fold up)

bocus_tag	old_bocus_tag	chrom	start	stop	strand	refseq_id	symbol	name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
ABUW_RS07250	ABUW_187	N2_CP008706.1	174382	174788	+	WP_000107904.1	cuuAB	Cuu fimbrial major subunit CuuAB	19.8 820395	4.46214754	1.24808658	3.575 90509	NA	NA
ABUW_RS1591	ABUW_191	N2_CP008706.1	176889	179387	+	WP_000603230.1	cuoD	Cuu fimbrial usher CuuD	970.57 1689	4.444351973	1.08725827	3.937404621	NA	NA
ABUW_RS07275	ABUW_192	N2_CP008706.1	179384	180383	+	WP_002017500.1	cuuE	Cuu fimbrial tip adhesin CuuE	294.43 1251	4.13760471	1.08965 179	3.8926294 12	NA	NA
ABUW_RS16040	ABUW_193	N2_CP008706.1	217368	217532	-	WP_001556890.1	cuuG	siderophore biosynthesis protein	2465.579755	3.964651477	0.628970056	6.303402587	2.9 E-10	8.44E-09
ABUW_RS07265	ABUW_190	N2_CP008706.1	176039	176872	+	WP_0019865 9.1	cuuC	Cuu fimbrial biogenesis chaperone CuuC	304.66605 12	3.892074696	1.12343832	3.464708698	0.000530806	0.002743062
ABUW_RS20 60	no	N2_CP008706.1	1697527	1697621	+			hypothetical protein	15 5 9729 29	3.5671957301	1.30662324	2.730670333	0.006320566	0.02195285
ABUW_RS016 5	ABUW_0307	N2_CP008706.1	330921	33116	-	WP_000289091.1		bacterioferritin-associated ferredoxin	600.0857499	4.496374042	0.72330092	4.833915447	1.34E-06	1.56E-05
ABUW_RS05760	ABUW_180	N2_CP008706.1	121043	12111	+	WP_000744369.1	baeE	(2,3-dihydroxyphenyl)lactate synthase BaeE	272.162465	3.259189472	0.73054105	4.46 133619	8.15E-06	7.53E-05
ABUW_RS16035	ABUW_238	N2_CP008706.1	2172 82	21736 15	-	WP_000836176.1		SidA/LucD/PvdA family monooxygenase	1174.867192	3.239833843	0.544409541	5.95 109674	2.66E-09	6.3 E-08
ABUW_RS16070	ABUW_2074	N2_CP008706.1	2056068	2056469	-	WP_002027886.1		transcriptional repressor	45.75954753	3.222030468	0.863474942	3.731469667	0.000190366	0.001017959
ABUW_RS16030	ABUW_2387	N2_CP008706.1	2170722	2172 81	-	WP_000442383.1		DHA2 family efflux MFS transporter/pemase subunit	947.7528411	3.190439	0.4604 596	6.929085097	4.24E-12	2.28E-10
ABUW_RS07265	ABUW_180	N2_CP008706.1	174793	175521	+	WP_0005771009.1	cuuA	Cuu fimbrial biogenesis protein CuuA	288.64 8321	3.108432704	1.276608415	2.458414555	0.01995 98	0.043724539
ABUW_RS07260	ABUW_180	N2_CP008706.1	175527	176045	+	WP_000876475.1	cuuB	Cuu fimbrial biogenesis protein CuuB	154.073787	3.083530557	1.030895947	2.3637277 01	0.01840847	0.033554711
ABUW_RS16040	ABUW_2454	N2_CP008706.1	244852	244855	+	WP_000191729.1		enoyl-CoA hydratase/isomerase family protein	974.636723	3.024246052	0.3247033	9.3 88787 14	1.23E-20	9.93E-18
ABUW_RS16020	ABUW_2794	N2_CP008706.1	2771943	2775932	+	WP_0003724 5.1		PxaA family phosphatase	33.1910234	2.9920903 53	0.56648 976	5.2933 17441	1.27E-07	2.86E-06
sRNA5														
ABUW_RS20 45	no	no	no	no	no	no	no	hypothetical protein	3.947 02552	2.952299377	1.440555179	2.037460457	0.041603621	0.102946783
ABUW_RS05725	ABUW_1173	N2_CP008706.1	191938	200079	+	WP_001010792.1	bauD	ferric acinetobactin ABC transporter pemase subunit BauD	44.87573437	2.919540003	0.534756095	5.459573 04	4.77E-08	8.89E-07
ABUW_RS05765	ABUW_181	N2_CP008706.1	121208	121298	+	WP_00161265.1	baeF	etobactin biosynthesis bifunctional isochromanotransferase carrier protein E	19.1841374	2.84 190456	0.61422483	4.626816639	3.7 E-06	3.75E-05
ABUW_RS05770	ABUW_182	N2_CP008706.1	121516	121627	+	WP_000603880.1	baeG	acinetobactin biosynthesis histidine decarboxylase BaeG	194.24 977	2.808545874	0.542686023	6.204 80671	5.50E-10	1.5 E-08
ABUW_RS16075	ABUW_185	N2_CP008706.1	200823	202953	+	WP_000582117.1	baeH	ferric acinetobactin ABC transporter ATP-binding protein BaeH	151074891	2.789109864	0.567990555	4.91047441	9.09E-07	1.6 E-05
ABUW_RS16040	ABUW_3780	N2_CP008706.1	3840068	384195	-	WP_00180766.1		acyl-CoA dehydrogenase family protein	643.959498	2.75855852	0.33094 015	8.335499204	7.72E-17	1.30E-14
ABUW_RS20 170	ABUW_1070	N2_CP008706.1	197277	199307	-	WP_000826026.1	baeB	acinetobactin non-ribosomal peptide synthetase subunit BaeB	497.0936901	2.74 195004	0.675002075	4.08 6955 12	4.87E-05	0.000346327
ABUW_RS12 725	ABUW_2621	N2_CP008706.1	281549	281907	+	WP_001027331.1		hypothetical protein	494.1499428	2.725879767	0.372266302	7.32 80 888	2.45E-10	1.73E-11
ABUW_RS05745	ABUW_1077	N2_CP008706.1	930364	930597	+	WP_00161265.1	bauA	TonB-dependent ferric acinetobactin receptor BauA	748.5593257	2.712284 86	0.357087365	7.595575905	3.06E-14	2.68E-12
ABUW_RS16075	ABUW_2075	N2_CP008706.1	2056937	2057578	-	WP_00026856.1		isochromanotransferase	469.7438 81	2.710037383	0.561955	4.82696955	1.37E-06	1.58E-05
ABUW_RS1945	ABUW_2455	N2_CP008706.1	244267	244458	+	WP_00046 1820.1		acetylpropionylmethylcrotonyl-CoA carboxylase subunit alpha	3837.508829	2.676281927	0.29302589	9.40083973	6.24E-20	3.14E-17
ABUW_RS16080	ABUW_2076	N2_CP008706.1	2057651	2058421	-	WP_00152748.1		SDF family oxidoreductase	273.1469539	2.652489 87	0.889039679	3.849544005	0.000188337	0.00075321
ABUW_RS16080	ABUW_0237	N2_CP008706.1	255242	255931	-	WP_000164598.1	aqpZ	aquaporin Z	107.12 60777	2.65 873291	0.288902208	9.20425031	3.44E-20	1.98E-17
ABUW_RS16085	ABUW_219	N2_CP008706.1	2180 69	218079	-	WP_000596873.1		acetyltransferase	16.9 420303	3.63898002	0.5629 0281	4.688 00588	2.76E-06	2.9 E-05
ABUW_RS07380	ABUW_184	N2_CP008706.1	121453	121523	+	WP_00108155.1	baeA	icinetobactin export ABC transporter pemase/ATP-binding subunit BaeA	296.300317	2.62146732	0.382875565	6.84790369	7.55E-12	3.68E-10
ABUW_RS07380	ABUW_1074	N2_CP008706.1	2008079	201026	+	WP_001223285.1	baeC	ferric acinetobactin ABC transporter pemase subunit BaeC	4.17186832	2.810554331	0.57291174	4.5644977 8	5.5 E-06	4.88E-05
ABUW_RS16195	ABUW_2449	N2_CP008706.1	243573	243646	-	WP_001029902.1		class I SAM-dependent methyltransferase	578.580408	2.6032 9195	0.2975914	8.747623822	2.18E-18	6.75E-16
sRNA75														
ABUW_RS16330	ABUW_3157	N2_CP008706.1	319336	3195072	-	WP_001091666.1		mechanosensitive ion channel	414.9 22788	2.51075838	0.30 833 816	8.339259466	7.48E-17	1.30E-14
ABUW_RS19560	ABUW_2456	N2_CP008706.1	2444655	2445557	+	WP_001988910.1		hydrosymethylglutaryl-CoA lyase	1900.797706	2.479601985	0.2887 0148	8.588282437	8.83E-18	2.22E-15
ABUW_RS0595	ABUW_1343	N2_CP008706.1	1188985	1190290	+	WP_000086869.1		YhdD/YXJ family protein	919.537678	2.464444345	0.30822 893	7.956882358	1.29E-15	1.62E-13
ABUW_RS12 715	ABUW_0260	N2_CP008706.1	276994	277874	-	WP_001635446.1		SDF family NAD(P)-dependent oxidoreductase	1475.56675	2.392255441	0.46 926575	5.96283594	2.16E-07	3.25E-06
ABUW_RS19075	ABUW_2453	N2_CP008706.1	2440041	244182	+	WP_001077777.1		methylcrotonyl-CoA carboxylase	2910.262352	2.387232669	0.338933961	7.04336635	1.89E-12	1.6 E-10
ABUW_RS16040	ABUW_3779	N2_CP008706.1	3839073	3840046	-	WP_001986919.1		enoyl-CoA hydratase	234.409676	3.283299084	0.32990365	7.235502 71	4.64E-10	3.1 E-11
ABUW_RS16040	ABUW_3814	N2_CP008706.1	387655	387852	-	WP_0017893 9.1	MP	L-lactate pemase	5075.979937	2.345324447	0.3464 7538	6.76909597 9	1.30E-11	5.74E-09
ABUW_RS07245	ABUW_1486	N2_CP008706.1	1473 40	147378	-	WP_000590096.1		TetR/AcrI family transcriptional regulator	44.50382304	2.338992704	1.809684409	2.0 8200737	0.044217745	0.107945495
ABUW_RS16040	ABUW_3810	N2_CP008706.1	3874665	387859	-	WP_000587286.1	MD	FMN-dependent, -lactate dehydrogenase LMD	2830.650457	2.365363348	0.339196874	8.806360794	6.88E-12	3.50E-10
ABUW_RS16040	ABUW_3810	N2_CP008706.1	3878615	3878655	-	WP_00122772.1	MR	transcriptional regulator LMR	1508.841212	2.318523422	0.329671025	7.01804 14	2.36E-12	1.40E-10
ABUW_RS16025	ABUW_2486	N2_CP008706.1	218869	219070	-	WP_000531152.1		siderophore achromobactin biosynthesis protein AcsC	1486.402731	2.289197363	0.29056229	7.87850921	3.3 E-15	3.7 E-13
sRNA76														
ABUW_RS05800	ABUW_188	N2_CP008706.1	121412	122081	+	WP_00093826.1	baeJ	acinetobactin biosynthesis isochromanotransferase BaeJ	975.9262847	2.779962893	0.493380777	4.621496347	3.8 E-06	3.84E-05
ABUW_RS19560	ABUW_2452	N2_CP008706.1	2440024	244026	+	WP_001053639.1		isovaleryl-CoA dehydrogenase	2343.051086	2.275175 08	0.36014994	6.97446559	2.66E-10	7.88E-09
ABUW_RS16020	ABUW_285	N2_CP008706.1	216949	2168859	+	WP_000993042.1		LuA/LucC family siderophore biosynthesis protein	1238.665621	2.271144712	0.282828957	6.030099552	9.74E-16	1.27E-13
ABUW_RS16020	ABUW_282	N2_CP008706.1	2163 81	2165479	+	WP_000410997.1		TonB-dependent receptor	7183.370963	2.234056379	0.3396257 12	6.5779954 9	4.77E-11	1.8 E-09
ABUW_RS06010	ABUW_1555	N2_CP008706.1	1588 63	1588323	-	WP_00099324 5.1		hemin uptake protein HemP	362.5923692	2.208420 86	0.44 836093	4.986270 08	5.78E-07	7.90E-06
ABUW_RS1490	ABUW_2984	N2_CP008706.1	3000533	3001024	-	WP_0019918 1.1		transformin-binding protein-like solute binding protein	7.14589986	2.98959259	0.44996 814	4.866 9224	1.16E-06	1.36E-05
ABUW_RS16050	ABUW_3811	N2_CP008706.1	3872632	3874338	-	WP_00193019.1	dd	D-lactate dehydrogenase	1286.2 0284	2.19318978	0.254987421	8.56 874807	1.11E-17	2.64E-15
ABUW_RS16080	ABUW_3351	N2_CP008706.1	3387 95	3388038	-	WP_000037364.1		hypothetical protein	980.7425242	2.154473382	0.42695262	5.02977 122	3.32E-07	5.05E-06
ABUW_RS16190	ABUW_2450	N2_CP008706.1	2436477	2438 71	+	WP_00183773.1		AMP-binding protein	176.17 6743	2.5493381	0.31860086	8.804835186	10. E-11	4.54E-10
ABUW_RS16085	ABUW_3778	N2_CP008706.1	3838235	3839260	-	WP_001991033.1		enoyl-CoA hydratase/isomerase family protein	119.23 898	2.50823575	0.244104233	8.78516524	3.02E-18	8.7 E-16
ABUW_RS16255	ABUW_3346	N2_CP008706.1	3379744	3382000	+	WP_001161980.1	acnA	acnitate hydratase AcnA	5478.768444	2.1 924807	0.265.			

ABUW_RS0560	ABUW_860	ABUW_RS0560	NZ_CP008706.1	292510	2927394	-	WP_000044866.1		TonB-dependent siderophore receptor	1861.672005	1.630917659	0.549032185	2.970532133	0.002972843	0.01823874
ABUW_RS0065	ABUW_862	NZ_CP008706.1	185484	185869	+	WP_0056937.1		aromatic- α -hydroxylating dioxygenase subunit beta	714.8232945	1.629818969	0.442504174	3.683171968	0.00023035	0.00137289	
ABUW_RS0235	ABUW_4042	NZ_CP008707.1	24979	25190	+	WP_000654348.1		hypothetical protein	367.3485986	1.628307809	0.334008496	4.888019479	1.0E-06	1.38E-05	
ABUW_RS0750	ABUW_1078	NZ_CP008706.1	120621	1207331	-	WP_000177756.1	bacC	putative histamine N-monooxygenase	1091.05642	1.622706469	0.320314548	5.065978049	4.08E-07	5.70E-06	
ABUW_RS0135	ABUW_2331	NZ_CP008706.1	231843	2314640	-	WP_000347804.1		amino acid ABC transporter permease	1107.819338	1.620874526	0.246480148	8.566495498	5.58E-11	1.90E-09	
ABUW_RS0130	ABUW_2330	NZ_CP008706.1	231406	2314169	-	WP_001932006.1		amino acid ABC transporter ATP-binding protein	368.5199521	1.618331743	0.236308163	8.8483395731	7.47E-12	3.68E-10	
ABUW_RS0430	ABUW_3581	NZ_CP008706.1	3633974	3641933	-	WP_001394933.1	hspG	molecular chaperone HspG	5586.8564906	1.603894269	0.322868536	4.817920717	1.45E-06	1.65E-05	
ABUW_RS0530	ABUW_2187	NZ_CP008706.1	214823	2149659	+	WP_000548727.1		PepSY domain-containing protein	263.4571508	1.603836723	0.291603554	3.493721025	3.94E-08	7.8E-07	
ABUW_RS1470	ABUW_2358	NZ_CP008706.1	2340767	2342074	+	WP_000816595.1		dicarboxylate/amine acid cation symporter	2310.976507	1.601354073	0.36598955	4.375409275	1.2E-05	0.00010057	
ABUW_RS0295	ABUW_2529	NZ_CP008706.1	2521057	2521848	-	WP_000386291.1		2-(1,2-epoxy-1,2-dihydrophenylacetyl)-CoA isomerase	1400.627279	1.596441756	0.422756882	3.776264363	0.00016998	0.00097831	
ABUW_RS0280	ABUW_2674	NZ_CP008706.1	2667054	2667332	-	WP_000072985.1		hypothetical protein	324.414494	1.594202863	0.479848164	3.322306892	0.000892764	0.00402301	
ABUW_RS1455	ABUW_2355	NZ_CP008706.1	2337728	2338213	-	WP_00066032.1		glutathione peroxidase	698.4107007	1.587456654	0.257392541	6.167454	6.94E-10	1.89E-08	
ABUW_RS0282	ABUW_2642	NZ_CP008706.1	2638887	2641677	-	WP_000003355.1		Hsp70 family type I secretin periplasmic adaptor subunit	2921445758	1.571919099	0.175065541	8.97903202	2.73E-19	1.22E-16	
ABUW_RS0790	ABUW_0169	NZ_CP008706.1	176219	178375	-	WP_000194085.1		TonB-dependent siderophore receptor	1688.219191	1.568994928	0.375612824	4.17718075	2.95E-05	0.000225236	
ABUW_RS0595	ABUW_2180	NZ_CP008706.1	2161259	2162782	-	WP_000110156.1		PepSY domain-containing protein	714.4884196	1.566421807	0.309518791	5.068028438	4.17E-07	5.84E-06	
ABUW_RS0220	ABUW_0490	NZ_CP008706.1	444102	444188	-		tRNA-Arg	2063.981742	1.559968294	0.46888838	3.326895209	0.000878021	0.004231513		
ABUW_RS0189	ABUW_2448	NZ_CP008706.1	2634239	2634592	-	WP_001891686.1		hypothetical protein	362.5669837	1.559651626	0.306673007	5.085715044	3.66E-07	5.21E-06	
ABUW_RS0680	ABUW_3106	NZ_CP008706.1	310950	310103	-	WP_000522218.1	lysM	peptidoglycan-binding protein LysM	1016.15442	1.557055055	0.264987422	5.876001984	4.20E-09	5.68E-08	
ABUW_RS0925	ABUW_2663	NZ_CP008706.1	2658162	2658652	-	WP_00060043.1		hypothetical protein	47.1346197	1.548732249	0.330187872	4.690557567	2.71E-06	2.88E-05	
sRNA3	no	no	no	no	no	no	no	no	255.7882435	1.545972919	0.28732007	5.386553493	7.42E-08	1.31E-06	
ABUW_RS0180	ABUW_0233	NZ_CP008706.1	252271	252714	-	WP_000581866.1		hypothetical protein	1282.899022	1.54540178	0.344881896	4.480959398	7.43E-06	6.91E-05	
ABUW_RS0600	ABUW_1144	NZ_CP008706.1	118458	118534	-		tRNA-Val	115.2002102	1.543735149	0.643455857	2.399191397	0.0163436	0.04873406		
ABUW_RS016	ABUW_2702	NZ_CP008706.1	2686206	2686535	+	WP_000980495.1		hypothetical protein	190.1027261	1.531489517	0.451063269	3.395031027	0.000885331	0.03401484	
ABUW_RS016	ABUW_2702	NZ_CP008706.1	259881	2599541	+	WP_001933098.1		TerR/AcrR family transcriptional regulator	217.8327628	1.530274758	0.957770752	1.597746387	0.10099431	0.18794186	
ABUW_RS0325	ABUW_2785	NZ_CP008706.1	2719566	2719119	+	WP_00110029.1		tanase/fenylserine family alpha/beta hydrolase	14.8193492	1.526919392	0.34218424	4.453703289	8.44E-06	7.75E-05	
ABUW_RS0525	ABUW_2186	NZ_CP008706.1	2147811	214810	-	WP_000091760.1		hypothetical protein	94.9704832	1.500319689	0.491869515	3.050239228	0.00228592	0.009536933	
ABUW_RS0205	ABUW_0449	NZ_CP008706.1	461097	463320	-	WP_000479308.1		hypothetical protein	13463.87897	1.498777275	0.26717812	5.609655692	2.03E-08	4.04E-07	
ABUW_RS0125	ABUW_0352	NZ_CP008706.1	374167	375198	-	WP_000973732.1	astA	asparagine N-succinyltransferase	7224.677006	1.492531669	0.255020832	8.852587235	3.84E-09	1.10E-07	
sRNA3	no	no	no	no	no	no	no	no	524.999025	1.490477957	0.401916105	3.710974659	0.000204029	0.001210654	
ABUW_RS0495	ABUW_2779	NZ_CP008706.1	2772544	2773995	+	WP_001181803.1		aldehyde dehydrogenase	2253.35107	1.489488871	0.280562344	5.3089401781	1.10E-07	1.8E-06	
ABUW_RS0490	ABUW_951	NZ_CP008706.1	953288	9533076	+	WP_075874752.1		hypothetical protein	92.7709314	1.489007477	0.297752263	4.973287067	6.58E-07	8.89E-06	
ABUW_RS0895	ABUW_0181	NZ_CP008706.1	181627	200194	-	WP_001026735.1		hypothetical protein	8155.1177251	1.478466912	0.306558808	4.822703999	1.42E-06	1.63E-05	
ABUW_RS1835	ABUW_2436	NZ_CP008706.1	2424078	2426222	-	WP_001985865.1	katE	catalase HPII	40275.84516	1.477287714	0.386038316	3.826790318	0.000129825	0.00081212	
ABUW_RS0730	ABUW_0555	NZ_CP008706.1	556947	557147	-	WP_001030085.1		TruR/CsA C4-type zinc finger protein	34.01935448	1.472914329	0.49052162	3.289355496	0.001977928	0.000052026	
ABUW_RS0645	ABUW_0775	NZ_CP008706.1	1714456	1714701	-	WP_000949688.1		hypothetical protein	26.49147444	1.471531928	0.264160477	5.568841269	2.55E-08	4.99E-07	
ABUW_RS1870	ABUW_3875	NZ_CP008706.1	3942924	3943164	-	WP_000733015.1		hypothetical protein	2195.81931	1.458469674	0.34691612	4.203551014	2.63E-05	0.000203845	
ABUW_RS0335	ABUW_3168	NZ_CP008706.1	3165300	3165527	-	WP_000543705.1		hypothetical protein	2152.154201	1.457065389	0.350185148	4.908841489	3.17E-05	0.000219679	
ABUW_RS0735	ABUW_0604	NZ_CP008706.1	1406073	1406174	-	WP_000167348.1	ushH	hydroxycoumarate hydrolase	72.14570907	1.449054961	0.240441674	6.026638133	1.67E-09	4.30E-08	
ABUW_RS0825	ABUW_2643	NZ_CP008706.1	2641074	2643215	-	WP_000988402.1		type I secretin system permease/ATPase	5868.688719	1.448737217	0.207342527	6.987168713	2.80E-12	1.61E-10	
ABUW_RS0730	ABUW_3569	NZ_CP008706.1	3626706	3627236	-	WP_000925953.1		peptidoglycan hydrolase	126.9702999	1.448476623	0.249557516	5.804175623	6.47E-09	1.42E-07	
ABUW_RS0500	ABUW_2780	NZ_CP008706.1	2746772	2775954	-	WP_07031869.1		AMP-binding protein	860.1609194	1.445028052	0.338106763	4.27385566	1.92E-05	0.000166692	
ABUW_RS1890	ABUW_2464	NZ_CP008706.1	2456665	2457318	-	WP_00018039.1		3-oxoacid CoA-transferase subunit B	74.4200576	1.44357227	0.314614914	4.588385435	4.47E-06	4.39E-05	
ABUW_RS0735	ABUW_0334	NZ_CP008706.1	376685	376828	+	WP_000678450.1	astB	N-succinylarginine dihydrolase	6654.628774	1.443331464	0.23836032	6.04004658	154E-09	4.00E-08	
ABUW_RS0130	ABUW_3161	NZ_CP008706.1	3174737	3178006	+	WP_000944599.1		TerR/AcrR family transcriptional regulator	795.0830323	1.441563142	0.296386776	4.863857827	1.16E-06	3.37E-05	
ABUW_RS0995	ABUW_2058	NZ_CP008706.1	2038261	2040162	-	WP_000632243.1		hypothetical protein	2180.471181	1.439739104	0.291028064	4.941921448	7.74E-07	1.03E-06	
ABUW_RS0745	ABUW_2828	NZ_CP008706.1	2833455	2835569	+	WP_000364482.1		TonB-dependent receptor	1231342145	1.43701055	0.4162347	3.452245829	0.000555941	0.002849728	
ABUW_RS0815	ABUW_932	NZ_CP008706.1	1872946	1872959	+	WP_000121760.1		CoA transferase subunit B	94.2964725	1.434499992	0.354546056	4.04015816	5.21E-05	0.000365967	
ABUW_RS0445	ABUW_2149	NZ_CP008706.1	210387	214053	-	WP_000917295.1		hypothetical protein	249.4309006	1.43306395	0.35234091	4.080082158	4.50E-05	0.000323901	
ABUW_RS0550	ABUW_3204	NZ_CP008706.1	323247	3233514	-	WP_000334411.1		amidohydrolase	486.482108	1.431663142	0.219739551	6.72794422	1.72E-11	7.38E-10	
ABUW_RS0600	ABUW_2181	NZ_CP008706.1	2162787	2163076	-	WP_000018791.1		hypothetical protein	60.86691226	1.42314889	0.470221197	3.025552486	0.002473599	0.0103016	
ABUW_RS0880	ABUW_0206	NZ_CP008706.1	1248971	1249512	-	WP_000872627.1		peptide MFS transporter	1391449195	1.422271738	0.229271657	6.206561914	5.45E-10	1.50E-08	
sRNA4	no	no	no	no	no	no	no	no	377.163104	1.419259596	0.283953856	4.988330414	5.78E-07	7.90E-06	
ABUW_RS0405	ABUW_0218	NZ_CP008706.1	923353	925189	+	WP_001274623.1	groL	chaperonin GroEL	52679.22472	1.41630074	0.300444534	4.716088248	2.47E-06	2.65E-05	
ABUW_RS0270	ABUW_0599	NZ_CP008706.1	274727	276199	+	WP_001110603.1		bifunctional SulP family inorganic anion transporter/carbonic anhydrase	4543.887225	1.410063149	0.283553482	4.972829606	6.60E-07	8.89E-06	
ABUW_RS0125	ABUW_2085	NZ_CP008706.1	206659	2067106	-	WP_000843218.1		transporter	47.6862662	1.40167424	0.325185486	4.332290232	1.48E-05	0.000104642	
ABUW_RS0495	ABUW_2985	NZ_CP008706.1	3001519	3004621	-	WP_085920715.1		TonB-dependent receptor	65.87468086	1.400651966	0.284800177	4.918011614	8.74E-07	1.16E-05	
ABUW_RS0510	ABUW_2782	NZ_CP008706.1	2777259	2778509	+	WP_000941502.1		GyrB family protein	102.4764982	1.397718131	0.354184843	3.94688182	7.82E-05	0.000530997	
ABUW_RS0740	ABUW_2827	NZ_CP008706.1	2833196	2833271	+		tRNA-Glu	27.481776383	1.396621887	0.619506004	2.274824491	0.02219146	0.06418347		
ABUW_RS0990	ABUW_2049	NZ_CP008706.1	2028487	2028705	-	WP_000303543.1		hypothetical protein	117.809019	1.391862127	0.516107093	2.69562548	0.00702423	0.024048194	
ABUW_RS0145	ABUW_4069	NZ_CP008707.1	40921	41418	+	WP_000758689.1		molecular chaperone DnaJ	220.6958265	1.388844315	0.441529368	3.14101289	0.00168373	0.007333707	
sRNA4	no	no	no	no	no	no	no	no	837.176015	1.385286539	0.303778779	5.56012064	5.1E-06	4.96E-05	
ABUW_RS0790	ABUW_1886	NZ_CP008706.1	1217787	1218521	+	WP_001932905.1	bashI	acinetobactin biosynthesis thioesterase BashI	141.4391154	1.372091994	0.273233358	5.021885517	5.1E-07	7.07E-06	
ABUW_RS0810	ABUW_2223	NZ_CP008706.1	2216694	2216694	-	WP_000818192.1		ABC transporter permease	1064.628047	1.35973806	0.190733445	6.8996			

ABUW_RS01005	ABUW_0203	NZ_CP008706.1	227864	229156	+	WP_000369968.1	gabT		4-aminobutyrate-- 2-oxoglutarate transaminase	1012.526494	1013324941	0.36256616	2.794889058	0.005192074	0.018627664
sRNA57	no	no	no	no	no	no	no	no	no	18.02129697	1013196104	0.853531836	1.87027902	0.235216615	0.372079993
ABUW_RS02375	ABUW_0484	NZ_CP008706.1	494759	496564	+	WP_000002862.1			DUF1446 domain-containing protein	270.2034319	1.01217531	0.369664855	2.738089101	0.006179733	0.021619572
ABUW_RS1500	ABUW_2364	NZ_CP008706.1	2350428	2352434	+	WP_000498041.1			alpha/beta fold hydrolase	626.1851044	1.011554463	0.248920064	4.063674755	4.83E-05	0.00034447
ABUW_RS1850	ABUW_3892	NZ_CP008706.1	3960342	3960707	+	WP_001256728.1			hypothetical protein	390.3394552	1.00287712	0.225937389	4.438739088	9.00E-06	8.11E-05
ABUW_RS03105	ABUW_0637	NZ_CP008706.1	638869	641004	-	WP_001274334.1			enoyl-CoA hydratase/isomerase family protein	431.7447847	1.001549387	0.182642684	5.483654572	4.17E-08	7.92E-07
ABUW_RS03360	ABUW_0683	NZ_CP008706.1	691552	692016	+	WP_000678916.1			hypothetical protein	751.0360837	1.001387188	0.182124624	5.498362406	3.83E-08	7.39E-07
ABUW_RS09905	ABUW_2040	NZ_CP008706.1	2022324	2022516	+	WP_000301761.1			hypothetical protein	1385.196488	1.000248866	0.250475308	3.993403075	6.51E-05	0.000441777

Table S10. RNA-seq data: Absolute and relative expression (LowFe/MEP > 2-fold down)

ABUW_RS01005	ABUW_0503	NZ_CP008706.1	1061640	1063160	+	WP_001212949.1	cgfA		Obg family GTPase CgfA	8813.541431	-1.002393235	0.189933008	-5.277161312	1.31E-07	2.19E-06
ABUW_RS18905	ABUW_3892	NZ_CP008706.1	3950667	3951053	+	WP_001985173.1			hypothetical protein	1450.553949	-1.003071366	0.316019703	-1.18416342	0.001451776	0.006434768
ABUW_RS19015	ABUW_3905	NZ_CP008706.1	3971540	3971832	-	WP_001240371.1	mpA		ribonuclease P protein component	15455.29991	-1.005419257	0.188207257	-5.342404292	9.17E-08	1.57E-06
ABUW_RS0460	ABUW_1644	NZ_CP008706.1	1943835	1944602	+	WP_001955308.1			NUC-X hydrolase	812.1859289	-1.006265649	0.315220822	-3.1212735486	0.001913473	0.009038589
ABUW_RS1785	ABUW_2635	NZ_CP008706.1	2634617	2635147	+	WP_085920603.1			GNA1 family N-acetyltransferase	865.1669934	-1.007601878	0.203680411	-4.848974636	7.54E-07	1.0E-05
ABUW_RS0200	ABUW_1889	NZ_CP008706.1	1890719	189125	-	WP_000477561.1			type 1 glutamine acyltransferase domain-containing protein	871.2684979	-1.008386305	0.26838011	-3.757122456	0.00107133	0.001308028
ABUW_RS17215	ABUW_2318	NZ_CP008706.1	2302706	2304121	+	WP_000378386.1			cysteine peptidase	585.1617479	-1.009191203	0.27742782	-3.633329943	0.000279787	0.001572192
ABUW_RS1705	ABUW_3436	NZ_CP008706.1	3478863	3480102	-	WP_000338961.1			RNA-binding protein	440.173254	-1.00950859	0.17561987	-5.756532582	8.58E-09	1.83E-07
ABUW_RS1365	ABUW_1164	NZ_CP008706.1	3189061	3189596	-	WP_001007343.1	upp		uracil phosphoribosyltransferase	5288.389926	-1.01981845	0.189385103	-5.07515913	3.86E-07	5.48E-06
ABUW_RS0215	ABUW_0471	NZ_CP008706.1	452883	453740	+	WP_001109438.1			23S rRNA (adenine(203)-N6)-methyltransferase RlmJ	2941.522604	-1.04261762	0.12912526	-7.854948301	4.00E-15	4.24E-13
ABUW_RS01960	ABUW_0399	NZ_CP008706.1	425919	426689	-	WP_001254461.1			Y1A family ribosome biogenesis GTP-binding protein	987.918087	-1.05689587	0.137020596	-7.41267821	1.24E-13	9.41E-12
sRNA7	no	no	no	no	no	no	no	no	no	1268.471058	-1.015971791	0.410663866	-2.461983891	0.013817087	0.042398358
ABUW_RS09220	ABUW_1893	NZ_CP008706.1	1894330	1894878	-	WP_000323486.1			Rif2 family transcriptional regulator	344.1923786	-1.01859198	0.15716073	-6.468531865	9.90E-11	3.47E-09
ABUW_RS0865	ABUW_1786	NZ_CP008706.1	1782197	1783030	-	WP_000616034.1			hypothetical protein	2409.906415	-1.017917829	0.299660484	-3.397080646	0.000681989	0.003383609
ABUW_RS04165	ABUW_0849	NZ_CP008706.1	829992	830249	-	WP_000201632.1	rpmA		50S ribosomal protein L27	30326.02303	-1.024808153	0.209957134	-4.88105191	1.06E-06	1.29E-05
ABUW_RS01770	ABUW_0361	NZ_CP008706.1	383324	384190	+	WP_000355668.1			LyfA family transcriptional regulator	78.1732917	-1.025253839	0.26803233	-3.825102588	0.00130712	0.000816496
ABUW_RS1605	ABUW_3111	NZ_CP008706.1	3192765	3193325	-	WP_001217512.1			DUF177 domain-containing protein	61220.7249	-1.026258897	0.218229687	-4.702654862	2.57E-06	2.75E-05
ABUW_RS17715	ABUW_2216	NZ_CP008706.1	2202330	2202596	+	WP_000901652.1	ipaT		50S ribosomal protein S20	5845.673991	-1.02815482	0.219765356	-4.679500731	2.88E-06	2.99E-05
ABUW_RS0565	ABUW_1777	NZ_CP008706.1	1775572	1776773	-	WP_001886681.1	bmQ		branched-chain amino acid transport system I carrier protein	4073.025376	-1.030314483	0.235444992	-4.376035965	1.21E-05	0.001056828
ABUW_RS02810	ABUW_0572	NZ_CP008706.1	570751	571087	-	WP_000990623.1			phage baseplate assembly protein V	17.26840201	-1.033330513	0.355516048	-2.906597229	0.000653833	0.01827431
ABUW_RS02270	ABUW_0462	NZ_CP008706.1	473894	474370	-	WP_000710357.1	ybeY		RNA maturation RNase YbeY	1479.000886	-1.034259999	0.164268329	-6.704292487	2.02E-11	8.49E-10
ABUW_RS03615	ABUW_0505	NZ_CP008706.1	518955	519338	+	WP_002040017.1			hypothetical protein	79.4818486	-1.035705705	0.30842004	-3.357862063	0.000778478	0.003840644
ABUW_RS02585	ABUW_1236	NZ_CP008706.1	534104	534975	+	WP_001191539.1			PHP domain-containing protein	683.8062704	-1.039195273	0.183437719	-5.66510227	1.47E-08	0.000100000
ABUW_RS1015	ABUW_0573	NZ_CP008706.1	574680	571909	-	WP_001059843.1			phage virion morphogenesis protein	103.373641	-1.040917843	0.379200565	-4.715919662	0.000047551	0.02169056
ABUW_RS1210	ABUW_2492	NZ_CP008706.1	2487739	2488786	-	WP_001171654.1			NAD-dependent succinate: semialdehyde dehydrogenase	136.520994	-1.046848804	0.324721184	-3.22338858	0.001268486	0.005745292
ABUW_RS04965	ABUW_1012	NZ_CP008706.1	1023999	1024670	-	WP_001247780.1	queC		7-cyano-7-deazaguanine synthase QueC	7161.687573	-1.047481993	0.194565127	-6.180710205	1.77E-09	4.44E-08
ABUW_RS15320	ABUW_3187	NZ_CP008706.1	3225637	3226630	-	WP_000735356.1			methionine synthase	7548.28151	-1.049195284	0.390422838	-6.087253878	0.007204217	0.024035068
ABUW_RS10125	ABUW_3175	NZ_CP008706.1	3195808	3196404	+	WP_000903856.1	scpB		SMC-Scp complex subunit ScpB	1800.246169	-1.055380437	0.161057785	-7.481910175	7.33E-14	5.90E-12
ABUW_RS18905	ABUW_3416	NZ_CP008706.1	3523372	3524244	+	WP_001088412.1			Rlx family pseudouridine synthase	590.107879	-1.059810272	0.184390705	-5.451968868	4.98E-08	9.16E-07
ABUW_RS14015	ABUW_2709	NZ_CP008706.1	2691763	2692722	-	WP_000423280.1			LyfA family transcriptional regulator	327.7681079	-1.064751142	0.25830271	-4.122105963	3.75E-05	0.000277539
ABUW_RS14465	ABUW_2184	NZ_CP008706.1	2120981	2121915	+	WP_000465013.1			hypothetical protein	157.3788477	-1.065358167	0.216494791	-4.520914949	8.61E-07	1.52E-05
ABUW_RS07495	ABUW_1635	NZ_CP008706.1	1621665	1622170	-	WP_000871703.1	pmaA		50S ribosomal protein L1 methyltransferase	2958.381955	-1.065881008	0.16195594	-7.527644591	5.17E-14	4.34E-12
ABUW_RS17825	no	NZ_CP008706.1	3721862	3721488	+				universal stress protein	439.6963096	-1.067634413	0.219264885	-4.844343713	7.64E-07	1.02E-05
ABUW_RS01400	ABUW_0415	NZ_CP008706.1	416929	417186	+	WP_001219145.1	rpsQ		30S ribosomal protein S17	35740.46642	-1.067805884	0.31018738	-3.453172777	0.000554034	0.002043571
ABUW_RS07020	ABUW_0170	NZ_CP008706.1	1030959	1031988	+	WP_001026192.1			cold-shock protein	35787.18034	-1.071338645	0.258290424	-4.147806295	3.36E-05	0.000252127
ABUW_RS04970	ABUW_1013	NZ_CP008706.1	1024711	1025421	-	WP_000957724.1	queE		7-carboxy-7-deazaguanine synthase QueE	5631.255099	-1.071624278	0.200464934	-5.216305883	1.84E-07	2.83E-06
ABUW_RS05065	ABUW_1032	NZ_CP008706.1	1034033	1034095	+	WP_000900691.1	mc		ribonuclease II	2696.635898	-1.073318804	0.188368135	-5.927144205	1.22E-08	2.53E-07
ABUW_RS17830	ABUW_3661	NZ_CP008706.1	3717458	3722837	+	WP_000317809.1			SL3-like element B/Pfu II family transposase	1077.6091856	-1.079988888	0.231812722	-4.658886939	3.18E-06	3.37E-05
sRNA43_uncloned	no	no	no	no	no	no	no	no	no	6.596721055	-1.080712229	0.69319623	-1.558074203	0.191265699	0.229072753
ABUW_RS19100	ABUW_3110	NZ_CP008706.1	3132505	3132690	-	WP_000290730.1	rpmF		50S ribosomal protein L32	27950.58697	-1.082900354	0.18100092	-5.972944605	2.33E-09	5.69E-08
ABUW_RS18270	ABUW_3753	NZ_CP008706.1	3880503	3880930	-	WP_001249720.1			PadrA family transcriptional regulator	476.9842168	-1.083347449	0.211748374	-4.989076915	6.07E-07	8.23E-06
ABUW_RS19210	ABUW_0307	NZ_CP008706.1	22207	22356	+	WP_001096423.1			helicase-helic transcriptional regulator	458.8004305	-1.085216019	0.345303706	-3.133467009	0.00127543	0.007002092
ABUW_RS02065	ABUW_0420	NZ_CP008706.1	438853	4392148	+	WP_000662616.1	rpsH		30S ribosomal protein S8	14.52166771	-1.092812445	0.253625822	-4.308916334	1.64E-05	0.00013517
ABUW_RS17920	ABUW_3659	NZ_CP008706.1	3719660	3721147	+	WP_000492599.1			SufP family inorganic anion transporter	2512.464287	-1.09621810	0.20508282	-5.345231051	9.03E-08	1.57E-06
ABUW_RS09335	ABUW_1895	NZ_CP008706.1	1892700	1892788	+	WP_001187843.1	foE		GTP cyclohydrolase FoE	1609.44445	-1.100419559	0.207874722	-5.291949086	1.21E-07	2.02E-06
ABUW_RS02150	no	NZ_CP008706.1	1343794	1343946	+	WP_001985370.1			hypothetical protein	3.773757164	-1.10180055	0.161034242	-6.681903698	0.495487186	0.634330249
ABUW_RS19975	ABUW_0362	NZ_CP008706.1	3321274	3321825	-	WP_001297364.1	infC		translation initiation factor IF-3	12125.63424	-1.102477826	0.188145561	-5.841067418	5.19E-09	1.17E-07
ABUW_RS01525	ABUW_1644	NZ_CP008706.1	1615797	1621596	+	WP_000391632.1			hypothetical protein	9812.788499	-1.104472509	0.22428965	-4.9241313	8.47E-07	1.93E-05
ABUW_RS05065	ABUW_1032	NZ_CP008706.1	1034033	1034095	+	WP_000900691.1			hypothetical protein	182.2292752	-1.105929739	0.233399058	-4.738364202	2.16E-06	2.36E-05
ABUW_RS01470	ABUW_0892	NZ_CP008706.1	887420	887836	-	WP_001180204.1	greA		transcription elongation factor GreA	4756.033008	-1.110244897	0.264298431	-4.199734226	2.67E-05	0.000205416
ABUW_RS18320	ABUW_3258	NZ_CP008706.1	3287973	3289508	-				16S ribosomal RNA	2511.896295	-1.114449613	0.584116282	-1.907933073	0.05640014	0.1265152
ABUW_RS04000	ABUW_1725	NZ_CP008706.1	1722653	1723144	+	WP_000949167.1			hypothetical protein	161.232879	-1.115182988	0.20512535	-5.436495246	5.43E-08	9.91E-07</

ABUW_RS02040	no	NZ_CP008706.1	2508 89	2508305	+	WP_00054392.1		hypothetical protein	198.047 592	-1.923 9272	0.5335 19367	-2.23484 9722	0.025427742	0.069456523
ABUW_RS17835	ABUW_3663	NZ_CP008706.1	3722859	3723371	-	WP_000002 828.1		signal peptidase I	237.543444	-1.93709704	0.324848407	-3.674666952	0.0002386	0.00786858
ABUW_RS14050	ABUW_2893	NZ_CP008706.1	290033	2901015	-	WP_00046229 8.1		hypothetical protein	623.8783973	-1.94532707	0.91078179	-5.589000798	4.46E-11	1.696E-09
ABUW_RS06075	ABUW_0016	NZ_CP008706.1	9232	92768	+			16S ribosomal RNA	2580.520421	-1.96002583	0.573088052	-2.092210541	0.0364 9418	0.0980923
ABUW_RS06390	ABUW_010	NZ_CP008706.1	922244	922759	+	WP_010185605.1		hypothetical protein	38.51604465	-1.03606328	0.55906328	-2.18107488	0.029987334	0.07726194
ABUW_RS19010	ABUW_3904	NZ_CP008706.1	397109	3971629	-	WP_00025 852.1	Ysd	membrane protein insertion efficiency factor Ysd	5043.093825	-1.20487 23	0.23552936	-5.15664725	3.10E-07	4.53E-06
ABUW_RS04990	ABUW_0107	NZ_CP008706.1	928440	929501	-	WP_000027499.1		sulfate ABC transporter ATP-binding protein	61.7620334	-1.20600 991	0.19362926	-8.637394991	5.75E-18	1.54E-15
ABUW_RS02050	ABUW_0417	NZ_CP008706.1	437657	437974	+	WP_000506885.1	tpx	50S ribosomal protein L24	44858.95409	-1.206707 12	0.229674791	-5.267043533	1.39E-07	2.23E-06
ABUW_RS19330	ABUW_0311	NZ_CP008706.1	334494	335 93	-	WP_000109373.1	gmk	guanylate kinase	2869.207226	-1.21166 842	0.59085033	-7.61680384	2.62E-14	2.39E-12
ABUW_RS17940	ABUW_3685	NZ_CP008706.1	3742844	3744 80	+	WP_000919004.1		CyD family outer membrane porin	6457.852532	-1.216357891	0.2335 17449	-5.20858225	1.90E-07	2.92E-06
ABUW_RS07555	ABUW_0348	NZ_CP008706.1	933487	933870	-	WP_00102 6678 1	galF	30S ribosomal protein S6	4316103465	-1.22196875	0.247346867	-4.939034782	7.85E-07	103E-05
ABUW_RS19860	ABUW_2851	NZ_CP008706.1	2663397	2664338	-	WP_000896578.1		cation transporter	480.262 1555	-1.22350634	0.29975432	-5.62011635	2.67E-08	5.17E-07
ABUW_RS19375	ABUW_2756	NZ_CP008706.1	2744837	2746 56	-	WP_000739960.1		NCB2 family permease	1374.132 945	-1.2321 87078	0.9895 919	-6.486886937	8.20E-11	2.95E-09
ABUW_RS19170	ABUW_2692	NZ_CP008706.1	2663061	2663562	+	WP_00007168 7.1	antB	anthranilate 1,3-dioxygenase small subunit	9.7094606	-1.234638609	0.63408 9757	-1.947 275582	0.0516 9681	0.90895922
ABUW_RS03970	ABUW_0611	NZ_CP008706.1	789307	789573	-	WP_000309102 1		hypothetical protein	1370.389959	-1.241010 707	0.233946464	-5.26189 853	1.43E-07	2.27E-06
ABUW_RS02330	ABUW_0474	NZ_CP008706.1	486 83	487699	+			16S ribosomal RNA	2574.938775	-1.24240777 8	0.564978559	-2.99042347	0.027874869	0.074573603
ABUW_RS02495	ABUW_0508	NZ_CP008706.1	5 8395	5 8931	+			16S ribosomal RNA	2586.4 8383	-1.242410676	0.578853153	-2.1426351	0.03214241	0.08322736
ABUW_RS05400	ABUW_1054	NZ_CP008706.1	102108	102278	+	WP_0011847890.1		ferritin reductase	19887.40143	-1.250393741	0.252322 953	-4.9266 9361	8.37E-07	1.00E-05
ABUW_RS02000	ABUW_0041	NZ_CP008706.1	48599	48789	+	WP_001097146.1		MFS transporter	339.7620582	-1.245487499	0.236927087	-5.26838176	1.47E-07	2.32E-06
ABUW_RS19360	ABUW_3163	NZ_CP008706.1	3188651	3189844	-	WP_000808037.1		cold shock domain-containing protein	1272.654885	-1.2523949 18	0.195307518	-6.42425532	1.43E-10	4.69E-09
ABUW_RS17320	ABUW_3541	NZ_CP008706.1	3599042	3601741	-	WP_0001930326.1	hfb	translation initiation factor IF-2	112708.337	-1.25473077	0.9855297	-6.349372396	2.63E-10	7.84E-09
ABUW_RS16225	ABUW_3168	NZ_CP008706.1	3226652	3227838	-	WP_00003 1855.1		DUF1852 domain-containing protein	3257.508337	-1.256337923	0.48703048	-3.01947767	0.002570235	0.90523859
ABUW_RS07465	ABUW_1629	NZ_CP008706.1	61471	615496	+	WP_000514025.1		methionine ABC transporter ATP-binding protein	5652 7508 6	-1.25781742	0.94429892	-6.820026801	9.10E-12	4.1E-10
ABUW_RS17330	ABUW_3561	NZ_CP008706.1	3617605	3618011	-	WP_0005036 13.1		DUF1856 domain-containing protein	722.3742173	-1.259599591	0.31076 1095	-4.054428807	5.03E-05	0.000355237
ABUW_RS06725	ABUW_1578	NZ_CP008706.1	191972	192423	+	WP_000200422.1	hfb	ATP-dependent RNA helicase RfbH	7104.22 88	-1.26104 089	0.84292983	-6.844215162	7.89E-12	3.69E-10
ABUW_RS205 5	ABUW_2517	NZ_CP008706.1	2508647	2508880	+	WP_01478 433.1		hypothetical protein	10.5253465	-1.268669528	0.360165271	-3.522464909	0.000427554	0.002266597
ABUW_RS07725	ABUW_1682	NZ_CP008706.1	1669758	1671797	+	WP_010230657.1	kdpB	potassium-transporting ATPase subunit KdpB	246.7248029	-1.268790304	0.19988482	-6.34749279	2.19E-10	6.89E-09
ABUW_RS02305	ABUW_0469	NZ_CP008706.1	481655	482092	-	WP_000021434.1		hypothetical protein	1430.738018	-1.271978194	0.392446605	-3.239489923	0.00197521	0.005488978
ABUW_RS19095	ABUW_3293	NZ_CP008706.1	3326304	3326663	+	WP_000567333.1		HP1 family phosphocarnitine protein	1107.674933	-1.27195736	0.1875867	-6.992438077	2.70E-12	1.58E-10
ABUW_RS14440	ABUW_2974	NZ_CP008706.1	2990622	2991992	+	WP_000199229.1		hypothetical protein	85.02492676	-1.2739207 13	0.263849926	-4.846668083	1.24E-06	1.47E-05
ABUW_RS20380	no	NZ_CP008706.1	2881956	2882174	-			hypothetical protein	55.44343002	-1.2852654 6	0.263226106	-4.882708405	1.05E-06	1.29E-05
ABUW_RS19205	ABUW_2200	NZ_CP008706.1	2186663	2187340	+	WP_000005344.1		hypothetical protein	705.4737883	-1.28733647	0.219373472	-6.0351951	1.82E-09	4.54E-08
ABUW_RS20320	ABUW_2512	NZ_CP008706.1	2505358	2505604	-	WP_000070368.1		hypothetical protein	194.203627	-1.2914085 97	0.686599076	-1.880871 956	0.059988631	0.151707018
ABUW_RS17225	ABUW_3540	NZ_CP008706.1	3598641	3599042	-	WP_000897048.1		ribosome-binding factor A	14401.45414	-1.29580277 6	0.1907837	-6.509954091	9.52E-11	2.73E-09
ABUW_RS17805	ABUW_3656	NZ_CP008706.1	3716336	3718563	+	WP_000845800.1		accessory factor/UBK family protein	259.9504031	-1.308243461	0.2538 1624	-5.968869528	2.48E-07	3.67E-06
ABUW_RS19675	ABUW_2610	NZ_CP008706.1	2603566	2603863	-	WP_000163420.1		hypothetical protein	626.6208053	-1.310205265	0.224660996	-5.399335585	5.22E-09	1.17E-07
ABUW_RS19330	ABUW_2370	NZ_CP008706.1	2357346	2357875	+	WP_000194197.1		metalloprotein AnpHSmf family transcription factor	19.08867301	-1.321950021	0.60250921	-2.93078545	0.02830 9721	0.07566501
ABUW_RS06195	ABUW_0224	NZ_CP008706.1	240408	240632	+	WP_000654507.1		helic_hmr-like transcriptional regulator	93.87726	-1.323723952	0.32296 299	-4.09870764	4.15E-05	0.002000521
ABUW_RS19725	ABUW_3542	NZ_CP008706.1	3601752	3603236	-	WP_0005632248.1	nusA	transcription termination/antitermination protein NusA	43971.56109	-1.335732065	0.203193 93	-6.573707045	4.91E-11	1.85E-09
ABUW_RS19370	ABUW_2754	NZ_CP008706.1	2743727	2744725	-	WP_00107714 2.1		adenosine deaminase	3552.053443	-1.3377300056	0.196336419	-6.81058449	9.67E-12	4.38E-10
ABUW_RS06980	ABUW_1928	NZ_CP008706.1	1926967	1927401	+	WP_001166495.1		DMT family transporter	91.45953033	-1.34458371	0.499606001	-2.654844381	0.007042054	0.024082521
ABUW_RS19445	ABUW_3484	NZ_CP008706.1	3535220	3533774	+	WP_0002779705.1	hemW	radical SAM family heme chaperone HemW	2448.016569	-1.353019972	0.31952127	-4.247864709	2.16E-05	0.000193952
ABUW_RS19645	ABUW_2096	NZ_CP008706.1	318069	322544	+	WP_001109947.1	gfbB	glutamate synthase large subunit	15107.44394	-1.353492563	0.261885006	-5.96229791	2.39E-07	3.56E-06
ABUW_RS19380	ABUW_0815	NZ_CP008706.1	790240	790644	+	WP_000854583.1		hypothetical protein	115.837329	-1.3642893 19	0.260970193	-4.559393906	4.35E-06	4.28E-05
ABUW_RS14405	ABUW_2967	NZ_CP008706.1	2979389	2980453	-	WP_000254582.1		Muc family protein	806.2335839	-1.374859309	0.18029659	-7.625542514	2.43E-14	2.28E-12
rRNA20										no				
ABUW_RS02270	no	NZ_CP008706.1	563924	564586	-			ATP-binding protein	4696.10362	-1.38319677	0.21938993	-6.463230961	1.02E-10	3.56E-09
ABUW_RS19340	ABUW_2169	NZ_CP008706.1	2160091	2160978	+	WP_000101876.1		sulfate exporter TauE/SatE family protein	1667.46087	-1.384824767	0.377887618	-3.66464711	0.00024768	0.00125074
ABUW_RS06710	ABUW_1975	NZ_CP008706.1	1893336	1900202	-	WP_001025339.1	spH	RNA polymerase sigma factor RpoH	4537.974002	-1.399550231	0.56654396	-8.940220261	1.88E-19	1.65E-16
ABUW_RS05405	ABUW_1105	NZ_CP008706.1	1127391	1128885	+	WP_001057073.1		acyl-CoA deuterase	19930.02931	-1.400574757	0.217198271	-5.94771597	2.41E-07	3.57E-06
ABUW_RS02775	ABUW_0565	NZ_CP008706.1	564579	565020	+	WP_00107 81E.1		phage tail assembly protein	5204.558227	-1.40306936	0.302774256	-4.63040445	3.99E-06	3.64E-05
ABUW_RS17240	ABUW_3543	NZ_CP008706.1	3603274	3603798	+	WP_000777730.1	impP	ribosome maturation factor RimpP	10056.9193	-1.416530095	0.244435957	-5.780920026	7.00E-09	1.52E-07
ABUW_RS04385	ABUW_0896	NZ_CP008706.1	893329	893885	-	WP_001079833.1		DOMON-like domain-containing protein	886.3284542	-1.427328996	0.1732 0526	-8.335422403	7.72E-17	1.30E-14
ABUW_RS05210	ABUW_0427	NZ_CP008706.1	442673	442789	+	WP_000869707.1	gpnJ	50S ribosomal protein L36	9327.939558	-1.430439956	0.228891676	-6.37344482	2.34E-10	7.16E-09
ABUW_RS19780	ABUW_2423	NZ_CP008706.1	2419066	2419731	+	WP_000418072.1		amino acid ABC transporter permease	888.1849133	-1.46598 975	0.467390871	-3.1065212	0.001098651	0.007430618
ABUW_RS03365	ABUW_0810	NZ_CP008706.1	788559	789101	+	WP_001019703.1		hypothetical protein	738.1219905	-1.473483737	0.272 162	-5.41551633	6.16E-08	1.11E-06
ABUW_RS01850	ABUW_0377	NZ_CP008706.1	402100	403050	-	WP_00116465 14.1	hemF	oxygen-dependent coproporphyrinogen oxidase	3815.627283	-1.479316033	0.300926237	-4.916872572	8.84E-07	1.01E-05
ABUW_RS20430	no	NZ_CP008706.1	564581	564676	-			GpE family phage tail protein	9556.075731	-1.493331275	0.260872192	-5.724378192	1.04E-08	2.16E-07
ABUW_RS04300	ABUW_0903	NZ_CP008706.1	898936	899021	-			rRNA-Lsu	26.65423437	-1.4950045 8	0.612206 94	-2.44199535	0.014606335	0.0443 9948
ABUW_RS16315	ABUW_3196	NZ_CP008706.1	3224490	3225401	+	WP_000204982.1		floxin reductase	1472.46474	-1.500821752	0.311650967	-6.877897842	1.45E-06	1.65E-05
ABUW_RS08150	ABUW_1673	NZ_CP008706.1	1655334	1655668	+	WP_004354454.1	acel	chitinase/hyaluronidase FAcE transporter AceI	90.49039243	-1.502258906	0.424802284	-3.537 19876	0.000404485	0.00270002
ABUW_RS02010	no	NZ_CP008706.1	333974	334 84	-			hypothetical protein	30.87189552	-1.50464824	0.26701951	-4.58496764	0.000373022	0.002035478
ABUW_RS06560	ABUW_0345	NZ_CP008706.1	956538	9571098	-	WP_000845861.1	yygQ	rRNA 5-hydroxymethyl modification protein YyqQ	19.81726209	-1.523405478				

ABUW_RS08030	ABUW_845	NZ_CP008706.1	640257	640811	+	WP_00103116.1		TeIRiAcrR family transcriptional regulator	113.245457	-2.276107121	1.02644806	-2.22789477	0.025887533	0.070425976
ABUW_RS10280	ABUW_2319	NZ_CP008706.1	2304179	2304616	-	WP_00161759.1		PACEEfflux transporter	486.7408237	-2.291580771	0.53531852	-4.280834841	1.8861-05	0.00025285
ABUW_RS10390	ABUW_2697	NZ_CP008706.1	2682890	2682966	-			IRNA-Met	582.975218	-2.293289331	0.41081815	-5.582335385	2.37E-08	4.66E-07
ABUW_RS14415	ABUW_2969	NZ_CP008706.1	2982649	2984271	-	WP_000243371.1		BCT family transporter	7253.254778	-2.30064846	0.337078566	-6.825259293	8.78E-12	4.18E-10
ABUW_RS18120	ABUW_2389	NZ_CP008706.1	2377512	2378957	+	WP_000552002.1		cytochrome ubiquinol oxidase subunit I	3322.882851	-2.321455943	0.398827945	-5.820695292	5.88E-09	1.30E-07
ABUW_RS04995	ABUW_1016	NZ_CP008706.1	1029513	1030397	-	WP_001048811.1	cysW	sulfate ABC transporter permease subunit CysW	95.90566251	-2.339323412	0.243524862	-9.606096857	7.54E-22	1.01E-18
ABUW_RS15175	ABUW_3125	NZ_CP008706.1	3146270	3146734	-	WP_0010214863.1	bfr	bactioferritin	12989.31849	-2.381249464	0.04101786	-5.892565972	3.80E-09	8.86E-08
sRNA72	no	no	no	no	no	no	no	no	227.9065322	-2.405222468	0.342054623	-7.037897004	2.04E-12	1.23E-10
ABUW_RS18170	ABUW_2439	NZ_CP008706.1	2428766	2428987	+	WP_000108365.1		hypothetical protein	139148.8858	-2.463774969	0.636882774	-3.868490515	0.000109511	0.000699224
ABUW_RS17440	ABUW_3583	NZ_CP008706.1	3641934	3642515	-	WP_000472947.1		outer membrane beta-barrel protein	17177.01316	-2.493796258	0.475609084	-5.243373906	1.58E-07	2.47E-06
ABUW_RS15160	ABUW_3122	NZ_CP008706.1	3142445	3143296	-	WP_001064773.1	otsB	tehalose-phosphatase	639.033208	-2.500744646	0.795442594	-3.143840505	0.0067463	0.007278666
ABUW_RS05005	ABUW_3020	NZ_CP008706.1	1031008	1031916	-	WP_000149921.1		alpha/beta hydrolase	280.8572397	-2.564949464	0.538512334	-4.763115637	1.91E-06	2.10E-05
ABUW_RS20285	ABUW_2687	NZ_CP008706.1	2676668	2676987	+	WP_001962898.1		hypothetical protein	186.0173126	-2.593631531	0.403898567	-6.421492291	1.35E-10	4.49E-09
ABUW_RS09450	ABUW_1942	NZ_CP008706.1	1941385	1942269	+	WP_001007514.1		ribose-phosphate pyrophosphokinase	1577.014582	-2.623389998	0.638229944	-4.1041151	3.95E-05	0.000287229
ABUW_RS13140	ABUW_2708	NZ_CP008706.1	2691513	2691713	+	WP_001985155.1		heavy-metal-associated domain-containing protein	1418.86303	-2.624103817	0.37142184	-7.065035418	1.61E-12	1.01E-10
ABUW_RS18655	ABUW_2438	NZ_CP008706.1	2428002	2428481	+	WP_000482091.1		Cna family protein	165.3707082	-2.625372688	1.279234062	-2.052300486	0.040140469	0.099612932
ABUW_RS05010	ABUW_3021	NZ_CP008706.1	1031947	1032954	-	WP_0010212600.1		sulfate ABC transporter substrate-binding protein	524.9851564	-2.650002292	0.584355478	-4.534914775	5.74E-06	5.51E-05
ABUW_RS12225	ABUW_2513	NZ_CP008706.1	2506724	2506933	-	WP_000072126.1		cold-shock protein	808.9924084	-2.657899103	0.823946007	-3.225626818	0.001256971	0.005715957
ABUW_RS15185	ABUW_2381	NZ_CP008706.1	2367863	2368657	-	WP_000114471.1		ATP-binding cassette domain-containing protein	719.963052	-2.685714231	0.453275343	-5.925195629	3.12E-09	7.35E-08
ABUW_RS15190	ABUW_2382	NZ_CP008706.1	2368667	2369707	-	WP_000651495.1	tauA	taurine ABC transporter substrate-binding protein	782.0023615	-2.758653948	0.541057788	-5.098630883	3.42E-07	4.92E-06
ABUW_RS05000	ABUW_1019	NZ_CP008706.1	1030394	1031227	-	WP_000083117.1	cysT	sulfate ABC transporter permease subunit CysT	116.0387869	-2.760709108	0.436053566	-6.344883572	2.23E-10	6.95E-09
ABUW_RS10055	ABUW_2680	NZ_CP008706.1	2678666	2678881	-	WP_000072767.1		cold-shock protein	458.1585517	-2.848610882	0.408322277	-6.461892718	1.03E-10	3.56E-09
ABUW_RS14430	ABUW_2972	NZ_CP008706.1	2986720	2988378	+	WP_001021934.1	betA	choline dehydrogenase	5009.587378	-2.954474293	0.449815281	-6.56814589	5.09E-11	1.90E-09
ABUW_RS14420	ABUW_2970	NZ_CP008706.1	2984536	2985159	+	WP_000166965.1	betI	transcriptional regulator BetI	4254.12659	-2.964629881	0.37555211	-7.894057311	2.93E-15	3.37E-13
ABUW_RS18115	ABUW_2387	NZ_CP008706.1	2376040	2376858	-	WP_000471020.1		hypothetical protein	610.4546051	-3.185350737	0.363530957	-8.782254439	1.91E-16	6.43E-16
ABUW_RS14425	ABUW_2971	NZ_CP008706.1	2985152	2986624	+	WP_0010286303.1	betB	betaine-aldehyde dehydrogenase	4266.030248	-3.186738468	0.393726888	-5.083779126	5.78E-16	8.20E-14
ABUW_RS12115	ABUW_2489	NZ_CP008706.1	2485285	2485881	-	WP_001062883.1		NAD(P)H-dependent oxidoreductase	443.6515256	-3.35922928	0.40459531	-8.302602626	1.02E-16	1.64E-14
sRNA56	no	no	no	no	no	no	no	no	13.12046502	-3.364442571	1.408792093	-2.3881975364	0.01693226	0.05008862
ABUW_RS20210	no	NZ_CP008706.1	2411445	2411558	+	WP_002019211.1		hypothetical protein	7.819497102	-3.468355385	0.898024616	-3.862205242	0.00102368	0.000716347
ABUW_RS09170	ABUW_0381	NZ_CP008706.1	407351	409198	+	WP_00047395.1		DEAD/DEAH box helicase	81860.12305	-3.581278376	0.402654583	-18.89419166	5.89E-19	2.16E-18
ABUW_RS10085	ABUW_2696	NZ_CP008706.1	2682483	2682716	-	WP_000636785.1		transposase	1546.096965	-3.80014147	0.587237057	-6.471222161	9.72E-11	3.44E-09
ABUW_RS06950	ABUW_1427	NZ_CP008706.1	1417703	1418155	+	WP_001088074.1		GNAT family N-acetyltransferase	6.777461437	-4.04108768	1.300047993	-3.108430449	0.00188039	0.008070182
ABUW_RS20235	ABUW_2515	NZ_CP008706.1	2502870	2508022	+	WP_001297964.1		hypothetical protein	1418609751	-4.172260226	1.394570827	-3.3864198	0.00070811	0.003504882
ABUW_RS12220	ABUW_2511	NZ_CP008706.1	2505791	2506261	-	WP_000008105.1		hypothetical protein	432.7391408	-5.26955379	1.43950539	-3.660669716	0.000251557	0.001447111

Table S11. RNA-seq data: Absolute and relative expression (Chl/MEP > 2-fold up)

locus_tag	old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	-log10
ABUW_RS20425	ABUW_0650	NZ_CP008706.1	655407	655565	-	WP_000692859.1		hypothetical protein	6450.455749	7.544513297	0.315836456	23.88704087	4.1E-126	4.17E-123	122.3798639
ABUW_RS03205	ABUW_0651	NZ_CP008706.1	655569	656774	-	WP_000512708.1		RcB family protein	16281.97678	7.286383328	0.343215687	21.23003039	5.05E-100	2.26E-97	96.64581969
ABUW_RS09950	ABUW_2049	NZ_CP008706.1	2028487	2028705	+	WP_002035543.1		hypothetical protein	117.7809016	7.032933674	0.460442224	5.27430221	1.10E-52	4.08E-51	50.38933984
ABUW_RS13100	ABUW_2703	NZ_CP008706.1	2687015	2687371	+	WP_001018862.1		four-helix bundle copper-binding protein	7279.866477	6.781623335	0.456675248	14.84991561	6.96E-50	2.12E-48	47.87366414
ABUW_RS09900	ABUW_2039	NZ_CP008706.1	2021992	2022210	-	WP_002035543.1		hypothetical protein	117.7699016	6.337262925	0.431681347	14.68041971	8.61E-49	2.42E-47	46.81618463
ABUW_RS20160	no	NZ_CP008706.1	1697527	1697621	+			hypothetical protein	15.51972919	6.221053464	1.256316852	4.95189845	7.35E-07	1.44E-06	5.841837508
ABUW_RS09895	ABUW_2038	NZ_CP008706.1	2020385	2021992	-	WP_0005501023.1		replication initiation factor domain-containing protein	908.1308232	5.951604983	0.212143723	28.05458907	3.15E-173	1.41E-169	168.8510708
sRNA5	no	no	no	no	no	no	no	no	3.947129552	5.706529253	1.309093724	4.359144916	1.31E-05	2.28E-05	4.62065153
ABUW_RS09945	ABUW_2048	NZ_CP008706.1	2027330	2028487	-	WP_0005501023.1		replication initiation factor domain-containing protein	906.4096723	5.675532682	0.215500856	25.85065156	2.39E-147	3.21E-144	143.493495
sRNA73	no	no	no	no	no	no	no	no	40.42812639	5.596002549	0.645447395	8.66995915	4.32E-18	2.00E-17	16.60897
sRNA75	no	no	no	no	no	no	no	no	461.5842247	5.500506026	0.407926806	11.48405362	1.94E-41	3.56E-40	39.44855
ABUW_RS19345	ABUW_4069	NZ_CP008707.1	40921	41418	+	WP_000758688.1		molecular chaperone DnaJ	220.6958265	5.373414137	0.420244626	12.78640079	1.95E-37	2.88E-36	35.54060751
ABUW_RS12150	ABUW_2313	NZ_CP008706.1	2298188	2299207	+	WP_000738477.1		fibrinolytic protein	1120.109986	5.271440666	0.347479953	15.17048861	5.55E-52	1.91E-50	49.71696663
ABUW_RS12615	ABUW_2596	NZ_CP008706.1	2589981	2590541	-	WP_001103098.1		TeIRiAcrR family transcriptional regulator	217.6133828	5.218928332	0.873619005	5.965899927	2.43E-09	5.87E-09	8.231561899
ABUW_RS19340	ABUW_4068	NZ_CP008707.1	40571	40885	+	WP_000708714.1		hypothetical protein	91.1146116	5.176703329	0.562462628	9.20363963	3.46E-20	1.84E-19	16.73501821
ABUW_RS09765	ABUW_2010	NZ_CP008706.1	2004664	2004482	-	WP_002074156.1		hypothetical protein	117.7422277	5.105144886	0.316987745	16.00420394	1.9E-57	5.77E-56	55.23828419
ABUW_RS06085	ABUW_1241	NZ_CP008706.1	1262739	1263161	-	WP_000635608.1		DUF962 domain-containing protein	639.0061519	5.079279715	0.259864184	19.54590411	4.47E-85	1.00E-82	82
sRNA56	no	no	no	no	no	no	no	no	13.12046502	5.056899629	0.77597438	6.516838389	7.18E-11	1.96E-10	9.707743929
ABUW_RS09715	ABUW_1999	NZ_CP008706.1	1998188	1998406	-	WP_002074156.1		hypothetical protein	120.2460439	4.94131235	0.317755348	15.84996459	1.41E-56	6.19E-55	54.20830935
ABUW_RS09815	ABUW_2021	NZ_CP008706.1	2011141	201359	-	WP_002074156.1		hypothetical protein	120.68455	4.920997618	0.367557749	13.38836565	7.07E-41	1.24E-39	38.9067831
ABUW_RS09310	ABUW_1912	NZ_CP008706.1	1913491	1914069	+	WP_002035810.1		TeIRiAcrR family transcriptional regulator	59.5115541	4.915741227	0.610704105	8.044427327	8.66E-16	3.47E-15	14.45967053
ABUW_RS13460	ABUW_2772	NZ_CP008706.1	2764930	2766726	-	WP_001986531.1		MFS transporter	243.5147894	4.869847313	0.28137321	17.30348803	4.43E-67	3.80E-65	64.4202184
ABUW_RS09865	ABUW_2032	NZ_CP008706.1	2017616	2017836	-	WP_002074156.1		hypothetical protein	117.0031058	4.852808151	0.35194341	13.8101353	1.98E-43	4.04E-42	41.39351963
ABUW_RS09965	ABUW_2052	NZ_CP008706.1	2030815	2031348	+	WP_000731919.1		type 1 fibrinolytic protein	6554.754857	4.763462575	0.590292759	8.0696112	7.05E-16	2.85E-15	14.54515514
ABUW_RS13855	ABUW_2850	NZ_CP008706.1	2862934	2863536	+	WP_000950253.1		amino acid transporter	602.7580995	4.762337781	0.2914861	16.34191389	4.97E-60	2.82E-58	57.54975089
ABUW_RS02710	ABUW_0552	NZ_CP008706.1	554968	555162	-	WP_000696053.1		hypothetical protein	192.87180432	4.753107869	0.356156688	13.34723741	1.23E-40	2.13E-39	38.6716204
ABUW_RS09640	ABUW_1982	NZ_CP008706.1	1987675	1988934	+	WP_001013990.1		outer membrane protein transport protein	832.0989161	4.733950457	0.210375334	22.50644649	3.59E-102	2.89E-109	108.531022
ABUW_RS12100	ABUW_2102	NZ_CP008706.1	2085633	2085854	-	WP_000685855.1		hypothetical protein	30.02055744	4.67631915	0.59843216	8.352908009	0.66E-17	2.86E-16	15.54363397
ABUW_RS13070	ABUW_2693	NZ_CP008706.1	2668067	2668106	+	WP_000421782.1		hypothetical protein	75.128006	4.649438437	0.27562323	6.868498907	7.67E-64	5.62E-62	61.25026398
ABUW_RS16290	ABUW_3353	NZ_CP008706.1	3389159	3389722	+	WP_001002215.1		TeIRiAcrR family transcriptional regulator	93.935587	4.52180382	0.387342484	116.7392623	1.73E-31	1.85E-30	29.73282827
ABUW_RS01750	ABUW_0357	NZ_CP008706.1	380432	380740	+	WP_001457108.1		hypothetical protein	96.32600432	4.51228031	0.39190196	11.5160955	1.30E-30	1.13E-29	28.9469256
ABUW_RS10460	ABUW_2152	NZ_CP008706.1	2168718	2167485	-	WP_000934174.1		methyltransferase domain-containing protein	83.53155449	4.485901162	0.337772707	13.28082776	2.99E-40	5.18E-39	38.2915791
ABUW_RS19220	ABUW_4039	NZ_CP008707.1	23096	23662	+	WP_000710385.1		hypothetical protein	497.827776	4.444950366	0.24703885	17.9929204	2.29E-72	2.70E-70	69.56613624
ABUW_RS12115	ABUW_2103	NZ_CP008706.1	208646	2086131	-	WP_000922099.1		hypothetical protein	7.57918899	4.433842463	0.94310355	4.70192926	2.58E-06	4.82E-06	5.36952962
ABUW_RS00420	ABUW_0085	NZ_CP008706.1	93475	93759	+	WP_000768201.1		hypothetical protein	29.3886579	4.366365944	0.36054398	12.1044949	9.29E-34	1.15E-32	31.9393021
ABUW_RS01645	ABUW_0212	NZ_CP008706.1	23720	237195	-			sRNA-Thr	320.919675	4.32445853	0.336850968	12.83802752	1.00E-37	1.46E-36	53.82681973
ABUW_RS13380	ABUW_2756	NZ_CP008706.1	2746479	2746708	+	WP_000608974.1		hypothetical protein	837.5659352	4.308586095	0.275454632	15.6472877	3.78E-55	1.56E-53	52.8068754
ABUW_RS19605	ABUW_5006	NZ_CP008706.1	2762	3049	+	WP_000438826.1		BlnT family toxin	329.834776	4.303004435	0.206954846	20.82822475	2.40E-96	8.80E-94	93.05551733
ABUW_RS12101	no	NZ_CP008706.1	250487	2505388	+	WP_04209871		TeIRiAcrR family transcriptional regulator	34.5200987	4.282624673	0.492937286	8.687970655	3.69E-18	1.70E-17	16.76447

ABLUW_RS8900	ABLUW_3881	NZ_CP008706.1	3949660	3950565	+	WP_00241061.1	matxin family metalloprotease	267.46299 E	4.21887597	0.28304178	4.88082982	4.395-50	1375-48	47.86327943
ABLUW_RS9375	ABLUW_2795	NZ_CP008706.1	2793499	2793837	-	WP_00067132.1	hypothetical protein	37.7235294	4.21885358	0.579734851	7.26515812	3.735-13	1245-12	1190567931
ABLUW_RS9380	ABLUW_5007	NZ_CP008706.1	3036	3350	+	WP_00198330.1	BlnA antitoxin family protein	1774.666793	4.173551802	0.204260406	20.4324862	8.605-93	2.675-90	89.9734874
ABLUW_RS9225	ABLUW_4040	NZ_CP008707.1	23711	23893	+	WP_000373385.1		952.3356475	4.16137037	0.383436924	10.8528151	1935-27	1595-26	25.79860288
ABLUW_RS9200	ABLUW_3538	NZ_CP008706.1	338532	3386792	-	WP_000790979.1	hypothetical protein	144.3185675	4.56260666	0.73770447	5.634042782	NA	NA	#VALUE!
ABLUW_RS1065	ABLUW_3505	NZ_CP008706.1	3547470	3550554	-	WP_00564374.1	hypothetical protein	105.935238	4.63868227	0.436021878	9.504545487	2.015-21	1.915-20	90.93554201
ABLUW_RS9405	ABLUW_4052	NZ_CP008707.1	51428	51850	-	WP_000770261.1	hypothetical protein	326.020942	4.83395055	0.350879304	11.69495552	1355-31	1465-30	29.93564774
ABLUW_RS9020	ABLUW_2896	NZ_CP008706.1	2893565	2893888	+	WP_000688341.1	hypothetical protein	132.3608328	4.40080381	0.335116602	11.5155356	1.915-30	1.115-29	28.95467702
ABLUW_RS9760	ABLUW_2009	NZ_CP008706.1	2003522	2004654	-	WP_00514263.1	replication initiation factor domain-containing protein	378.6741663	4.07632553	0.230240541	9.70463842	3.805-70	3.995-68	67.390271
ABLUW_RS1860	ABLUW_2437	NZ_CP008706.1	2426277	2427686	-	WP_00145690.1	iron-containing redox enzyme family protein	6730.655542	4.038412202	0.414688548	9.738422302	2.075-22	1.275-21	20.89619628
ABLUW_RS9755	ABLUW_2639	NZ_CP008706.1	2626050	2626004	-	WP_000321024.1	TerR/AcR family transcriptional regulator	27.46681933	4.037709246	0.459923342	8.778095626	1.655-18	7.845-18	17.10568368
ABLUW_RS9285	ABLUW_3352	NZ_CP008706.1	3388369	3388941	+	WP_000043984.1	TerR/AcR family transcriptional regulator	492.5632601	4.033709191	0.327547924	8.213486699	7.535-35	9.885-34	33.00603309
ABLUW_RS1835	ABLUW_4032	NZ_CP008706.1	2420572	2420808	+	WP_00079595.1	hypothetical protein	217.5339558	4.008324603	0.294476964	9.61867458	3.415-42	4.645-41	40.18976748
ABLUW_RS9235	ABLUW_0479	NZ_CP008706.1	491708	492058	+	WP_00045587.1	GFA family protein	103.9145529	3.969089107	0.37504033	10.58039495	3.575-26	2.815-25	24.55210368
ABLUW_RS9025	ABLUW_2054	NZ_CP008706.1	2045977	2046213	-	WP_000044010.1	hypothetical protein	395.3538908	3.963090653	0.69719821	5.68623869	1305-08	2.965-08	7.528708289
ABLUW_RS1455	ABLUW_2771	NZ_CP008706.1	2763698	2763898	-	WP_00073356.1	OptD family outer membrane porin	95.7648798	3.952599354	0.328003328	8.28888553	1.115-34	1435-33	32.84466306
ABLUW_RS9205	no	NZ_CP008706.1	048830	1048964	+	WP_08591873.1	hypothetical protein	15.93345802	3.94405807	0.91343759	4.319208263	1575-05	2.725-05	4.565431096
ABLUW_RS9235	ABLUW_4042	NZ_CP008707.1	24797	25190	+	WP_00056438.1	hypothetical protein	367.3845986	9.254565299	0.326737548	12.0109515	3.915-33	3.755-32	3142596873
ABLUW_RS9330	ABLUW_2952	NZ_CP008706.1	3019145	3019429	+	WP_000675270.1	hypothetical protein	42.9674725	3.885664548	0.539901	7.107550201	6.105-13	11.69897	
rRNA4														
ABLUW_RS9160	ABLUW_5122	NZ_CP008706.1	3142445	3143296	+	WP_001904773.1	otfB	4.738178009	8.855333595	1.30418046	2.956281603	0.00010732	0.00431076	2.35345199
ABLUW_RS9420	ABLUW_2144	NZ_CP008706.1	210994	210266	+	WP_000367442.1	tehalohalo-phosphatase	1639.033208	3.84184916	0.579389805	6.62947274	3.375-11	9.505-11	10.0227639
ABLUW_RS9215	ABLUW_2510	NZ_CP008706.1	2505452	2505643	-	WP_000201779.1	hypothetical protein	1326.84819	4.831917362	0.12441858	9.602186582	5.335-73	6.715-71	70.17327748
ABLUW_RS9360	ABLUW_4072	NZ_CP008707.1	42340	42534	+	WP_000560244.1	hypothetical protein	93.78452307	3.831643369	0.834203806	4.593174184	4.375-06	7.975-06	5.098845703
ABLUW_RS9360	ABLUW_2031	NZ_CP008706.1	2018476	2017618	-	WP_00514263.1	replication initiation factor domain-containing protein	267.489145	3.803117693	0.341012494	11.23196382	2.855-29	2.565-28	27.59197077
rRNA14														
ABLUW_RS9225	ABLUW_0451	NZ_CP008706.1	464311	465003	-	WP_000007407.1	nitroreductase family protein	213.9151874	3.80309092	0.512101479	7.426440025	1.015-13	8.855-13	12.14153927
ABLUW_RS9355	ABLUW_4071	NZ_CP008707.1	41992	42324	-	WP_000597531.1	hypothetical protein	295.4502953	3.76125172	0.27660359	9.59783759	4.105-42	7.765-41	40.1910328
ABLUW_RS9300	ABLUW_9104	NZ_CP008706.1	911984	912576	-	WP_000340497.1	amidohydrolase	60.1501692	3.75720221	0.344495243	9.90639795	1075-27	9.005-27	26.04597749
ABLUW_RS9460	ABLUW_0244	NZ_CP008706.1	938270	938206	+	WP_000182024.1	hypothetical protein	280.5165212	3.75182603	0.37084297	9.11072772	4.645-24	3.245-23	22.48504499
ABLUW_RS9200	ABLUW_2463	NZ_CP008706.1	259710	259874	-	WP_000086293.1	hypothetical protein	24.0535948	3.748737807	0.533730319	7.023767759	2.165-12	1.17	11.58747
ABLUW_RS9060	ABLUW_0558	NZ_CP008706.1	934750	935940	-	WP_000453627.1	hypothetical protein	2812.67964	4.073396635	0.337183431	10.9630269	1365-28	1.915-27	26.5240344
ABLUW_RS9445	ABLUW_0255	NZ_CP008706.1	938623	938841	+	WP_00198363.1	hypothetical protein	19.42723645	3.72068287	0.560192332	6.641795429	3.155-11	8.795-11	10.0560112
ABLUW_RS9940	ABLUW_2047	NZ_CP008706.1	2027031	2027327	-	WP_000983197.1	hypothetical protein	93.4438502	3.706619835	0.383621631	9.662155882	4.375-22	2.695-21	20.58027665
ABLUW_RS9090	ABLUW_4020	NZ_CP008706.1	2009999	201141	-	WP_00514263.1	replication initiation factor domain-containing protein	434.131054	3.705198842	0.22528486	9.44893816	8.415-61	9.585-59	58.30720066
ABLUW_RS9235	ABLUW_2051	NZ_CP008707.1	55668	56327	-	WP_000581089.1	hypothetical protein	504.8974197	3.691335857	0.20716374	9.72362159	4.635-71	5.055-69	68.29670862
ABLUW_RS97300	no	NZ_CP008706.1	1484140	1484282	-		ADP-ribose pyrophosphatase	594.2973545	3.685325558	0.31319013	11.76213601	5.755-32	6.295-31	30.20140393
ABLUW_RS9785	ABLUW_1474	NZ_CP008706.1	146212	1462727	-	WP_000429477.1	LydE family translocator	32.9782845	3.67610742	0.456447676	8.053974172	8.035-16	3.225-16	3.448097748
ABLUW_RS9370	ABLUW_9598	NZ_CP008706.1	9597045	9598188	-	WP_00514263.1	replication initiation factor domain-containing protein	454.4090042	3.674863392	0.205691644	9.76585857	2.975-71	2.435-69	6.81439373
ABLUW_RS9230	ABLUW_2504	NZ_CP008706.1	2507164	2507484	-	WP_000338517.1	hypothetical protein	200.4946675	3.658699349	0.667962628	5.477396779	4.325-08	9.415-08	7.026410377
ABLUW_RS9230	ABLUW_2512	NZ_CP008706.1	2506358	2506504	-	WP_000676368.1	hypothetical protein	1144.293627	3.65738923	0.612020458	5.945017262	2.765-09	6.645-09	8.17831921
ABLUW_RS9390	ABLUW_2037	NZ_CP008706.1	2020536	2020832	-	WP_000983197.1	hypothetical protein	436.7770889	3.625624764	0.22642951	16.10041915	1565-58	8.065-57	56.00936496
ABLUW_RS9320	ABLUW_0800	NZ_CP008706.1	776544	776714	+	WP_000533615.1	Ans family DNA-binding protein	144.8159932	3.641233663	0.365053227	9.45255343	1875-23	12.8724	21.87943507
ABLUW_RS9795	no	NZ_CP008706.1	9665836	9665833	+		GNA1 family N-acetyltransferase	28.12022194	3.64055195	0.448662721	8.114237875	4.895-16	2.005-16	14.69897
ABLUW_RS9370	ABLUW_4074	NZ_CP008707.1	43471	43941	+	WP_000182272.1	hypothetical protein	96.7334883	3.63324885	0.399450815	9.099610063	9.415-20	4.835-19	9.83905287
ABLUW_RS9065	ABLUW_2692	NZ_CP008706.1	2680084	2680629	-	WP_000196811.1	N-acetylurea hydrolase	177.5177091	3.630776997	0.23266573	9.605192163	6.725-55	5.217-53	52.96703071
ABLUW_RS9160	ABLUW_0337	NZ_CP008706.1	358322	359551	+	WP_000790198.1	MFS transporter	448.1337556	3.625666884	0.419688418	8.635024504	5.865-18	7.205-17	9.58683624
ABLUW_RS1825	ABLUW_2430	NZ_CP008706.1	2418995	2419606	+	WP_000885227.1	LydE family translocator	145.6287038	3.618889886	0.269127804	9.42807472	4.145-41	7.415-40	39.101879
rRNA32														
ABLUW_RS9130	no	NZ_CP008707.1	11984	11994	+	WP_001998891.1	SAM-dependent DNA methyltransferase	927.2963753	3.55253319	0.343129845	10.35279572	4.005-25	3.015-24	23.6214335
ABLUW_RS9975	ABLUW_2008	NZ_CP008706.1	2003224	2003499	-	WP_000697348.1	hypothetical protein	303.3044455	3.546799836	0.238567853	14.86704845	5.335-50	1.665-48	47.77899191
ABLUW_RS9115	ABLUW_2702	NZ_CP008706.1	2686206	2686535	+	WP_000980495.1	hypothetical protein	90.1267261	3.545576411	0.427801002	8.78791497	1.555-16	4.875-16	15.15247104
ABLUW_RS90530	ABLUW_9559	NZ_CP008706.1	963555	963551	+	WP_002010791.1	TerR/AcR family transcriptional regulator	65.66696081	3.53661951	0.45418023	7.786796388	6.875-15	2.885-14	15.88383029
ABLUW_RS9125	ABLUW_4021	NZ_CP008707.1	10568	11165	+	WP_001987227.1	hypothetical protein	138.9104617	3.52929311	0.36192638	9.762200768	1.645-22	1.025-21	20.99139883
ABLUW_RS9070	ABLUW_2053	NZ_CP008706.1	2019437	2019771	+	WP_000714206.1	molecular chaperone	62.81755828	3.519326704	0.608971671	8.807742264	6.335-09	1485-08	7.829732865
ABLUW_RS9590	ABLUW_0763	NZ_CP008706.1	976945	976188	-	WP_000102225.1	universal stress protein	1077.486001	3.517296972	0.363350554				

ABUW_RS0890	ABUW_E31	NZ_CP008706.1	1827256	927927	+	WP_000566027.1		3-oxoacyl-CoA transferase subunit A	93.0585272	3.225943902	0.32486759	9.930026881	3.08E-23	2.00E-22	21.69897
ABUW_RS0970	ABUW_2672	NZ_CP008706.1	2666673	266607	-	WP_001004672.1		hypothetical protein	70.76252331	3.223950959	0.549028761	5.872077607	4.30E-09	1.02E-08	7.90198928
ABUW_RS0940	ABUW_2474	NZ_CP008706.1	2467451	2468422	-	WP_000805368.1		nitrate monooxygenase	226.607258	3.223425086	0.25029303	0.27858377	5.94E-38	9.03E-37	36.0443125
ABUW_RS0930	ABUW_860	NZ_CP008706.1	916528	866901	+	WP_001059828.1		FAD-binding oxidoreductase	1020.0796	3.20015885	0.21486724	95.2256170	2.39E-52	8.45E-51	50.97034329
ABUW_RS0920	no	no	no	no	no	no	no	no	4.05750211	3.20875547	0.935677899	3.42774474	0.00006844	0.000020628	3.03595921
ABUW_RS0385	ABUW_2548	NZ_CP008706.1	2539900	2540832	-	WP_000859578.1		4-hydroxyphenyl epimerase	75.59996242	3.203473865	0.270439901	11.8454972	2.27E-32	2.80E-31	30.58505865
ABUW_RS0975	ABUW_4030	NZ_CP008707.1	8647	8904	+	WP_000834290.1		hypothetical protein	22.2985908	3.200005662	0.87043049	5.81903206	2.02E-08	4.40E-08	7.34773659
ABUW_RS0970	ABUW_897	NZ_CP008706.1	1906747	897043	-	WP_00086387.1		hypothetical protein	398.3938284	3.850886077	0.240176489	13.261424	3.87E-40	6.56E-39	88.3830618
ABUW_RS0380	ABUW_2547	NZ_CP008706.1	2538890	2539903	-	WP_001059833.1		FAD-binding oxidoreductase	61.0490195	3.173022963	0.338521111	9.373760787	7.04E-21	3.94E-20	19.40450378
ABUW_RS0945	ABUW_4093	NZ_CP008707.1	57264	57695	-	WP_00190819.1		hypothetical protein	227.3754781	3.170154176	0.222459395	14.25083434	4.43E-46	1.09E-44	43.9625735
ABUW_RS02475	ABUW_2443	NZ_CP008706.1	2435053	2430646	-	WP_000205935.1		hypothetical protein	183.02491	3.169160182	0.894333885	3.543598463	0.000394706	0.00004895	3.18320005
ABUW_RS0930	ABUW_4001	NZ_CP008707.1	1	1076	-	WP_0002031424.1		replication initiation protein	4.4.2896586	3.16458261	0.330550205	9.543033413	1.19E-21	8.10E-21	20.0191938
ABUW_RS0995	ABUW_2642	NZ_CP008706.1	2023029	2024246	-	WP_000884016.1		DNA replication protein	187.545187	3.100565391	0.98593078	16.8848527	5.83E-64	4.35E-62	61.6361674
ABUW_RS0970	no	no	no	no	no	no	no	no	2018.99062	3.14828206	0.298312496	10.52003336	6.65E-26	4.79E-25	24.3966449
ABUW_RS025	ABUW_4038	NZ_CP008707.1	22356	22895	-	WP_000302250.1		type II toxin-antitoxin system RelE/Paef family toxin	6.103.43259	3.14043257	0.301602703	10.4248152	2.17E-25	1.65E-24	23.7825806
ABUW_RS0490	ABUW_0935	NZ_CP008706.1	944654	945046	-	WP_000406450.1		hypothetical protein	9.783974076	3.1655000	0.879835463	3.564073444	0.000363893	0.000559983	3.252461574
ABUW_RS0385	ABUW_2395	NZ_CP008706.1	2383496	2383897	-	WP_000587903.1	matL	malonate transporter subunit MatL	58.182647	3.127200711	0.263917518	11.84916929	2.17E-32	2.50E-31	30.60209999
ABUW_RS0718	ABUW_1459	NZ_CP008706.1	1450338	1450411	+			RNA-Tp	6075.739836	3.15723557	0.31026272	9.98625053	1.55E-23	1.05E-22	21.9788107
ABUW_RS0960	ABUW_2670	NZ_CP008706.1	2664443	2664625	-	WP_000110266.1		DUF2280 domain-containing protein	53.10069024	3.10285639	0.388685874	8.006805036	1.15E-15	8.40E-15	14.33743217
ABUW_RS0718	ABUW_3843	NZ_CP008706.1	391259	391854	-	WP_000954544.1		formycin dehydrogenase	8777.296432	3.110249952	0.214891621	14.4720008	1.69E-47	4.44E-46	45.35261793
ABUW_RS02180	ABUW_918	NZ_CP008706.1	197241	917381	+	WP_000710284.1		hypothetical protein	87.0702377	3.10649202	0.44519266	6.98804873	2.79E-12	8.52E-12	11.065094041
ABUW_RS0978	ABUW_2015	NZ_CP008706.1	2007127	2007411	-	WP_000505042.1		DUF2523 domain-containing protein	19.52970962	3.098891042	0.549904436	5.633326055	1.75E-08	3.92E-08	7.06749333
ABUW_RS0005	ABUW_2678	NZ_CP008706.1	2669697	2670326	-	WP_000247196.1		hypothetical protein	772.2338274	3.092601749	0.393940185	7.852981008	4.00E-15	1.55E-14	13.8096863
ABUW_RS0485	ABUW_0914	NZ_CP008706.1	91874	91812	+	WP_001047651.1		NAD(+)-NADH kinase	725.9338092	3.090904239	0.200807406	14.9980258	7.59E-51	2.42E-49	48.619463
ABUW_RS0135	ABUW_2310	NZ_CP008706.1	224255	224791	+	WP_000710430.1		type I fibrinolytic protein	14.842952	3.075858628	0.394392992	7.79897685	6.24E-15	2.35E-14	13.8299324
ABUW_RS02200	ABUW_0448	NZ_CP008706.1	460444	461037	+	WP_001046666.1		HAD-like hydrolase	576.096304	3.073691873	0.238607527	12.8818798	5.70E-38	8.70E-37	36.06404075
ABUW_RS0385	ABUW_0749	NZ_CP008706.1	744822	744868	-	WP_000005986.1		hypothetical protein	2.13703708	3.089467176	0.262140183	11.70925941	1.14E-31	1.23E-30	29.9100489
ABUW_RS0718	ABUW_164	NZ_CP008706.1	1543227	154795	+	WP_000181272.1		CoA-acylating methylmalonate-semialdehyde dehydrogenase	524.0297573	3.067106723	0.274827287	11.0023361	6.38E-29	5.66E-28	27.140719357
ABUW_RS0718	no	no	no	no	no	no	no	no	229.3661001	3.065807731	0.372244986	8.2359947	1.17E-16	7.43E-16	95.020118
ABUW_RS0335	ABUW_0068	NZ_CP008706.1	72582	73100	-	WP_000181645.1		VOC family protein	24.8.56693	3.06022224	0.353673876	8.652384102	5.04E-18	2.32E-17	46.4562002
ABUW_RS0490	ABUW_851	NZ_CP008706.1	952288	953076	+	WP_075874782.1		hypothetical protein	92.7709314	3.047300652	0.27645567	10.0259816	3.75E-28	3.9E-27	26.4923603
ABUW_RS0900	ABUW_2658	NZ_CP008706.1	2654223	2654996	-	WP_000710284.1		DUF4882 family protein	375.14869	3.02763888	0.28718564	13.84274716	1.45E-43	2.95E-42	11.53610701
ABUW_RS0800	ABUW_851	NZ_CP008706.1	1645792	1646262	+	WP_001023841.1		hypothetical protein	984.5032291	3.017389602	0.53632269	5.90810777	3.49E-09	8.30E-09	8.080921908
ABUW_RS0440	ABUW_3383	NZ_CP008706.1	3421482	3422033	-	WP_000696965.1		phosphatase PAP family protein	303.0802145	3.015894884	0.260297074	11.28672803	1.53E-29	1.40E-28	27.85387196
ABUW_RS0425	ABUW_0902	NZ_CP008706.1	89856	898860	-	WP_03208192.1		hypothetical protein	453.7988756	3.008095293	0.248565142	12.88994	9.48E-34	1.07E-32	31933.94
ABUW_RS0145	ABUW_2333	NZ_CP008706.1	2318780	2318673	-	WP_000830363.1		amino acid ABC transporter substrate-binding protein	5036.286782	3.00623282	0.9504065	18.245132	3.96E-74	5.50E-72	71.25963731
ABUW_RS0695	ABUW_17297	NZ_CP008706.1	178297	1783030	-	WP_000616034.1		hypothetical protein	2409.106415	2.9990143	0.290065402	10.9257072	4.08E-24	2.86E-23	22.54363397
ABUW_RS0085	ABUW_859	NZ_CP008706.1	952339	952770	+	WP_000720299.1		hypothetical protein	280.6947332	2.99659889	0.507530814	5.904271853	3.54E-09	8.42E-09	8.074687605
ABUW_RS0718	ABUW_618	NZ_CP008706.1	1053894	1054400	-	WP_000894317.1		GNA1 family N-acetyltransferase	25.3651604	2.992609506	0.95771238	5.006814037	5.53E-07	1.0E-06	5.98780736
ABUW_RS0440	ABUW_4092	NZ_CP008707.1	55684	57222	+	WP_001995382.1		recombinase family protein	1737.259632	2.988920642	0.290299878	14.2805566	2.89E-46	7.15E-45	44.1465936
ABUW_RS0975	ABUW_2054	NZ_CP008706.1	2032229	2034787	+	WP_0010214963.1		fimbrial biogenesis outer membrane usher protein	1242.003872	2.97793711	0.415285805	7.17081057	7.46E-13	2.4E-12	11.0793296
ABUW_RS0390	ABUW_010	NZ_CP008706.1	132244	1322759	+	WP_001815605.1		hypothetical protein	38.51904485	2.977927357	0.42184755	7.061673968	1.58E-12	4.94E-12	13.0627305
ABUW_RS0560	ABUW_186	NZ_CP008706.1	194180	195088	-	WP_000089887.1	ydsG	aromatic amino acid DMF transporter YdsG	77.3532657	2.9741789	0.323685022	9.88319449	3.99E-20	2.1E-19	9.8731754
ABUW_RS0440	ABUW_812	NZ_CP008706.1	1324105	1325064	-	WP_000608509.1		ORF49 domain-containing protein	182.409187	2.969651706	0.234415568	13.2382397	5.67E-40	9.44E-39	38.0502801
ABUW_RS0900	ABUW_857	NZ_CP008706.1	853946	855055	+	WP_001021599.1		amidase	4.8.3031482	2.96324193	0.519923878	7.78841108	7.05E-09	7.78E-08	16.53276056
ABUW_RS0310	ABUW_0640	NZ_CP008706.1	643821	644739	+	WP_000205332.1		CoA transferase	398.78373	2.954943454	0.200784411	1.7.8099637	5.05E-49	1.44E-47	46.8413751
ABUW_RS0245	ABUW_2588	NZ_CP008706.1	2581405	258930	-	WP_001000626.1		hypothetical protein	10.6523299	2.93866786	0.59160493	4.969310276	6.72E-07	1.32E-06	5.87942066
ABUW_RS0165	ABUW_2348	NZ_CP008706.1	2428002	2428481	+	WP_000440209.1		CoA family protein	165.3707082	2.939341489	0.7816397	3.760345556	0.000199666	0.000288283	61.70400249
ABUW_RS09720	ABUW_2000	NZ_CP008706.1	99857	998723	+	WP_0000747909.1		hypothetical protein	335.06638	2.934381068	0.200997566	14.59909899	2.85E-48	7.80E-47	46.1070054
ABUW_RS0300	ABUW_2600	NZ_CP008706.1	259375	2593145	-	WP_0004044788.1		hypothetical protein	1115733008	2.934267019	0.37145371	7.773846024	7.61E-15	2.85E-14	43.5105154
ABUW_RS0900	ABUW_2484	NZ_CP008706.1	2478806	2481008	-	WP_001968006.1		ATP-binding cassette domain-containing protein	27.8776587	2.934137773	0.40421668	7.258914268	3.90E-10	1.29E-12	11.8884291
ABUW_RS0405	ABUW_3009	NZ_CP008706.1	3036911	3037189	-	WP_001064707.1		hypothetical protein	57.25395468	2.9128332	0.38731262	7.52775278	5.40E-14	19E-13	12.0789663
ABUW_RS0718	ABUW_3842	NZ_CP008706.1	391986	3919218	-	WP_000592706.1		acyl-CoA deacylase	899.550841	2.901861217	0.20474795	14.17284623	1.35E-45	3.22E-44	43.4921441
ABUW_RS0940	ABUW_4003	NZ_CP008707.1	741	2556	+	WP_000258411.1		zeta toxin family protein	558.2889829	2.900584203	0.256555736	11.30586378	1.23E-29	1.05E-28	27.95480256
ABUW_RS0915	ABUW_832	NZ_CP008706.1	827946	828099	+	WP_001021760.1		CoA transferase subunit B	94.29694725	2.899503438	0.373795545	8.583782348	9.18E-18	4.20E-17	9.5673071
ABUW_RS0380	ABUW_0077	NZ_CP008706.1	82160	83827	+	WP_0000208428.1	hufJ	uncoupled hydrolase	7983.6429	2.89528793	0.447791952	6.46557694	1.05E-10	2.73E-10	8.636337353
ABUW_RS02360	ABUW_0480	NZ_CP008706.1	482078	482641	+	WP_000988414.1		DUF4256 domain-containing protein	222.226919	2.881970681	0.307330256	9.377100974	6.78E-21	3.80E-20	19.4202184
ABUW_RS0310	no	no	no	no	no	no	no	no	11.9376122	2.848653792	0.86042859	3.31063371	0.00093085	0.001089035	2.857286811
ABUW_RS0295	ABUW_831	NZ_CP008706.1	1039258	1039728	+	WP_000210566.1		DUF2280 domain-containing protein	60.9985082	2.84186103	0.37269958	7.625761888	2.43E-14	8.8E-14	13.05502409
ABUW_RS0450	ABUW_4094	NZ_CP008707.1	57721	58056	-	WP_001074611									

ABLUW_RS0355	ABLUW_2101	NZ_CP008706.1	216856	21178	-	WP_00117575.1	thiamine pyrophosphate-dependent dehydrogenase E1 component sub	638.366658	2.70745 13 9	0.592032921	4.573 143 87	4.80E-06	5.058488567
ABLUW_RS0225	ABLUW_2510	NZ_CP008706.1	2506933	-	WP_00007326.1		cold-shock protein	808.9924084	2.706370085	0.75004196	3.608425289	0.000308061	0.000476277
ABLUW_RS0620	ABLUW_2522	NZ_CP008706.1	201470	201176	+	WP_000747909.1		hypothetical protein	325.7507229	2.704044072	0.190959097	4.1280460	2.55E-45
ABLUW_RS0505	ABLUW_1419	NZ_CP008706.1	141867	141897	+	WP_000333834.1		hypothetical protein	0.72746627	2.627 102 92	1.77 000565	1525079 92	0. 0.7239351
ABLUW_RS0385	ABLUW_2503	NZ_CP008706.1	297594	297276	+	WP_000267738.1	cdtA	8195 9705	2.70 833 863	0.358264465	7.539207951	4.73E-14	1.68E-13
ABLUW_RS0340	ABLUW_2560	NZ_CP008706.1	151816	151741	-	WP_000692540.1		stress-responsive nuclear envelope protein	20.43787207	2.686 96502	0.397733508	6.7839 13954	1.17E-11
ABLUW_RS0170	ABLUW_2094	NZ_CP008706.1	207685	207297	-	WP_00101659.1		hypothetical protein	510162548	2.6976 9 89	0.356096547	7.57535285	3.58E-14
sRNA8	no	no	no	no	no	no	no	no	975.7787727	2.68502 047	0.292554444	9.17785 829	4.40E-20
ABLUW_RS0516	ABLUW_1642	NZ_CP008706.1	105072	105042	+	WP_001014257.1		GFA family protein	393.7295252	2.68 107 001	0.249088238	0.76434328	5.07E-27
ABLUW_RS1055	ABLUW_2314	NZ_CP008706.1	2299784	2299963	+	WP_000905609.1		hypothetical protein	14.5470 8678	2.68063 718	0.5847888 3	4.58394049	4.56E-06
ABLUW_RS0240	ABLUW_0750	NZ_CP008706.1	748784	748951	+	WP_000047869.1		hypothetical protein	67.1245086	2.668552559	0.29190463	9.94285578	4.99E-20
ABLUW_RS0760	ABLUW_2831	NZ_CP008706.1	2837325	2842124	-	WP_002017455.1		RHS repeat protein	6937.8793 9	2.667 020385	0.18247604	4.61627272	2.2 9E-48
ABLUW_RS0385	ABLUW_2757	NZ_CP008706.1	2747075	2748625	-	WP_000256739.1		NAD(P)FAD-dependent oxidoreductase	177.4189627	2.664408651	0.267473061	9.961409366	2.25E-23
ABLUW_RS0450	ABLUW_0339	NZ_CP008706.1	152572	153357	+	WP_000155840.1		ABC transporter substrate-binding protein	187.63 0355	2.66 826701	0.180827624	4.72079674	4.74E-49
ABLUW_RS0395	ABLUW_2965	NZ_CP008706.1	2978751	2978951	+	WP_0007676 577.1		hypothetical protein	1338.562044	2.65828942	0.6 9582238	4.31659514	159E-05
ABLUW_RS0335	ABLUW_2537	NZ_CP008706.1	2528673	2530052	-	WP_000470954.1		L-serine ammonia- lyase	1739.075033	2.65691671	0.195755785	97.098 8783	3.04E-65
ABLUW_RS0385	ABLUW_3372	NZ_CP008706.1	341016	341871	+	WP_00 1058070.1		4'-phosphopartheninyltransferase superfamily protein	7613.980876	2.655990407	0.908609002	15.63626693	4.52E-55
ABLUW_RS0125	ABLUW_1432	NZ_CP008706.1	14507 9	145 9336	-	WP_000802669.1		LydX family transcriptional regulator	356.45 0262	2.645382317	0.278261949	9.520968634	1.72E-21
ABLUW_RS0705	ABLUW_9638	NZ_CP008706.1	930917	931 906	-	WP_00105399.2		acyltensorase	49.82046937	2.64283 826	0.466728781	5.664577877	147E-08
ABLUW_RS0335	ABLUW_3706	NZ_CP008706.1	387776	387843	-	WP_00 026649.1		4'-phosphopartheninyltransferase superfamily protein	568.5876529	2.643422762	0.2939824	9.0 6307893	159E-9
ABLUW_RS0360	ABLUW_1922	NZ_CP008706.1	1920270	192 862	-	WP_000955626.1		amidobifidolase family protein	18. 8665277	2.631070066	0.269528326	9.17225 812	4.63E-20
ABLUW_RS0830	ABLUW_0723	NZ_CP008706.1	1017691	172 697	-	WP_000707849.1		hypothetical protein	89.84832779	2.628070763	0.425772567	6.172295495	6.73E-10
ABLUW_RS1965	ABLUW_4028	NZ_CP008707.1	1 936	1740	+	WP_000933769.1		toxic anion resistance protein	223.3066202	2.623598859	0.299031168	8.736638643	1.73E-18
ABLUW_RS0100	ABLUW_1000	NZ_CP008706.1	2607851	230874	-	WP_001024339.1		hypothetical protein	279.4984583	2.621456328	0.27579138	9.507070355	139E-21
ABLUW_RS0700	ABLUW_0557	NZ_CP008706.1	541838	164276	+	WP_000913301.1	pgaA	poly-beta-18 N-acetyl-D-glucosamine exporter pom PgaA	185.4306274	2.62184606	0.270400578	9.693740296	3.2 9E-22
ABLUW_RS0395	ABLUW_4079	NZ_CP008706.1	406326	50892	-	WP_00 0930170.1		hypothetical protein	346.323507	2.618702439	0.264496199	9.90072 981	4.0E-23
ABLUW_RS0230	ABLUW_0327	NZ_CP008706.1	316045	316 168	-	WP_000797882.1		hypothetical protein	206.898549	2.608208775	0.273555979	9.370047593	7.25E-24
ABLUW_RS0275	ABLUW_1200	NZ_CP008706.1	276984	277874	-	WP_00 035486.1		SDR family NAD(P)-dependent oxidoreductase	1478.5875	2.605580001	0.46 033 9 18	5.65 94508	159E-08
ABLUW_RS0235	ABLUW_2506	NZ_CP008706.1	2507870	2508022	+	WP_001279164.1		hypothetical protein	141.8609751	2.598 14298	0.753664624	3.447347 48	0.000566 12
ABLUW_RS0285	ABLUW_3704	NZ_CP008706.1	3763092	3764351	-	WP_000330488.1		ectonase-like activity of phylase family protein	300.5509652	2.596078969	0.27967224	11.9340984	104E-32
ABLUW_RS0290	ABLUW_0703	NZ_CP008706.1	896629	896970	-	WP_000146559.1		hypothetical protein	51.6 936545	2.592765943	0.760236338	3.43734885	0.000648736
ABLUW_RS0990	ABLUW_2055	NZ_CP008706.1	2034784	2035794	+	WP_000821735.1		type I fibrinolytic protein	524.47 6817	2.59 027204	0.325494909	7.96 699041	1.75E-15
ABLUW_RS0245	ABLUW_3140	NZ_CP008706.1	316474	3166807	-	WP_000209696.1		hypothetical protein	1319.458006	2.55628063	0.22 839087	11.52312999	10 4E-30
ABLUW_RS0240	ABLUW_3109	NZ_CP008706.1	3163973	3164698	-	WP_000724344.1		hypothetical protein	488.2637173	2.55466 848	0.218542279	11.6895341	144E-31
ABLUW_RS0565	ABLUW_2654	NZ_CP008706.1	2662975	2664465	-	WP_00 0568439.1	tet.	phage terminase large subunit	61.5922403	2.540720789	0.31697853	8.15 922687	3.60E-16
ABLUW_RS1030	ABLUW_2308	NZ_CP008706.1	2230458	2230808	+	WP_0006 8911.1		hypothetical protein	924.18701	2.540686432	0.287288208	8.843622402	9.27E-19
ABLUW_RS02375	ABLUW_0484	NZ_CP008706.1	494759	495654	+	WP_000002382.1		DUF 1448 domain-containing protein	270.20343 9	2.5319999 9	0.363628853	6.982943999	2.89E-12
ABLUW_RS0170	ABLUW_2016	NZ_CP008706.1	2007414	2008865	-	WP_000996660.1		hypothetical protein	264.6104591	2.538179978	0.93 83485	11.4364704	194E-39
sRNA65	no	no	no	no	no	no	no	no	3728.887349	2.53691647	0.44145431	5.74671 079	9.90E-09
ABLUW_RS0040	ABLUW_0069	NZ_CP008706.1	73148	73780	-	WP_000781235.1	maIA	maltylecylacetate isomerase	4447. 88804	2.536817 07	0.373876895	6.785 66876	1.9E-11
ABLUW_RS0270	ABLUW_2861	NZ_CP008706.1	2871422	287 635	-	WP_00166305.1		hypothetical protein	163.9444459	2.52555907	0.29243 906	8.67298567	4.21E-18
ABLUW_RS0880	ABLUW_2654	NZ_CP008706.1	2651966	2662094	+	WP_000471735.1		hypothetical protein	124.681945	2.533375291	0.355667255	7.12934107	106E-12
ABLUW_RS124 9	ABLUW_2550	NZ_CP008706.1	2545458	2545910	-	WP_000004126.1	soxR	redox-sensitive transcriptional activator SoxR	939.537116	2.532257383	0.234267881	10.8902338	3.11E-27
ABLUW_RS0655	ABLUW_2811	NZ_CP008706.1	28 5801	28 9341	-	WP_000773509.1		hypothetical protein	438.0046081	2.528588298	0.234 82384	7.800719528	6.17E-15
ABLUW_RS0560	ABLUW_2589	NZ_CP008706.1	2581722	2582075	-	WP_001198143.1		helicum-helic transcriptional regulator	40.38 100387	2.519665922	0.304283506	8.280350894	123E-16
ABLUW_RS0390	ABLUW_0803	NZ_CP008706.1	778043	778390	+	WP_000103334.1		hypothetical protein	13.16379345	2.5149 6395	0.80566421	4.82328243	3.29E-05
ABLUW_RS0700	ABLUW_1437	NZ_CP008706.1	142904	1430894	-	WP_000159883.1		hypothetical protein	302.673212	2.514250834	0.228 006474	10.02228866	2.98E-28
ABLUW_RS1070	ABLUW_2833	NZ_CP008706.1	2842664	2842993	-	WP_000255936.1		hypothetical protein	838.799548	2.510803875	0.2343786	10.72539844	7.74E-27
ABLUW_RS0525	ABLUW_2785	NZ_CP008706.1	2775566	27813 17	+	WP_001100209.1		taninase/fenylol esterase family alpha/beta hydrolase	148.390482	2.510072 5	0.3357545	4.745849451	1.67E-14
ABLUW_RS0765	ABLUW_2832	NZ_CP008706.1	2842332	2842655	+	WP_000725059.1		hypothetical protein	261.085951	2.507485782	0.306438363	8.1826 17395	2.78E-16
ABLUW_RS0110	ABLUW_0227	NZ_CP008706.1	247400	247735	-	WP_000168772.1		helicum-helic transcriptional regulator	1025. 960451	2.506337492	0.27925841	6.97 46656	2.93E-19
ABLUW_RS0380	ABLUW_0646	NZ_CP008706.1	165174	65 917	-	WP_001195885.1		VOC family protein	1234.266871	2.504 1071	0.3518 8563	7.1107054 16	1.16E-12
ABLUW_RS0165	ABLUW_1612	NZ_CP008706.1	1606447	1606647	+	WP_000462396.1		hypothetical protein	4.998927239	2.495507059	1.047270365	2.382936769	0.01757844
sRNA 61	no	no	no	no	no	no	no	no	781.687 0224	2.496463429	0.25579257	9.756630 82	175E-22
ABLUW_RS1955	ABLUW_2091	NZ_CP008706.1	2077290	2077376	-	WP_00 1985605.1		hypothetical transcriptional regulator	383.0860923	2.488925726	0.274700081	9.060520544	130E-19
ABLUW_RS0535	ABLUW_3201	NZ_CP008706.1	3229 91	3229739	+	WP_000807295.1		LydX family translocator	33.53337078	2.488753784	0.333656002	7.45904 119	8.72E-14
ABLUW_RS0750	no	NZ_CP008706.1	3273353	3274195	-			CDF family peptidase	308.9784756	2.48796 9764	0.28849373	8.62397 970	6.47E-18
ABLUW_RS1640	ABLUW_2372	NZ_CP008706.1	2358457	23586 8	-	WP_000784879.1		DUF1217 family protein	88.86948507	2.479695392	0.43920197	5.644774648	165E-08
ABLUW_RS0370	ABLUW_0685	NZ_CP008706.1	693671	694552	-	WP_000022 05.1		alpha/beta fold hydrolase	287.600 099	2.479286949	0.42059 856	5.894759629	3.75E-09
ABLUW_RS1075	ABLUW_2834	NZ_CP008706.1	2841439	2843508	+	WP_000744506.1		hypothetical protein	388.7433293	2.4719 5 86	0.297307901	8.338667391	7.51E-17
ABLUW_RS0180	ABLUW_1675	NZ_CP008706.1	162278	1636 34	-	WP_000097870.1		AraC family transcriptional regulator	133.9551333	2.47740045	0.2 6528487	1147329074	1.80E-30
ABLUW_RS12 9	ABLUW_4037	NZ_CP008707.1	22237	22336	-	WP_00 1096429.1		helicum-helic transcriptional regulator	498.8084305	2.47665259	0.337797033	7.33177725	2.27E-13
ABLUW_RS0005	ABLUW_2437	NZ_CP008706.1	2469376	2460530	-	WP_000517392.1		acyl-CoA dehydrogenase family protein	69.0664786	2.475624876	0.34460924	7.183860884	6.78E-13
ABLUW_RS0265	ABLUW_2523	NZ_CP008706.1	2514893	2516276	-	WP_001191041.1		Psad family thioesterase	68.1266657	2.47 98 12	0.4018 5296	6.15542325	7.50E-10
ABLUW_RS0305	ABLUW_1866	NZ_CP008706.1	18978 9	1898 00	-	WP_0005523 0.1		hypothetical protein	91492 9891	2.471 9277	0.273900764	0.024197944	1.8E-19
ABLUW_RS0630	ABLUW_1855	NZ_CP008706.1	185167	18529 16	-	WP_00 076622.1		MFS transporter	75.5304 872	2.469830232	0.354817424	6.960848221	3.38E-12
ABLUW_RS0745	ABLUW_3243	NZ_CP008706.1	3273792	32737307	-	WP_000370427.1		hypothetical protein	503.034285	2.468650865	0.9648 909	4.83434972	8.79E-50
ABLUW_RS0670	ABLUW_1823	NZ_CP008706.1	1818802	1819647	-	WP_000844943.1		metal-dependent hydrolase	164.2458599				

ABUW_RS10670	ABUW_2495	NZ_CP008706.1	218189	218242	-	WP_000993356.1		alkane 1-monooxygenase	236.1810285	2.59649492	0.256302627	9.206497502	3.37E-20	1.79E-19	8.74714697
ABUW_RS0920	ABUW_933	NZ_CP008706.1	929623	929623	+	WP_000772916.1	pcrF	3'-oxoadipyl-CoA thiolase	94.45037377	2.89891641	0.33781929	6.982755163	2.89E-12	8.83E-12	11.0540393
ABUW_RS0285	ABUW_072	NZ_CP008706.1	916654	699244	-	WP_010125253.1		ANTAR domain-containing protein	32.76561499	2.5838543	0.32196639	7.324250263	2.40E-13	8.06E-13	12.0936496
ABUW_RS1580	ABUW_1702	NZ_CP008706.1	215690	215693	-	WP_051016784.1		HAD1 family hydrolase	101.276091	3.28482346	0.148272083	5.84805548	1.45E-56	6.28E-55	54.2020430
ABUW_RS1460	ABUW_231	NZ_CP008706.1	293281	293328	+	WP_000706047.1		fomylglycine-generating enzyme family protein	91.51041604	2.34190636	0.264359555	8.844761973	6.40E-19	3.1E-18	17.5072361
ABUW_RS3235	ABUW_3038	NZ_CP008706.1	916329	916340	+	WP_010336911.1		hydropetalin protein	1054.91233	3.247805491	0.85918763	12.6283294	1.47E-36	2.8E-35	34.57778271
ABUW_RS0995	ABUW_2592	NZ_CP008706.1	2586352	2587005	-	WP_000217385.1		DUF1989 domain-containing protein	3.480806754	2.34433623	0.007550291	2.32075845	0.070977592	0.025947685	158590.583
ABUW_RS0385	ABUW_2636	NZ_CP008706.1	268243	268276	+	WP_000636785.1		transposase	1646.09965	2.34168899	0.570023204	4.108059054	3.99E-05	6.70E-05	4.73925197
ABUW_RS0265	ABUW_0481	NZ_CP008706.1	452778	493941	+	WP_010176667.1		acyl-CoA dehydrogenase family protein	478.7224629	2.390480022	0.235433952	9.935049732	2.93E-23	1.91E-22	21.7896663
ABUW_RS0580	ABUW_181	NZ_CP008706.1	187842	188457	+	WP_000725511.1		hydropetalin protein	90.4343304	2.338849424	0.31848012	7.34378508	2.08E-10	7.00E-10	12.6490196
ABUW_RS1675	ABUW_2400	NZ_CP008706.1	238783	2387462	+	WP_000448952.1		malonate decarboxylase subunit delta	85.82535069	2.33816745	0.484720068	4.823641008	1.41E-06	2.7E-06	5.567030709
ABUW_RS1035	ABUW_2229	NZ_CP008706.1	221907	2219623	+	WP_000525882.1		energy transducer TonB	67.8827213	2.336982333	0.254024731	9.69822109	3.59E-20	1.90E-19	8.7210444
ABUW_RS0630	ABUW_092	NZ_CP008706.1	1009718	111145	+	WP_000102080.1	terL	phage terminase large subunit	10.2523942	2.336483059	0.25278255	9.24305518	2.40E-20	1.29E-19	8.88941929
ABUW_RS8290	ABUW_3757	NZ_CP008706.1	381340	381377	-	WP_000483007.1		DoxA family protein	80.6206763	2.33375631	0.204356934	11.4200059	3.32E-30	3.96E-29	28.4962032
ABUW_RS0790	ABUW_937	NZ_CP008706.1	913540	935723	+	WP_000920714.1		SDR family NAD(P)-dependent oxidoreductase	232.5891553	2.33272402	0.314067497	7.427440797	1.18E-13	3.83E-13	12.4168023
ABUW_RS0560	ABUW_184	NZ_CP008706.1	192271	193443	+	WP_000049455.1		hydropetalin protein	105.4800381	2.328250079	0.248670164	9.362804304	7.76E-21	4.32E-20	9.36451825
ABUW_RS0245	ABUW_933	NZ_CP008706.1	916047	916910	+	WP_000037356.1		iron-containing redox enzyme family protein	1093.800821	2.316693331	0.203493939	11.38458148	4.99E-30	4.75E-29	28.32330639
ABUW_RS0595	ABUW_027	NZ_CP008706.1	102720	102975	-	WP_000516644.1		acyl-CoA dehydrogenase	2404.047217	2.316430246	0.334678592	6.9243255	4.47E-12	1.34E-11	10.872852
ABUW_RS0755	ABUW_0358	NZ_CP008706.1	380776	382121	+	WP_010198448.1		S8 family serine peptidase	272.4159303	2.316772986	0.205670342	11.29963568	2.08E-29	1.88E-28	27.2584125
ABUW_RS0495	ABUW_260	NZ_CP008706.1	2140911	2142017	+	WP_000734971.1		poim	318.0805505	2.31059185	0.077224493	8.04034859	7.21E-39	1.14E-37	36.54035916
ABUW_RS0960	ABUW_986	NZ_CP008706.1	190238	191686	+	WP_034805894.1		replication initiation factor domain-containing protein	454.6804761	2.310489548	0.28189579	8.216819164	2.09E-10	8.7E-10	15.0599614
ABUW_RS0760	ABUW_931	NZ_CP008706.1	912652	925092	+	WP_000750672.1		spore coat protein I domain-containing protein	7973.259285	2.308874279	0.419132727	5.51080693	3.57E-08	7.82E-08	7.10679247
ABUW_RS1845	ABUW_3344	NZ_CP008706.1	3373701	3378400	+	WP_001885447.1		LydR family transcriptional regulator	244.838216	2.30918547	0.268709535	8.59332892	8.45E-18	3.87E-17	16.1229033
ABUW_RS0845	ABUW_1403	NZ_CP008706.1	104825	105097	+	WP_000090108.1		hydropetalin protein	104.2236246	2.308712295	0.280485728	8.243152219	1.85E-16	7.74E-15	15.1102904
ABUW_RS09740	ABUW_2005	NZ_CP008706.1	200938	202238	+	WP_000996660.1		hydropetalin protein	2614413877	2.303834819	0.96078244	1177277382	5.59E-32	5.92E-31	30.2276728
ABUW_RS0025	ABUW_0233	NZ_CP008706.1	1275970	127708	-	WP_000978625.1		OmpW family protein	350.0831077	2.305540801	0.261974307	8.804807381	1.27E-18	6.06E-18	12.0752733
ABUW_RS0476	ABUW_061	NZ_CP008706.1	917189	917235	-	WP_010188098.1		glycylserine family 39 protein	80.1549504	2.302572016	0.228858802	10.0610317	8.21E-24	5.62E-23	22.2502363
ABUW_RS1410	ABUW_3781	NZ_CP008706.1	384207	3842856	+	WP_000695976.1		AMP-binding protein	693.131288	2.30145195	0.387566211	5.93897271	6.87E-09	8.83043263	
ABUW_RS0300	ABUW_2684	NZ_CP008706.1	2674083	2675189	-	WP_000790402.1		minor capsid protein	424.6528204	2.300779312	0.369518591	6.22642698	4.77E-10	1.22E-09	8.91640919
ABUW_RS0440	ABUW_2027	NZ_CP008706.1	201391	2015342	+	WP_000996660.1		hydropetalin protein	261518347	2.296571793	0.77606738	10.305668	3.02E-38	4.65E-37	36.33254705
ABUW_RS0340	ABUW_258	NZ_CP008706.1	216282	2114725	-	WP_010287542.1	tpdA	thylacoid protein/dehydrogenase	665.6628746	2.294754251	0.45719393	9.019344748	5.1E-07	1.04E-06	15.82966661
ABUW_RS0576	ABUW_935	NZ_CP008706.1	912690	927840	+	WP_010295091.1		citriculic permuted type 2 ATP-grasp protein	880.15665	2.294557198	0.241735531	9.279602552	1.77E-20	8.60E-20	10.0728871
ABUW_RS0370	ABUW_2545	NZ_CP008706.1	2537307	2538569	-	WP_000416230.1		NAD(P)FAD-dependent oxidoreductase	80.35791419	2.294444206	0.235008504	9.763222034	1.62E-22	10.1E-21	20.95967863
ABUW_RS1400	ABUW_2344	NZ_CP008706.1	2374461	2328168	+	WP_000342693.1		Cyp11r family transcriptional regulator	212.8547762	2.287845048	0.216534222	10.56734347	4.30E-26	3.36E-25	24.47360072
ABUW_RS1880	ABUW_4031	NZ_CP008707.1	91809	9481	+	WP_000443897.1		hydropetalin protein	102.5020344	2.285546646	0.289628323	7.89109196	2.99E-15	1.16E-14	13.0930216
ABUW_RS0355	ABUW_0621	NZ_CP008706.1	622271	623330	+	WP_010155158.1		AraC family transcriptional regulator	275.6878074	2.284896562	0.191059664	11.84367656	7.01E-33	8.28E-32	31.0819686
ABUW_RS0065	ABUW_962	NZ_CP008706.1	915844	915869	+	WP_01056937.1		aromatic-type hydroxylating dioxygenase subunit beta	714.732945	2.28158406	0.420862659	5.308334556	1.1E-07	2.34E-07	6.03078143
ABUW_RS0945	ABUW_2056	NZ_CP008706.1	2035907	2036884	+	WP_000701847.1		DUF4882 family protein	429.0684263	2.27723989	0.29887357	7.59400313	3.1E-14	1.1E-13	12.6546702
ABUW_RS1445	ABUW_2394	NZ_CP008706.1	2382690	2383451	+	WP_000338773.1	madM	malonate transporter subunit MadM	177.8893506	2.276500534	0.235374698	9.6781601	3.97E-22	2.39E-21	10.9260181
ABUW_RS1470	ABUW_3039	NZ_CP008706.1	3065316	3066097	-	WP_000895283.1		GNAT family N-acetyltransferase	103.858804	2.276201921	0.257804814	8.829516755	1.05E-18	5.03E-18	17.29843201
ABUW_RS1470	ABUW_2165	NZ_CP008706.1	218211	1218435	+	WP_000848151.1		hydropetalin protein	1012.573221	2.276062895	0.262902277	10.587448395	8.42E-18	2.23E-17	6.61595194
ABUW_RS1085	ABUW_2817	NZ_CP008706.1	2819808	2823302	+	WP_000488285.1		type IV secretion system pil protein VgrG	3702.318214	2.27195364	0.2219276	10.25337895	1.1E-24	8.1E-24	23.0009719
ABUW_RS0745	ABUW_0693	NZ_CP008706.1	973225	974205	-	WP_010224031.1		glycylserine family 2 protein	90.86496627	2.271491107	0.255719169	8.896678385	5.75E-19	2.80E-18	17.55284197
ABUW_RS0300	ABUW_0620	NZ_CP008706.1	612715	621190	-	WP_000919281.1		metal-dependent hydrolase	304.3910207	2.273238445	0.233263195	9.745334359	1.93E-22	1.96E-21	10.92445304
ABUW_RS0710	ABUW_0279	NZ_CP008706.1	296818	297107	-	WP_000690905.1		hydropetalin protein	3293.81873	2.267922532	0.8160428	11.6214069	3.21E-31	3.33E-30	29.4775577
ABUW_RS0800	ABUW_960	NZ_CP008706.1	9152359	9154422	-	WP_000103596.1		ABC-F family ATP-binding cassette domain-containing protein	749.2875832	2.265638082	0.266753063	8.493319069	2.01E-17	8.93E-17	16.0418854
ABUW_RS1780	ABUW_3646	NZ_CP008706.1	3749142	3772394	+	WP_017695121.1		universal stress protein	311.957817	2.263394835	0.1891941	11.9661052	5.55E-33	6.37E-32	31.9586057
ABUW_RS1250	ABUW_3749	NZ_CP008706.1	3805847	380615	-	WP_000626445.1		glutathione S-transferase	938.01993	2.2618198	0.159872002	14.1773241	1.93E-45	4.47E-44	43.34960248
ABUW_RS0980	ABUW_965	NZ_CP008706.1	9160751	916107	+	WP_010183767.1		flavin reductase family protein	25.7643261	2.26076697	0.386296488	5.52441094	4.84E-09	1.14E-08	7.94309510
ABUW_RS0920	ABUW_4041	NZ_CP008707.1	23960	24658	+	WP_000879188.1		glycylserine family 2 protein	378.4862268	2.258838736	0.302124008	7.460179433	8.64E-14	3.02E-13	11.92993036
ABUW_RS0480	ABUW_2167	NZ_CP008706.1	2192625	219860	+	WP_000652121.1		GFA family protein	72.482608	2.251978773	0.388862809	5.71972779	6.99E-09	1.63E-08	17.78782396
ABUW_RS0320	ABUW_3341	NZ_CP008706.1	3374349	3375497	+	WP_000534868.1		lysine-type racemase/epimerase	168.99801	2.251564899	0.93728516	11.62227343	3.1E-31	3.29E-30	29.4828041
ABUW_RS0350	ABUW_2100	NZ_CP008706.1	216823	2118842	+	WP_010133050.1		alpha-ketoadipyl dehydrogenase subunit beta	780.165996	2.248789874	0.572267116	3.262678152	8.83E-05	0.000100551	3.8521606
ABUW_RS1075	ABUW_4011	NZ_CP008706.1	41649	6684	+	WP_010118847.1		type-F conjugative transfer system secretin Trak	523.0528661	2.245809213	0.273352469	8.81866037	2.1E-16	5.04E-16	10.54272756
ABUW_RS0950	ABUW_959	NZ_CP008706.1	9156269	9156628	+	WP_000387550.1		hydropetalin protein	559.554375	2.24465335	0.530594381	4.230281093	2.33E-05	3.98E-05	4.40119828
ABUW_RS0710	ABUW_1440	NZ_CP008706.1	1432445	132987	+	WP_010118740.1		hydropetalin protein	32.2415925	2.243388829	0.34965033	6.45725645	1.39E-10	3.70E-10	9.43192176
ABUW_RS0280	ABUW_0583	NZ_CP008706.1	577412	579230	+	WP_000289874.1		terminase family protein	18.3857239	2.241964715	0.239214445	9.37980133	7.1E-21	4.00E-20	19.39710001
ABUW_RS0720	ABUW_1801	NZ_CP008706.1	159760	1597868	+	WP_000351255.1		hydropetalin protein	102.3187892	2.238187844	0.446192055	5.01851663	5.26E-07	1.05E-06	5.97881871
ABUW_RS0045	ABUW_0009	NZ_CP008706.1	11026	12103	+										

ABUW_RS1000	ABUW_2699	NZ_CP008706.1	2684478	2686472	+	WP_000998366.1		exodeoxyribonuclease V1small subunit	35.42714579	2.344597309	0.408884028	5.24500142	1.56E-07	3.26E-07	6.4867824
ABUW_RS06025	ABUW_1421	NZ_CP008706.1	1412739	1412324	+	WP_000610266.1		hypothetical protein	12.47077006	2.109244175	0.4875172	4.388038359	1.9E-05	2.0E-05	4.69680343
ABUW_RS1890	ABUW_3068	NZ_CP008706.1	3095513	3096091	+	WP_001968486.1		hypothetical protein	242.7292224	2.109097318	0.301867012	7.086224185	1.38E-12	4.35E-12	1.13615074
ABUW_RS07630	ABUW_1432	NZ_CP008706.1	1423885	1424109	+	WP_000850407.1		hypothetical protein	318.601445	2.108992006	0.227808619	9.38942565	6.03E-21	3.40E-20	9.46385108
ABUW_RS07630	ABUW_1463	NZ_CP008706.1	1517054	1512207	-	WP_000783724.1		hypothetical protein	307.0754027	2.10765221	0.321928613	6.64043567	3.18E-11	8.87E-11	10.05203468
ABUW_RS07630	ABUW_1469	NZ_CP008706.1	1576720	1557859	-	WP_000583581		ABC transporter permease	63.53833372	2.127377394	0.273067605	8.72690439	5.00E-15	1.90E-14	3.072494
ABUW_RS06920	ABUW_1957	NZ_CP008706.1	1959292	1959366	-	WP_000193129.1		HD domain-containing protein	145.0659345	2.106264996	0.219332036	9.939203607	2.81E-23	1.84E-22	2.17359218
ABUW_RS1815	ABUW_3331	NZ_CP008706.1	3366235	3366848	-	WP_001991904.1		hypothetical protein	189.4607777	2.105523048	0.43857807	4.869230371	1.02E-04	2.16E-08	5.665544249
ABUW_RS1625	ABUW_2359	NZ_CP008706.1	2356407	2357441	-	WP_001966574.1		anrB	28.28076534	2.103322302	0.36194122	5.906935049	3.49E-09	8.29E-09	8.081454469
sRNA39	no	no	no	no	no	no	no	no	17.05571931	2.104543371	1.427838369	1.494884447	0.134944602	0.17959816	0.801458082
ABUW_RS10395	ABUW_2759	NZ_CP008706.1	2749545	2750507	-	WP_000226456.1		metal-dependent hydrolase	39.96014067	2.11110081	0.300610734	7.089278052	1.35E-12	4.26E-12	11.3759904
ABUW_RS03665	ABUW_1744	NZ_CP008706.1	744323	744514	-	WP_001076118.1		hypothetical protein	59.99241438	2.129679529	0.27036885	8.78733576	3.31E-15	1.27E-14	13.8919628
ABUW_RS04940	ABUW_1330	NZ_CP008706.1	1340816	1341451	-	WP_161283661.1		hypothetical protein	164.1097805	2.128685786	0.250708347	4.890685721	2.05E-17	9.14E-17	16.0390538
ABUW_RS00785	ABUW_1058	NZ_CP008706.1	1175884	1176169	+	WP_001614984.1		TMM165/GDT1 family protein	1985.723301	2.108810486	0.249975453	8.508089333	1.77E-17	7.90E-17	16.9237291
ABUW_RS03175	ABUW_1625	NZ_CP008706.1	1623316	1624194	+	WP_000404161.1		SMP-303glucanactonase,RE family protein	339.8893349	2.122947105	0.22343018	9.479815839	2.55E-21	1.46E-20	19.83564714
ABUW_RS20450	ABUW_1069	NZ_CP008706.1	1098999	1099272	+	WP_001070707.1		hypothetical protein	20.39343546	2.122033254	0.40690443	5.216065495	1.84E-07	3.82E-07	6.41936637
ABUW_RS18940	ABUW_3282	NZ_CP008706.1	3318205	3317206	+	WP_001027236.1		hypothetical protein	818.5007425	2.118688782	0.195284866	13.4086472	2.06E-40	3.55E-39	38.44077185
ABUW_RS01790	ABUW_10773	NZ_CP008706.1	759531	760172	+	WP_000373122.1		hypothetical protein	57.0619432	2.116190403	0.238008454	8.90345097	5.35E-19	2.63E-19	17.69004425
ABUW_RS01360	ABUW_2152	NZ_CP008706.1	2118183	2119189	+	WP_000364558.1		lpA	500.7776	2.118773353	0.338846793	6.237735268	3.91E-10	1.9E-09	8.99567626
ABUW_RS10300	ABUW_4056	NZ_CP008707.1	33741	34544	-	WP_025464697.1		aph(3")-b	857.2807749	2.118533268	0.440060305	4.14296932	1.40E-06	2.83E-06	5.544210564
ABUW_RS08545	ABUW_1754	NZ_CP008706.1	1749578	1750114	-	WP_000573225.1		GNA1 family N-acetyltransferase	304.760239	2.118518638	0.24211653	8.78237856	2.58E-18	1.21E-17	16.91721463
ABUW_RS10545	ABUW_2894	NZ_CP008706.1	2901934	2902486	+	WP_001929889.1		DUF2233 family protein	1012.105045	2.117818034	0.279819074	7.568529565	3.77E-14	1.35E-13	12.8666623
ABUW_RS01360	ABUW_10809	NZ_CP008706.1	718187	718856	+	WP_000443302.1		hypothetical protein	6153287307	2.115075753	0.330071922	6.41519511	14.1E-10	3.75E-10	9.425968732
ABUW_RS02020	ABUW_2438	NZ_CP008706.1	2443352	2445284	-	WP_000433921.1		flavin nucleotide family protein	126.777809	2.116339184	0.276393611	7.656975525	1.90E-14	6.98E-14	13.1614458
ABUW_RS00405	ABUW_1237	NZ_CP008706.1	1208161	1210646	+	WP_000192520.1		DUF3465 domain-containing protein	331.393969	2.116137017	0.19316319	9.9551809	6.21E-28	5.32E-27	26.27408337
ABUW_RS10295	ABUW_1925	NZ_CP008706.1	2307578	2307654	+	WP_000230765.1		rRNA-1e	34.1674799	2.114719144	0.489350552	4.32141062	1.55E-05	2.70E-05	4.566363236
ABUW_RS14270	ABUW_2940	NZ_CP008706.1	2954180	2955376	-	WP_000753778.1		hypothetical protein	611.8467862	2.114220029	0.26319515	8.030531755	3.36E-16	3.74E-16	14.4271884
ABUW_RS10190	ABUW_2505	NZ_CP008706.1	2500023	2501539	-	WP_000600070.1		MFS transporter	77.97504362	2.117422289	0.276477036	7.645272527	2.09E-14	7.61E-14	11.186934
ABUW_RS18220	ABUW_3339	NZ_CP008706.1	3373304	3374074	+	WP_00170388.1		hypothetical protein	571.610489	2.106570452	0.193093441	6.019594863	9.25E-28	7.80E-27	26.1079054
ABUW_RS18195	ABUW_3333	NZ_CP008706.1	3357191	3358204	-	WP_001937473.1		hypothetical protein	316.0100858	2.10835373	0.487967075	4.320685804	1.56E-05	2.70E-05	4.566363236
ABUW_RS01360	ABUW_10809	NZ_CP008706.1	718187	718856	-	WP_000443302.1		hypothetical protein	34.2634944	2.107006632	0.417608137	5.045415659	4.53E-07	9.09E-07	6.014361197
ABUW_RS01360	ABUW_10809	NZ_CP008706.1	718187	718856	-	WP_000443302.1		hypothetical protein	87.47102003	2.106459996	0.261691572	8.049922303	8.55E-16	3.44E-16	14.48341195
ABUW_RS10545	ABUW_1754	NZ_CP008706.1	1749578	1750114	-	WP_000573225.1		GNA1 family N-acetyltransferase	563.1809335	2.105423316	0.21750976	9.942921429	2.71E-23	1.78E-22	2.174958
ABUW_RS00910	ABUW_1418	NZ_CP008706.1	1416544	1416667	+	WP_000729216.1		hypothetical protein	6.532604237	2.101878299	0.64719429	3.247681076	0.001163493	0.0017198	2.764522055
ABUW_RS10345	ABUW_2608	NZ_CP008706.1	2608775	2609167	+	WP_001733094.1		minor capsid protein	76.16448541	2.11077441	0.369610164	5.686473525	1.30E-08	2.95E-08	7.530177078
ABUW_RS01730	ABUW_1541	NZ_CP008706.1	1527863	1528459	+	WP_000243522.1		alpha-E domain-containing protein	218.0434316	2.109683835	0.278544721	7.527826629	5.16E-14	1.83E-13	12.73754891
ABUW_RS02690	ABUW_10548	NZ_CP008706.1	1053035	1053226	-	WP_001043481.1		hypothetical protein	63.58032267	2.109241956	0.304953385	6.873883889	6.25E-12	1.86E-11	19.70404706
ABUW_RS01360	ABUW_10809	NZ_CP008706.1	718187	718856	-	WP_000443302.1		hypothetical protein	21.62374114	2.109598753	0.37051591	5.656762915	1.54E-08	3.48E-08	7.45842071
ABUW_RS01730	ABUW_1469	NZ_CP008706.1	1576720	1557859	-	WP_000583581.1		cusB	104.377787	2.109249885	0.130782883	1.961060242	0.109164002	0.109164002	8.88838831
ABUW_RS18195	ABUW_3333	NZ_CP008706.1	3357191	3358204	-	WP_001937473.1		hypothetical protein	21.72729493	2.109153345	0.21720735	9.740807488	2.02E-22	1.25E-21	20.30039699
ABUW_RS18195	ABUW_3333	NZ_CP008706.1	3357191	3358204	-	WP_001937473.1		hypothetical protein	176.1718743	2.108255331	0.31673502	6.629726216	3.46E-11	9.72E-11	10.01233374
ABUW_RS18195	ABUW_3333	NZ_CP008706.1	3357191	3358204	-	WP_001937473.1		hypothetical protein	171.1168368	2.108233072	0.290990414	7.165011651	8.31E-13	2.68E-12	15.77186521
ABUW_RS18195	ABUW_3333	NZ_CP008706.1	3357191	3358204	-	WP_001937473.1		hypothetical protein	59.5045679	2.107954592	0.31912683	5.619326409	7.21E-11	1.97E-10	9.705533774
ABUW_RS14135	ABUW_2949	NZ_CP008706.1	2964221	2965190	-	WP_000637783.1		VOC family protein	64.1632417	2.107496041	0.304523992	6.868996927	8.57E-12	2.52E-11	10.58895946
ABUW_RS01360	ABUW_10809	NZ_CP008706.1	718187	718856	-	WP_000443302.1		hypothetical protein	98.07908245	2.107371662	0.310538857	8.000199704	5.20E-12	1.55E-11	10.096683
ABUW_RS02035	ABUW_1356	NZ_CP008706.1	1353907	1353267	-	WP_000742883.1		hypothetical protein	226.3425616	2.107723473	0.317798011	6.536373655	6.30E-11	1.74E-10	9.758407752
ABUW_RS01730	ABUW_1469	NZ_CP008706.1	1576720	1557859	-	WP_000583581.1		phage tail protein	410.0273942	2.107633	0.248534722	6.030430344	6.25E-17	2.69E-16	9.57024712
ABUW_RS02380	ABUW_1495	NZ_CP008706.1	1495685	1497496	+	WP_000121938.1		SDR family oxidoreductase	134.988263	2.107561445	0.369577106	5.616187025	1.95E-08	4.35E-08	7.361910743
sRNA4	no	no	no	no	no	no	no	no	28.4677612	2.107329956	0.412338483	5.02843705	4.95E-07	9.91E-07	6.003926436
ABUW_RS08555	ABUW_1756	NZ_CP008706.1	1750756	1752006	+	WP_000632782.1		lynJ	291.009204	2.107185005	0.172284893	12.02592389	2.60E-33	3.15E-32	31.50168945
ABUW_RS08535	ABUW_1340	NZ_CP008706.1	1334449	1334108	+	WP_000103375.1		hlsQ	26.58724874	2.107492103	0.358898163	5.76755106	8.04E-09	1.86E-08	7.730487056
ABUW_RS18175	ABUW_2237	NZ_CP008706.1	2226621	2228168	+	WP_000920587.1		NAD(P)FAD-dependent oxidoreductase	75.9668729	2.107294966	0.239224361	6.654210675	4.96E-18	2.28E-17	16.6404562
ABUW_RS04730	ABUW_1964	NZ_CP008706.1	1974202	1974996	+	WP_001104939.1		ChdGlpH-like family deacetylase	176.187345	2.106974616	0.228014418	9.045918437	1.48E-19	7.47E-19	18.066794
ABUW_RS10405	ABUW_3768	NZ_CP008706.1	3766359	3766967	+	WP_000667181.1		transglycolase family domain-containing protein	200.181111	2.106500468	0.247148217	8.36181246	6.20E-17	6.76E-16	15.73448874
ABUW_RS01360	ABUW_10809	NZ_CP008706.1	718187	718856	-	WP_000443302.1		hypothetical protein	238.0684581	2.106408441	0.302309399	6.827617184	8.63E-12	2.53E-11	10.5668748
ABUW_RS04145	ABUW_1008	NZ_CP008706.1	1021621	1022190	-	WP_001950712.1		CAP-domain-containing protein	322.411472	2.106376934	0.190539405	11.43061779	2.94E-30	2.83E-29	28.58421536
ABUW_RS10300	ABUW_2530	NZ_CP008706.1	2521948	2523621	-	WP_001168442.1		enrG	794.633576	2.106330044	0.52160219	3.956418889	7.61E-05	0.000194708	3.904105686
ABUW_RS10190	ABUW_2679	NZ_CP008706.1	2670707	2671500	+	WP_000644336.1		DUF1142 domain-containing protein	1255.378016	2.105648525	0.604471845	3.4020916	0.000668722	0.001008951	2.9987427
ABUW_RS10190	ABUW_2679	NZ_CP008706.1	2668857	2668848	-	WP									

ABUW_RS1000	ABUW_2466	NZ_CP008706.1	2458034	2459371	-	WP_000208930.1		MFS transporter	63.19331237	1.965078967	0.283752292	6.92532484	4.35E-12	1.3E-11	10.8827287
ABUW_RS1430	ABUW_2948	NZ_CP008706.1	2962980	2964191	-	WP_00041872.1		FAD-dependent oxidoreductase	98.40976079	1.96234208	3.0244333	6.18859999	1.0E-09	2.52E-09	8.59549459
ABUW_RS02730	ABUW_0555	NZ_CP008706.1	559447	557447	-	WP_000300085.1		TraT/DiisA_Ca-type zinc finger protein	34.01885448	1.961867084	4.29018999	4.57205516	4.85E-06	8.8E-06	5.055024902
ABUW_RS14365	ABUW_4066	NZ_CP008706.1	2194	21707	+	WP_000731978.1		hypothetical protein	94.4831502	1.96964276	3.32510388	6.270594201	3.60E-10	9.30E-10	17.03387951
ABUW_RS0555	ABUW_0890	NZ_CP008706.1	886151	886588	-	WP_000966782.1		universal stress protein	1098.074839	1.957893443	0.232520349	8.79355211	1.96E-18	9.25E-18	17.03387951
ABUW_RS1650	ABUW_4106	NZ_CP008706.1	66902	67297	+	WP_000717812.1		hypothetical protein	1013658584	1.954740414	0.25207212	7.765014497	8.15E-15	3.04E-14	13.5170462
ABUW_RS0925	ABUW_8554	NZ_CP008706.1	855094	851450	-	WP_000421436.1		OpiD family outer membrane protein	88.10095702	1.953069493	0.31188258	6.276281975	3.47E-10	8.97E-10	9.047207567
ABUW_RS1073	ABUW_2176	NZ_CP008706.1	216699	215785	-	WP_000249278.1		2'-5' RNA ligase family protein	330.0841259	1.950600573	0.2192631	8.976008783	2.81E-19	1.39E-18	17.85685652
ABUW_RS07285	ABUW_1494	NZ_CP008706.1	148195	148192	+	WP_000097611.1		hypothetical protein	124.5089825	1.95027452	0.337437597	5.77965819	7.49E-09	1.74E-08	7.759450752
ABUW_RS07865	ABUW_610	NZ_CP008706.1	604758	605615	+	WP_000242911.1		DMT family transporter	215.9416099	1.949715481	0.89765682	11.48474447	1.07E-30	1.55E-29	28.1096683
ABUW_RS0955	ABUW_1665	NZ_CP008706.1	1667276	1668199	-	WP_000860138.1		alpha/beta hydrolase	12117160811	1.949331726	0.234424028	8.31540924	9.16E-17	3.90E-16	15.40083539
ABUW_RS1520	ABUW_1341	NZ_CP008706.1	3167036	3168385	-	WP_001024874.1		hypothetical protein	1021666093	1.944705834	0.165050797	12.26898869	1.33E-34	1.72E-33	32.76447155
ABUW_RS10815	ABUW_1666	NZ_CP008706.1	1657273	1660029	+	WP_000617512.1	mgfA	magnesium-translocating P-type ATPase	349.4186194	1.944053666	0.200229032	9.29191017	1.52E-20	8.30E-20	10.08092191
ABUW_RS1840	ABUW_4096	NZ_CP008707.1	58930	5996	-	WP_001978617.1		hypothetical protein	84.05733059	1.94385769	0.41023885	4.738359396	2.16E-06	4.05E-06	5.924540977
ABUW_RS17335	ABUW_3562	NZ_CP008706.1	3618004	3620193	-	WP_000925020.1		FUSC family protein	755.4744807	1.943274528	0.2237243	8.699706241	3.33E-18	1.55E-17	8.1096683
ABUW_RS07255	ABUW_1488	NZ_CP008706.1	1474973	1475521	-	WP_000577009.1	csuA	Cou fibrinolyticogenesis protein CsuA	288.6416321	1.942144961	1.276656817	1.521274109	0.028191065	0.150446189	0.82281781
ABUW_RS16740	ABUW_3242	NZ_CP008706.1	3270425	3272089	+	WP_003118848.1		outer membrane protein transport protein	1058.666229	1.940359434	0.17104697	16.48497884	4.70E-61	2.87E-59	58.542198
ABUW_RS0320	ABUW_0665	NZ_CP008706.1	70383	71438	-	WP_000353193.1	hgpD	4-hydroxyphenylpyruvate decarboxinase	9134.533215	1.940350539	0.325057428	5.961002345	2.15E-09	1.04E-09	6.219630051
ABUW_RS04920	ABUW_0057	NZ_CP008706.1	6500884	6601754	+	WP_000222616.1		hspC/ScpB family protein	12411765712	1.940190906	0.94969096	9.96519446	2.17E-33	1.44E-32	21.91423751
ABUW_RS18995	ABUW_3474	NZ_CP008706.1	3521872	3522567	-	WP_000001416.1		YnfF family transhydroxylase	481491475	1.938897921	0.18519729	9.030913746	2.89E-23	1.89E-22	21.72594215
ABUW_RS02830	ABUW_0576	NZ_CP008706.1	572527	573526	-	WP_000571491.1		phage holin family protein	12.89085996	1.938623137	0.548606997	3.524600532	0.000424114	0.000448977	3.187770694
ABUW_RS1415	ABUW_3782	NZ_CP008706.1	3842938	3843828	-	WP_001017291.1	mmB	3-hydroxyisobutyrate dehydrogenase	414.5369476	1.933397701	0.471488633	4.100624204	4.12E-05	6.91E-05	10.40083539
ABUW_RS07140	ABUW_1465	NZ_CP008706.1	1454899	1462396	+	WP_001010195.1		amino acid permease	1151931751	1.932472666	0.28919556	7.194494531	7.00E-13	2.27E-12	11.64391741
ABUW_RS10850	ABUW_1666	NZ_CP008706.1	1667276	1668199	-	WP_000860138.1		LysR family transcriptional regulator ArgP	1021053241	1.928625173	0.228950151	8.423710057	3.65E-17	1.61E-16	13.5170412
ABUW_RS1605	ABUW_2385	NZ_CP008706.1	2373057	2374448	-	WP_001988580.1		LLM class flavin-dependent oxidoreductase	109.691487	1.92807268	0.19940199	9.066453238	4.19E-22	2.15E-21	20.00326029
ABUW_RS05235	ABUW_0666	NZ_CP008706.1	1076659	1077399	-	WP_001186266.1		outer membrane protein transport protein	389.380916	1.92621994	0.309105346	6.21853994	4.62E-10	9.89E-09	8.92454039
ABUW_RS1840	ABUW_2454	NZ_CP008706.1	2441852	2442655	+	WP_001017291.1		enoyl-CoA hydratase/isomerase family protein	1274.636723	1.924714539	0.324629716	5.588935646	3.05E-09	7.29E-09	8.12772472
ABUW_RS04720	ABUW_0662	NZ_CP008706.1	673225	673725	+	WP_000457363.1		GNA1 family N-acetyltransferase	24.46197772	1.922630941	0.406955121	4.7244498	2.31E-06	4.32E-06	5.54519253
rsNA7.4	no	no	no	no	no	no	no	no	67.06410898	1.920281703	0.316404483	6.088314543	1.14E-09	2.84E-09	8.54668166
ABUW_RS17915	ABUW_3679	NZ_CP008706.1	3737151	3737834	+	WP_0010131947.1		ATP-binding protein	110.6546619	1.917263056	0.279345369	6.863642803	6.71E-12	1.99E-11	10.7104692
ABUW_RS1920	ABUW_2322	NZ_CP008706.1	2306186	2307420	-	WP_000108033.1		integrase family protein	464.4314373	1.913308963	0.2693287	6.740075499	12.1E-12	3.84E-12	14.1566678
ABUW_RS17910	ABUW_3678	NZ_CP008706.1	3736316	3737026	-	WP_000736404.1		heterotrimeric transposase/endonuclease subunit TnsA	623.4275564	1.910067121	0.214416098	7.813193854	4.81E-15	1.83E-14	8.17374991
ABUW_RS1910	ABUW_4029	NZ_CP008707.1	17282	18542	+	WP_0010103370.1		hypothetical protein	285.058449	1.908394566	0.26184488	7.301687074	2.85E-13	9.53E-13	12.0209711
ABUW_RS07145	ABUW_1686	NZ_CP008706.1	1679193	1677337	-	WP_001010560.1		glutamine synthetase	142.2008056	1.907591971	0.186558008	9.704960171	2.87E-22	1.75E-21	20.7669196
ABUW_RS03310	ABUW_0673	NZ_CP008706.1	617616	6176357	+	WP_000929502.1		YnfJ family protein	186.384408	1.907186641	0.299472565	6.389751846	1.66E-10	4.40E-10	9.356547324
ABUW_RS1025	ABUW_0230	NZ_CP008706.1	2149413	2149955	-	WP_000604276.1		GNA1 family N-acetyltransferase	215.1843526	1.905338222	0.226343306	8.471910832	3.83E-17	1.69E-16	15.172103
ABUW_RS02425	ABUW_1888	NZ_CP008706.1	1889880	1890446	-	WP_001024903.1		acetoacetate decarboxylase family protein	25.36452373	1.905314046	0.401340603	4.732006347	2.32E-06	4.35E-06	5.51910743
ABUW_RS1550	ABUW_2374	NZ_CP008706.1	2360880	2361666	-	WP_001043288.1		hydrolase	277.700869	1.9019332	0.167777071	11.33262013	9.05E-30	8.48E-29	28.07160415
ABUW_RS20165	no	NZ_CP008706.1	171821	1731637	+	WP_002010156.1		hypothetical protein	612105089	1.898954703	0.370954445	5.180099335	3.07E-07	6.28E-07	0.02040356
ABUW_RS15900	ABUW_1392	NZ_CP008706.1	3222203	3222487	-	WP_000605927.1		hypothetical protein	120.119904	1.898796193	0.370538174	5.64427836	2.98E-07	6.1E-07	6.21995979
ABUW_RS07785	ABUW_1694	NZ_CP008706.1	1591355	1591789	+	WP_000925881.1		hypothetical protein	387.5819161	1.895901929	0.248788803	7.62058883	2.53E-14	9.16E-14	13.03819453
ABUW_RS17310	ABUW_1499	NZ_CP008706.1	1485710	1486600	+	WP_000340891.1		DMT family transporter	397.8976008	1.892973182	0.224532418	6.03734535	3.44E-17	1.52E-16	8.5191641
ABUW_RS18870	ABUW_3875	NZ_CP008706.1	3942934	3943154	-	WP_000733016.1		hypothetical protein	2956.89131	1.892602086	0.346348553	5.464733313	4.64E-08	10E-07	6.995671626
ABUW_RS03650	ABUW_0742	NZ_CP008706.1	743342	744103	-	WP_000731940.1		hypothetical protein	8124372504	1.890983465	0.322238411	5.867454625	4.43E-09	1.04E-08	7.88296661
ABUW_RS04300	ABUW_0985	NZ_CP008706.1	997995	1000436	+	WP_000807799.1		CSLREA domain-containing protein	1770.14582	1.890223699	0.207597748	9.9961209	5.80E-19	8.29E-19	10.2942392
ABUW_RS03880	ABUW_0791	NZ_CP008706.1	771497	772144	+	WP_000094258.1		hypothetical protein	17.64543608	1.890010156	0.40190712	4.706318903	2.52E-06	4.70E-06	5.327902142
ABUW_RS0260	ABUW_0053	NZ_CP008706.1	56624	56782	-	WP_000490267.1		DUF1228 domain-containing protein	5808.425003	1.888970061	0.354816795	5.323804888	1.02E-07	2.16E-07	6.665540129
ABUW_RS11635	ABUW_3622	NZ_CP008706.1	3608364	3608945	-	WP_000998201.1		TetR/RacR family transcriptional regulator	713.42519151	1.888526007	0.31028238	6.068471715	1.65E-09	2.88E-09	5.660507542
ABUW_RS10330	ABUW_2536	NZ_CP008706.1	2526527	2528629	+	WP_000892952.1		phenylacetic acid degradation bifunctional protein PaaZ	4627.007006	1.887167276	0.40184721	4.696610568	2.65E-06	4.92E-06	5.308034877
ABUW_RS09060	ABUW_0611	NZ_CP008706.1	657196	658473	+	WP_001084464.1		aromatic ring-hydroxylating dehydrogenase subunit alpha	1047.429429	1.886638222	0.439632269	4.29490069	1.78E-05	3.06E-05	0.000415974
ABUW_RS05625	ABUW_0338	NZ_CP008706.1	135166	152397	+	WP_002018708.1	adeL	multidrug efflux transcriptional repressor AdeL	678.8224756	1.884942485	0.92039344	9.816387717	9.67E-23	6.12E-22	21.0244885
ABUW_RS18210	ABUW_2429	NZ_CP008706.1	2418383	2418838	-	WP_000737621.1		LysR/KacC family transcriptional regulator	148.5105337	1.882452032	0.244314652	7.704190957	1.32E-14	4.88E-14	8.1168019
ABUW_RS1700	ABUW_2519	NZ_CP008706.1	2524478	2524744	+	WP_000730423.1		hypothetical protein	28.5727978	1.87711651	0.418894779	4.50261921	6.71E-06	12.1E-05	4.9172163
ABUW_RS1320	ABUW_2834	NZ_CP008706.1	2820050	2825230	+	WP_000318648.1	paalB	12-phenylacetyl-CoA epoxidease subunit B	2333.557698	1.87706546	0.602039456	3.11974473	0.000217788	0.00244086	2.57724423
ABUW_RS1365	ABUW_2193	NZ_CP008706.1	219327	2150466	-	WP_000307591.1		transcriptional regulator	716.4408741	1.878722437	0.223701791	8.389300875	4.89E-17	2.12E-16	15.6736144
ABUW_RS1050	ABUW_2089	NZ_CP008706.1	2078239	2078463	+	WP_000310300.1		hypothetical protein	226.7599471	1.875301087	0.42679125	4.405433526	1.06E-05	1.86E-05	4.704817056
ABUW_RS1570	ABUW_2587	NZ_CP008706.1	2580696	2581900	-	WP_001198705.1		hypothetical protein	23.4161906	1.875193281	0.375358827	4.99561218	5.86E-07	1.95E-06	5.935542011
ABUW_RS18995	ABUW_3880	NZ_CP008706.1	3948556	3949473	+	WP_000714235.1		matrix family metalloprotease	5.144406483	1.874949106	0.368063288	5.09409433	3.50E-07	7.1E-07	8.1610399
ABUW_RS1820	ABUW_2112	NZ_CP008706.1	2												

ABLUW_RS0405	ABLUW_0082	NZ_CP008706.1	89373	9199	+	WP_000797607.1		DUF885 domain-containing protein	346.606194	1.803860086	0.249181301	7.23947079	4.525e-13	1.496e-12	11.82681073
ABLUW_RS10410	ABLUW_2762	NZ_CP008706.1	2752956	2733915	+	WP_000626189.1		metal-dependent hydrolase	85.38504811	1.803453368	0.227949069	7.91850521	2.546e-15	9.846e-15	6.4007049
ABLUW_RS0305	ABLUW_4057	NZ_CP008707.1	34574	35365	-	WP_001261740.1		ANT(27) is family aminoglycoside nucleotidyltransferase AAdA	653.4054952	1.802341798	0.4223493	4.267419882	1.985e-05	3.406e-05	4.46682183
ABLUW_RS12220	ABLUW_2734	NZ_CP008706.1	2715557	2710061	+	WP_001037898.1			7937.004811	1.799603549	0.384836323	4.676282966	2.926e-06	5.416e-06	5.26800735
ABLUW_RS07605	ABLUW_956	NZ_CP008706.1	958246	928580	+	WP_000812727.1		hydrophobic protein	106.775428	1.79737688	0.243508053	7.38180447	1.575e-13	5.355e-13	9.27184622
ABLUW_RS04040	ABLUW_967	NZ_CP008706.1	920960	921650	+	WP_001891084.1		nicotinate-nicotinamide nucleotide adenylyltransferase	3815.919797	1.79693463	0.90532109	11.93550818	6.336e-33	7.586e-32	31.0330379
ABLUW_RS1950	ABLUW_4025	NZ_CP008707.1	16320	9549	+	WP_001024502.1		hydrophobic protein	648.6433325	1.796781213	0.221972903	8.094583798	5.755e-16	2.335e-16	4.63264408
ABLUW_RS0605	ABLUW_2801	NZ_CP008706.1	2799502	2799924	+	WP_000368712.1		LiprA/C family transcriptional regulator	211.8438137	1.796488198	0.33658576	5.338451805	9.375e-08	2.005e-07	6.896970004
ABLUW_RS0560	ABLUW_2585	NZ_CP008706.1	2578123	2579145	-	WP_00059142.1		ABC transporter substrate-binding protein	51042171362	1.795846271	0.297525064	6.035929376	1.585e-09	3.895e-09	8.410050399
ABLUW_RS07970	ABLUW_933	NZ_CP008706.1	928979	932338	+	WP_000873962.1		fibrinol biosynthesis outer membrane usher protein	2018.72232	1.794714276	0.35166219	5.103519998	3.335e-07	6.785e-07	6.168770306
ABLUW_RS07605	ABLUW_956	NZ_CP008706.1	958246	928580	+	WP_000812727.1	pgdB	poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgdB	133.0239142	1.793157564	0.242545185	7.393161558	14.35e-13	4.905e-13	12.30803032
ABLUW_RS4250	ABLUW_2935	NZ_CP008706.1	2948484	2950634	+	WP_001285133.1		helicium-helic transcriptional regulator	653.5758009	1.790938849	0.167671504	1.15868719	6.725e-30	6.355e-29	28.1722627
ABLUW_RS1240	ABLUW_2494	NZ_CP008706.1	2490120	2491526	-	WP_000081863.1		cytosine permease	63.84070017	1.790328414	0.254865988	7.024591347	2.155e-12	6.645e-12	11.17783192
ABLUW_RS07155	ABLUW_1468	NZ_CP008706.1	1457399	1458733	+	WP_000536984.1		PGD-1 family deacetylase	1665.513356	1.788328338	0.444379007	4.02431282	5.718e-05	9.455e-05	4.02456819
ABLUW_RS07645	ABLUW_965	NZ_CP008706.1	953062	953964	+	WP_000089880.1		LyxR family transcriptional regulator	318.4143163	1.786644955	0.21867133	8.442812006	3.105e-17	1.375e-16	5.86327943
ABLUW_RS0580	ABLUW_3411	NZ_CP008706.1	3458639	3458857	+	WP_000908011.1		Sec-independent protein translocase subunit TatA	35.10996885	1.785599612	0.375835837	4.751009443	2.025e-06	3.825e-06	5.47936637
ABLUW_RS1550	ABLUW_3204	NZ_CP008706.1	3232147	3233514	-	WP_001033441.1		amidohydrolase	486.4821068	1.785248258	0.208280447	8.57136752	1.025e-17	4.635e-17	16.3341901
ABLUW_RS1955	ABLUW_2093	NZ_CP008706.1	2074919	2076730	-	WP_000263726.1		GmpP family permease	768.2064039	1.779374963	0.266717435	6.671386002	2.535e-11	7.225e-11	10.1416428
ABLUW_RS1845	ABLUW_2501	NZ_CP008706.1	971486	971745	+	WP_000089496.1		hydrophobic protein	23.23437616	1.777339973	0.388894428	4.57119252	4.855e-05	5.05453154	5.9258466
ABLUW_RS1665	ABLUW_0339	NZ_CP008706.1	355699	361719	-	WP_001051826.1	ycgS	TCR90/656 family membrane protein	740.35361	1.77635948	0.91918195	9.285231637	1.615e-20	8.795e-20	10.0560112
ABLUW_RS16300	ABLUW_3161	NZ_CP008706.1	3173743	3178006	+	WP_000044599.1		TerR/AcrR family transcriptional regulator	795.0830323	1.775943304	0.295239804	6.015257027	1.805e-09	4.405e-09	8.396547134
ABLUW_RS16300	ABLUW_3161	NZ_CP008706.1	3173743	3178006	+	WP_001056663.1		hydrophobic protein	72.32947648	1.770519501	0.240442732	7.363545314	1.795e-13	6.075e-13	12.216811
ABLUW_RS0690	ABLUW_183	NZ_CP008706.1	190332	190895	+	WP_001033225.1		TerR/AcrR family transcriptional regulator	26.71217692	1.770252984	0.387138637	4.565617353	4.985e-06	9.035e-06	5.0443125
ABLUW_RS0570	ABLUW_1920	NZ_CP008706.1	970193	971033	+	WP_000872857.1		SDR family NAD(P)-dependent oxidoreductase	5.7559531	1.769995869	0.472926244	3.742646747	0.000280902	0.000280902	5.94225816
ABLUW_RS08705	ABLUW_1780	NZ_CP008706.1	1781706	1784032	+	WP_000955082.1		hydrophobic protein	1895.663958	1.767645396	0.878889976	9.407814915	5.065e-21	2.885e-20	9.54361397
ABLUW_RS07605	ABLUW_956	NZ_CP008706.1	958246	928580	+	WP_000812727.1		penicillin acylase family protein	170.6877036	1.766789572	0.25216105	7.006405005	2.445e-12	7.10237216	9.1282762
ABLUW_RS0525	ABLUW_900	NZ_CP008706.1	900527	901756	+	WP_000078402.1		NADH-flavin oxidoreductase/NADH oxidase family protein	2314219551	1.766435262	0.19714136	8.947898496	3.625e-19	1.275e-18	17.74958
ABLUW_RS1025	ABLUW_2085	NZ_CP008706.1	2065159	2067106	-	WP_000844321.1		transporter	47.6862662	1.764751405	0.30791833	5.73142103	9.975e-09	2.886e-08	7.640164518
ABLUW_RS02390	ABLUW_0487	NZ_CP008706.1	499163	500330	+	WP_000673015.1		acyl-CoA dehydrogenase family protein	363.2200255	1.764522691	0.287186249	6.34971683	8.055e-10	2.035e-09	8.692503962
ABLUW_RS2035	no	NZ_CP008706.1	281029	281348	-			hydrophobic protein	324.7326784	1.762637502	0.360558633	4.888629304	1.025e-06	1.975e-06	5.07553774
ABLUW_RS0260	ABLUW_0582	NZ_CP008706.1	574447	577274	-	WP_000748563.1		GPD family capsid scaffolding protein	57.38702469	1.76181793	0.344537055	5.19019694	3.225e-07	6.575e-07	6.1624345
ABLUW_RS0400	ABLUW_2551	NZ_CP008706.1	2543067	2544002	+	WP_000058199.1		dihydrodipicolinate synthase family protein	572.7056997	1.76013935	0.174203486	10.16403887	5.255e-24	3.645e-23	22.4889862
ABLUW_RS105	ABLUW_2711	NZ_CP008706.1	2694385	2694885	+	WP_000167002.1	benB	benzoate 1,2-dioxygenase small subunit	65.80197187	1.759908853	0.262178281	6.698844263	2.155e-11	6.005e-11	10.22184875
ABLUW_RS0165	no	NZ_CP008706.1	982167	983471	+		abaQ	multidrug efflux MFS transporter ABAQ	30.58900082	1.75796154	0.352941978	4.98089587	6.335e-07	1.255e-06	5.90389987
ABLUW_RS07340	ABLUW_905	NZ_CP008706.1	919088	919176	+	WP_001033800.1		heme-binding protein	31.1802242	1.75710741	0.319592235	5.499727296	3.805e-08	6.325e-08	7.07987461
ABLUW_RS1960	ABLUW_2092	NZ_CP008706.1	2074150	2074885	+	WP_000163854.1		3-hydroxyisovalerate dehydrogenase	900.3414066	1.756730157	0.288719059	6.083051081	1.98e-09	2.935e-09	8.53310238
ABLUW_RS06190	ABLUW_0285	NZ_CP008706.1	1208295	1208525	+	WP_000160425.1		hydrophobic protein	32.0322643	1.753863267	0.36471156	4.808910394	1.525e-06	2.905e-06	5.53760202
ABLUW_RS0260	ABLUW_2543	NZ_CP008706.1	253154	253443	+	WP_000214021.1	abaF	fosfomycin efflux MFS transporter ABAF	153.0008989	1.749810067	0.230342692	7.59655125	3.045e-14	1.085e-13	12.962875
ABLUW_RS0330	ABLUW_3157	NZ_CP008706.1	318336	3195072	+	WP_001001666.1		mechanosensitive ion channel	414.229178	1.7487172075	0.30172855	5.795841617	6.805e-09	1.680e-08	7.80104291
ABLUW_RS0970	ABLUW_963	NZ_CP008706.1	958580	959717	+	WP_000816905.1		SDR family oxidoreductase	595.5863172	1.748239863	0.42882627	4.079243858	4.525e-05	7.565e-05	4.121478204
ABLUW_RS0430	ABLUW_0205	NZ_CP008706.1	1019736	1020053	+	WP_000918029.1		NF1	843.1842883	1.746069516	0.163660593	10.66884512	1.425e-26	1.155e-25	24.9303216
ABLUW_RS140	ABLUW_2290	NZ_CP008706.1	2278041	2278271	+	WP_000116739.1		hydrophobic protein	696.4527119	1.745654809	0.420328576	7.001386825	2.535e-12	7.795e-12	11.9084524
ABLUW_RS0400	ABLUW_3707	NZ_CP008706.1	3765487	3766053	+	WP_000859337.1		flavodoxin family protein	60.27448759	1.745336984	0.383760282	4.547897549	5.425e-06	9.815e-06	5.008330993
ABLUW_RS0360	ABLUW_0889	NZ_CP008706.1	881766	886995	+	WP_001986539.1		MCM7 family protein	172.5077969	1.744753833	0.254172448	6.849663668	7.415e-12	2.185e-11	10.6595589
ABLUW_RS1970	ABLUW_3104	NZ_CP008706.1	3141782	3149975	+	WP_001992311.1		MFS transporter	835.9180038	1.742554354	0.283651572	6.143291973	8.085e-10	2.045e-09	8.89036833
ABLUW_RS0230	ABLUW_0433	NZ_CP008706.1	441990	447390	+	WP_000415133.1		NAD(P)FAD-dependent oxidoreductase	15015.78082	1.741890974	0.17998677	9.677883404	3.745e-22	2.265e-21	20.64589156
ABLUW_RS0180	ABLUW_0237	NZ_CP008706.1	255242	255931	+	WP_001045986.1	agp2	aquaporin 2	107.1219277	1.73969513	0.287826266	6.044254249	1.505e-09	3.175e-09	4.83062099
ABLUW_RS01760	ABLUW_0767	NZ_CP008706.1	756626	756901	+	WP_001003942.1		DUF968 domain-containing protein	23.53521829	1.739653245	0.37047092	4.663301965	3.115e-05	5.240332105	
ABLUW_RS12715	ABLUW_2619	NZ_CP008706.1	2618733	2619780	+	WP_000217666.1		serine hydrolase	411.0488039	1.738602876	0.310058131	11.35919169	6.685e-30	6.345e-29	28.9791074
ABLUW_RS09800	ABLUW_2018	NZ_CP008706.1	2009188	2009392	-	WP_000367699.1		hydrophobic protein	10.1837693	1.737456402	0.23238617	1.274606923	7.635e-14	2.575e-13	9.7518621
ABLUW_RS0270	ABLUW_0753	NZ_CP008706.1	3805053	3809030	+	WP_001049720.1		PaeR1 family transcriptional regulator	476.984268	1.7330574242	0.205949708	8.147463936	3.855e-17	1.695e-16	6.172103
ABLUW_RS08530	ABLUW_1751	NZ_CP008706.1	1748425	1748784	+	WP_000798370.1		hydrophobic protein	139.7445939	1.732996383	0.370392106	4.677735469	2.905e-06	5.385e-06	5.269271724
ABLUW_RS08540	ABLUW_1753	NZ_CP008706.1	1749233	1749526	+	WP_000898660.1		hydrophobic protein	493.54717	1.731855043	0.319439032	5.524400881	3.305e-08	7.265e-08	7.193063378
ABLUW_RS08600	ABLUW_921	NZ_CP008706.1	917635	917635	+	WP_000266302.1		SGN1/GDSL hydrolase family protein	295.188001	1.730887182	0.162203054	10.671104	1.395e-26	1.125e-25	24.9083999
ABLUW_RS0920	ABLUW_1420	NZ_CP008706.1	141999	142742	+	WP_001029311.1		head-tail connector protein	11.8291448	1.730363553	0.31056407	5.53434768	3.55e-08	6.885e-08	7.9241262
ABLUW_RS1915	ABLUW_3702	NZ_CP008706.1	3756885	3760195	-	WP_001029128.1		DUF1726 domain-containing protein	455.4398762	1.727698198	0.21943769	6.702801974	6.685e-16	2.795e-16	4.86862404
ABLUW_RS0925	ABLUW_934	NZ_CP008706.1	923926	931181	+	WP_000809893.1		3-carboxy-cis,cis-muconate cyclomerase	167.403773	1.727186401	0.260519702	6.627380949	3.425e-11	9.625e-11	10.1618493
ABLUW_RS1905	ABLUW_2447	NZ_CP008706.1	2432924	2434162	+	WP_000781162.1		SGN1/GDSL							

ABUW_RS0870	ABUW_E77	NZ_CP008706.1	167032	W74891	+	WP_000588779.1		serine hydrolase	857.35759 9	1660368289	0.166 9382 9	9.995702 177	1.595-23	1.07E-22	2.1970E 622
ABUW_RS07295	ABUW_E46	NZ_CP008706.1	141282	W43799	-	WP_001020052.1	proP	glycine betaine:-,proline transporter ProP	678.2205604	1657106 11	0.19922487	8.38009591	8.94E-17	3.82E-16	6.4793664
ABUW_RS07900	ABUW_E9	NZ_CP008706.1	61954	151339	-	WP_000102142.1		ethanone/ammonia-lyase subunit EutB	5148723832	16567515 13	0.322590 84	5.15377841	2.81E-07	5.77E-07	6.238824 987
ABUW_RS02625	ABUW_E03	NZ_CP008706.1	903508	W03093	-	WP_000706933.1		hyothetical protein	18.6996649	1656096899	0.476262 97	3.479003696	0.00053282	0.00077786	3.14759811
ABUW_RS04275	ABUW_E032	NZ_CP008706.1	939255	143523	-	WP_001971462.1		non-ribosomal peptide synthetase	296.056442	165482965	0.98956489	8.3754551	8.98E-17	3.83E-16	6.1608213
ABUW_RS0575	ABUW_E78	NZ_CP008706.1	973639	W12107	-	WP_000323307.1		TetR family transcriptional regulator	909.4294833	165028679	0.23014243	7.17783646	7.08E-13	2.30E-12	11.63821726
ABUW_RS03490	ABUW_0709	NZ_CP008706.1	716374	716441	+	WP_000789875.1		DUF1176 domain-containing protein	538.05647102	1651461 234	0.174332695	9.472816475	2.72E-21	1.55E-20	9.8068754
ABUW_RS09995	ABUW_2058	NZ_CP008706.1	2038281	2040162	-	WP_000632243.1		hyothetical protein	2580.471881	1651070286	0.289974401	5.694882998	1.23E-08	2.81E-08	7.55102368
ABUW_RS1635	ABUW_2453	NZ_CP008706.1	2440241	2441842	+	WP_001072777.1		methylcrotonyl-CoA carboxylase	2910.262352	1651317399	0.338604393	4.876833943	1.08E-06	2.08E-06	5.68193565
ABUW_RS00050	ABUW_0010	NZ_CP008706.1	15476	15480	-	WP_001021535.1		hyothetical protein	17.4015563	165101064	0.235977906	6.996470258	2.62E-12	8.05E-12	11.094204 12
ABUW_RS0810	ABUW_E62	NZ_CP008706.1	165544	1655641	+	WP_000774578.1		hyothetical protein	12.02631639	1650562732	0.531897911	3.103157015	0.0019468	0.002776907	2.556438665
ABUW_RS09850	ABUW_2029	NZ_CP008706.1	2016665	2015859	-	WP_000367699.1		hyothetical protein	110.514011	164915323	0.221472391	7.446315123	9.60E-14	3.34E-13	12.47620333
ABUW_RS1925	ABUW_4109	NZ_CP008707.1	68467	69510	+	WP_000710320.1		TraI family protein	186.1718664	1647640164	0.173038883	9.518765968	1.73E-21	1.02E-20	99.99193983
ABUW_RS04935	ABUW_E06	NZ_CP008706.1	1020050	1020850	-	WP_000175548.1		enoyl-CoA hydratase/isomerase family protein	714.2874083	1645567373	0.227709003	7.226881193	4.94E-13	1.63E-12	11.8787014
ABUW_RS09475	ABUW_E48	NZ_CP008706.1	1947325	1948785	+	WP_000003670.1	iaaH	indoleacetamide hydrolase	87.1563057	1641828954	0.267041852	6.184206088	7.84E-10	1.98E-09	8.73033481
ABUW_RS03005	ABUW_E69	NZ_CP008706.1	111192	112593	-	WP_001028352.1		DUF4055 domain-containing protein	61.8254398	1641678513	0.246225716	6.666641245	2.62E-11	7.44E-11	10.12847208
ABUW_RS02765	ABUW_Q39	NZ_CP008706.1	1971084	1971998	-	WP_024436202.1		alpha/beta fold hydrolase	26.55957756	1641552023	0.425029915	3.862203497	0.00012369	0.00018049	3.74243819
ABUW_RS04475	ABUW_0910	NZ_CP008706.1	1970791	1980608	+	WP_000868053.1	glyD	glycyl-S- phosphate dehydrogenase	5006.051678	164102022	0.208748547	7.861023404	3.80E-15	1.46E-14	13.53564714
ABUW_RS05910	ABUW_E87	NZ_CP008706.1	1893336	1895274	+	WP_000862283.1		NADH:flavin oxidoreductase/NADH:oxidase family protein	188.036116	1619392879	0.273057462	6.003165974	1.94E-09	4.72E-09	8.326059001
rsNAG3	no	no	no	no	no	no	no	no	84.75569652	1637421775	0.31979174	5.494211859	2.81E-07	5.37E-07	6.270025774
ABUW_RS06440	ABUW_E20	NZ_CP008706.1	1335301	1333899	+	WP_000277446.1		hyothetical protein	45.1310301	1634372109	0.327688676	4.987423594	6.12E-07	1.21E-06	5.91721463
ABUW_RS02665	ABUW_E286	NZ_CP008706.1	257942	2580953	-	WP_000918646.1	atpF	aliphosphate hydrolase	63.45488333	1634170085	0.235988319	6.924702255	4.37E-12	1.31E-11	10.8627287
ABUW_RS01105	ABUW_0226	NZ_CP008706.1	247164	247372	-	WP_001021535.1		hyothetical protein	294.4005845	1632469819	0.288679308	5.694098898	1.59E-08	3.52E-08	7.453457337
ABUW_RS07870	ABUW_2014	NZ_CP008706.1	2005890	2007104	-	WP_000600368.1		hyothetical protein	484.2183719	1632184492	0.173201217	9.42363138	4.36E-21	2.48E-20	9.65054832
ABUW_RS1910	ABUW_2326	NZ_CP008706.1	2309736	2310281	-	WP_000710973.1		1-acyl-sn-glycerol-3-phosphate acyltransferase	352.2496348	1631801702	0.308264246	5.293519594	1.20E-07	2.53E-07	6.598879479
ABUW_RS12765	no	NZ_CP008706.1	2028331	2028679	-			EAL domain-containing protein	68.195964	16310205	0.250030097	6.152404058	6.84E-11	1.88E-10	9.72084251
ABUW_RS07620	ABUW_E61	NZ_CP008706.1	1549854	1550417	-	WP_000201771.1		hyothetical protein	311.4948929	162914908	0.249178833	7.5781071	3.50E-14	1.25E-13	10.92039662
ABUW_RS09955	ABUW_2030	NZ_CP008706.1	2028819	2029013	-	WP_000301761.1		hyothetical protein	1090.801872	1627668611	0.249951013	6.518426311	7.42E-11	2.03E-10	6.65050399
ABUW_RS01000	ABUW_2677	NZ_CP008706.1	2668857	2669210	-	WP_001106451.1		hyothetical protein	311.4473985	1626027672	0.248316543	6.54823185	5.82E-11	1.61E-10	9.793147104
ABUW_RS19600	ABUW_2408	NZ_CP008706.1	2445037	2445037	+	WP_001017562.1		indolopyruvate leu:indole oxidoreductase family protein	10779.54597	1624556459	0.302854666	5.364189304	8.51E-08	1.74E-07	6.749045252
ABUW_RS01405	ABUW_3191	NZ_CP008706.1	3221607	3222191	-	WP_000639507.1		hyothetical protein	281.0565794	1622123406	0.311025659	5.754005593	1.83E-07	3.81E-07	6.419071024
ABUW_RS09015	ABUW_4105	NZ_CP008707.1	64179	66995	+	WP_000147416.1	traC	type IV secretion system protein TraC	812.6100325	1620863987	0.1614919	11.96558013	5.32E-33	6.36E-32	3.119654289
ABUW_RS08055	ABUW_E52	NZ_CP008706.1	1944451	1946732	+	WP_000605375.1		hyothetical protein	148.5893081	1619991928	0.360487823	4.493880778	6.99E-06	1.26E-05	4.899629455
ABUW_RS19390	ABUW_4078	NZ_CP008707.1	41962	50288	-	WP_001132522.1		hyothetical protein	230.9157814	1618876386	0.989508481	8.140087339	3.95E-16	1.63E-15	14.7878104
ABUW_RS02160	ABUW_0440	NZ_CP008706.1	432140	434335	-	WP_001154905.1		TRAP transporter large permease subunit	1082.852946	1612219966	0.21955052	7.344749378	2.06E-09	1.02E-08	12.6739676
ABUW_RS07005	ABUW_E320	NZ_CP008706.1	913356	914792	-	WP_001075439.1	eat	ethanolamine permease	85.25975536	1611480288	0.358189773	4.489318852	7.15E-05	1.28E-05	4.88270033
ABUW_RS02025	ABUW_0449	NZ_CP008706.1	461097	463320	-	WP_000471938.1		hyothetical protein	13463.97897	1611029191	0.267088551	6.032710332	1.61E-09	3.97E-09	8.44020493
ABUW_RS09905	ABUW_2640	NZ_CP008706.1	2022324	2022518	-	WP_000304176.1		hyothetical protein	1385.166488	1610572943	0.249571893	6.453342649	1.09E-10	2.94E-10	9.51362787
ABUW_RS14220	ABUW_2929	NZ_CP008706.1	2943470	2944771	+	WP_000381885.1	MFS transporter	63.13644023	1606844803	0.28619316	6.725041608	1.85E-08	4.15E-08	7.136581903	
ABUW_RS08165	ABUW_E51	NZ_CP008706.1	1291897	1291912	-	WP_001291999.1		hyothetical protein	100.6671710	1606350746	0.233054727	6.892397182	5.49E-12	1.63E-11	10.7878104
ABUW_RS04845	ABUW_E50	NZ_CP008706.1	1055520	10552100	+	WP_001032988.1		ChA2 family efflux MFS transporter permease subunit	22.35890705	1606231161	0.439504616	3.654640685	0.000257542	0.000410252	3.38665279
ABUW_RS19150	ABUW_2497	NZ_CP008706.1	2493312	2494349	-	WP_001021565.1		LLM class flavin-dependent oxidoreductase	82.0183624	1605996871	0.246424787	6.51718884	7.16E-11	1.96E-10	9.707713029
ABUW_RS09605	ABUW_E42	NZ_CP008706.1	1837997	1838916	-	WP_001142561.1		carbohydrate pin	249.4563322	1604826901	0.18891216	6.850505696	1.98E-17	8.81E-17	10.45024961
ABUW_RS13915	ABUW_3776	NZ_CP008706.1	3836184	3836670	+	WP_000381873.1	abai	acyl-homoserine-lactone synthase Abai	45.91964997	1603282334	0.349670478	4.585123525	4.54E-06	8.28E-06	5.98106663
ABUW_RS05990	ABUW_3798	NZ_CP008706.1	2795179	2795641	-	WP_000410289.1		amino acid permease	986.0586309	1600103437	0.358233003	4.466710089	7.94E-06	1.42E-05	8.447711856
ABUW_RS12250	ABUW_2730	NZ_CP008706.1	2718760	2718175	-	WP_000261486.1		OmpA family protein	759.248195	15986047035	0.20503046	7.794193306	6.48E-16	2.44E-14	1.510261017
ABUW_RS19390	ABUW_3777	NZ_CP008706.1	3836763	3838116	-	WP_001193286.1		Mds family MFS transporter	209.0296393	1597904349	0.272909886	8.850081474	4.77E-09	1.02E-08	7.95047891
ABUW_RS13915	ABUW_2550	NZ_CP008706.1	2542102	2543010	+	WP_000106675.1		EamA family MFS transporter	85.86495227	1594804961	0.228946726	6.965834324	3.20E-12	9.90E-12	11.04203481
ABUW_RS07275	ABUW_E92	NZ_CP008706.1	1479364	1480383	+	WP_0002017500.1	cusE	Cus ferrihalophilus adhesin CusE	294.4310251	1594634853	0.110028686	1.436317935	NA	NA	!VALUE!
ABUW_RS14245	ABUW_2765	NZ_CP008706.1	2766470	2767345	+	WP_000586808.1		hyothetical protein	18.9525938	159389188	0.438856102	3.61922038	0.000281918	0.000437102	3.350497271
ABUW_RS19110	ABUW_4018	NZ_CP008707.1	8888	95775	-	WP_000389996.1		class I/AM- dependent methyltransferase	66.9843844	1590844671	0.24383157	6.524358901	6.83E-11	1.88E-10	9.72084251
ABUW_RS04995	ABUW_0636	NZ_CP008706.1	1415094	1415366	-	WP_000320571.1		DUF2786 domain-containing protein	61.5278281	1590863325	0.246677694	6.484427913	1.15E-10	3.04E-10	9.51702416
ABUW_RS03235	ABUW_E97	NZ_CP008706.1	1314084	1314885	+	WP_001130861.1		hyothetical protein	38.06633297	1589896413	0.452444591	5.310415826	0.00044193	0.00067464	3.17092338
ABUW_RS03235	ABUW_E97	NZ_CP008706.1	1314084	1314885	+	WP_001130861.1		hyothetical protein	5.954870032	1589178063	0.684332442	2.32312008	0.020193192	0.026187917	1.585230466
ABUW_RS01710	ABUW_E60	NZ_CP008706.1	1410439	1450023	-			RNA- Leu	793.7242603	1589017613	0.417456819	3.806409524	0.00040999	0.000224895	3.6440202
ABUW_RS03835	ABUW_1827	NZ_CP008706.1	1925935	1926867	-	WP_000366426.1		LyxJ family transcriptional regulator	98.41122967	1587687781	0.28888856	7.650809196	2.83E-14	1.02E-13	12.91919383
ABUW_RS19250	ABUW_4108	NZ_CP008707.1	67832	68470	+	WP_000672680.1	traW	type-F conjugative transfer system protein TraW	73.26654751	158817541	0.241587034	6.573026194	4.90E-11	1.36E-10	9.866461092
ABUW_RS12845	ABUW_2603	NZ_CP008706.1	2595821	2597539	-	WP_001019100.1		ATP- group domain-containing protein	2210.223486	158595988	0.316218621	5.030015625	4.90E-07	9.83E-07	6.007446842
ABUW_RS04730	ABUW_2003	NZ_CP008706.1	199944												

ABUW_RS4525	ABUW_2591	NZ_CP008706.1	301953	301609	+	WP_000464231.1	OpD family outer membrane porin	58.04278998	1522761943	0.308273191	4.9396509	7.835e-17	1.635e-06	5.81630869
ABUW_RS1905	ABUW_2700	NZ_CP008706.1	2684897	2685121	-	WP_000828869.1	hypothetical protein	704.876478	1520088799	0.223258925	6.80808745	9.855e-12	2.885e-11	10.54060751
ABUW_RS1740	ABUW_3535	NZ_CP008706.1	3634022	3634669	-	WP_002018000.1	serine hydrolase family protein	563.3272485	1518820378	0.405595299	4.73715093	0.000178866	0.000282055	3.54666907
ABUW_RS0479	ABUW_0983	NZ_CP008706.1	1006094	1006921	-	WP_000543905.1	hypothetical protein	32.81956342	1519555082	0.32456929	4.727074303	2.218e-06	4.272e-06	3.56957125
ABUW_RS1700	ABUW_2507	NZ_CP008706.1	2002712	2002906	-	WP_000367899.1	hypothetical protein	109.6806405	151912171	0.24713772	6.25890189	3.885e-10	9.995e-10	9.05043192
ABUW_RS0850	ABUW_819	NZ_CP008706.1	918373	918397	+	WP_000061168.1	NAD(P)-dependent 2,4-dienol-CoA reductase	731.8025046	151853151	0.318237876	4.77186924	1.835e-06	3.476e-06	5.450667525
ABUW_RS1905	ABUW_2550	NZ_CP008706.1	2871932	2871949	-	WP_000650363.1	hypothetical protein	74.33741955	151700851	0.337777912	4.058560835	4.945e-05	8.235e-05	4.488460185
ABUW_RS1840	ABUW_2433	NZ_CP008706.1	2420869	2422164	-	WP_000524222.1	stress-induced protein	101047.252	1519953839	0.527843286	2.871877119	0.004079125	0.005750453	2.240297942
ABUW_RS0520	ABUW_2784	NZ_CP008706.1	2779143	2779352	+	WP_000372418.1	phosphatidylthioesterase	33.8192834	1518410005	0.570223144	2.657577161	0.007870457	0.010702019	1.970534445
ABUW_RS0555	ABUW_2172	NZ_CP008706.1	215310	2164678	-	WP_001023024.1	histidine-type phosphatase	165.0082565	1518469996	0.267500361	5.662971785	1.495e-08	3.375e-08	7.472370099
ABUW_RS0735	ABUW_2624	NZ_CP008706.1	2620818	2621511	+	WP_000185559.1	DUF B26 domain-containing protein	121.2319113	1519372754	0.240161268	6.30148553	2.955e-10	7.685e-10	9.14638878
ABUW_RS0680	ABUW_1369	NZ_CP008706.1	1364959	1369159	-	WP_000920236.1	MBL fold metallo-hydrolase	409.3807034	1511947948	0.10015849	10.06725811	7.71e-24	5.295e-23	22.27654433
ABUW_RS11725	ABUW_2410	NZ_CP008706.1	2396784	2397410	+	WP_001058576.1	glutathione transferase	705.3962451	1509832235	0.258449977	5.84187410	5.165e-09	1.21e-08	7.9172463
ABUW_RS07190	ABUW_1574	NZ_CP008706.1	1564241	1564064	+	WP_000853306.1	AMP-binding protein	1264.602328	1509043116	0.282304843	5.345438284	9.025e-08	1.935e-07	6.714442691
ABUW_RS0525	ABUW_1958	NZ_CP008706.1	1959771	1962767	+	WP_000192636.1	DEAD/DEAH box helicase family protein	1472.244893	1508852245	0.162802272	7.825904883	5.048e-15	1.925e-14	13.76398877
ABUW_RS0445	ABUW_1317	NZ_CP008706.1	131205	131896	+	WP_000142495.1	hypothetical protein	3185.732323	1507418298	0.276810094	5.445617654	5.16e-08	1.12e-07	6.95077817
ABUW_RS02042	no	NZ_CP008706.1	951089	2503305	+	WP_000543392.1	hypothetical protein	198.0471592	1504264007	0.463226903	3.247384509	0.001847191	0.001720287	2.764399993
ABUW_RS07195	ABUW_1618	NZ_CP008706.1	161128	161843	-	WP_000774022.1	eutC	125.951749	1503353574	0.269737311	5.574069176	2.495e-08	5.51e-08	7.25884401
ABUW_RS1740	ABUW_2410	NZ_CP008706.1	2396838	2400105	+	WP_001027342.1	SCR family oxidoreductase	68.87187484	1500919585	0.289737535	5.17756699	2.235e-07	4.655e-07	6.338254747
ABUW_RS07195	ABUW_8336	NZ_CP008706.1	834259	835030	+	WP_000154428.1	SCR family NAD(P)-dependent oxidoreductase	290.9334479	1497582055	0.318374665	4.733571055	2.21e-06	4.41e-06	5.32999959
ABUW_RS0440	ABUW_0916	NZ_CP008706.1	91193	912551	+	WP_000524131.1	metallophosphatase	684.584949	1495671079	0.18163301	8.243306758	1.65e-16	6.895e-16	16.187087
ABUW_RS0430	ABUW_0903	NZ_CP008706.1	899636	899921	-	WP_000524131.1	SRNA-Leu	26.65423437	1495810256	0.522682554	2.862203658	0.004207065	0.005912195	2.22825105
ABUW_RS07840	ABUW_1605	NZ_CP008706.1	159962	1600536	-	WP_000097958.1	pseudouridine synthase	250.59588707	1492885133	0.21091466	7.074817769	1.445e-12	4.605e-12	11.33724217
ABUW_RS03810	ABUW_8773	NZ_CP008706.1	763388	764494	+	WP_000149698.1	minor capsid protein	97.918123	1492013230	0.176256626	8.404999994	2.565e-17	1.141e-16	19.3430915
ABUW_RS08935	ABUW_8336	NZ_CP008706.1	832006	833351	-	WP_000101823.1	MFS transporter	10159398	149189426	0.318285352	4.73125184	2.235e-06	4.185e-06	5.377785977
ABUW_RS0595	ABUW_3210	NZ_CP008706.1	321478	3215404	-	WP_0001058249.1	MFS transporter	8168467794	1491220371	0.304010859	4.908154957	9.345e-07	5.78232126	1.96
ABUW_RS03430	ABUW_0697	NZ_CP008706.1	69903	700088	-	WP_001181817.1	YnfC family protein	415.0640924	1491084863	0.29192418	5.1234321	3.005e-07	6.41e-07	6.21831829
ABUW_RS1420	ABUW_2557	NZ_CP008706.1	2546184	2547473	+	WP_000107559.1	epoxyurease/nitrate reductase QueH	2542.090483	1490639902	0.319356735	4.66763258	3.055e-06	5.635e-06	5.24949105
ABUW_RS0695	ABUW_3414	NZ_CP008706.1	3460247	3462447	+	WP_000205448.1	DUF338 domain-containing protein	270.5251623	1489941256	0.1626829	9.16794425	5.305e-20	2.755e-19	15.9509092
ABUW_RS07625	ABUW_1652	NZ_CP008706.1	1650565	1651629	-	WP_0001925789.1	LLM class flavin-dependent oxidoreductase	337.4961003	1489219528	0.247133687	6.022951854	1.685e-09	4.915e-09	8.384004948
ABUW_RS01950	ABUW_2090	NZ_CP008706.1	207377	2077270	+	WP_000484256.1	MFS transporter	76.28271015	1488633777	0.272434842	5.46493426	4.635e-08	1.01e-07	6.99567626
ABUW_RS12445	ABUW_2934	NZ_CP008706.1	2948519	2949739	-	WP_000102444.1	MFS transporter	390.6085919	148827457	0.31818636	8.173194601	4.395e-16	1.805e-16	14.74472749
ABUW_RS08316	ABUW_1708	NZ_CP008706.1	1707738	1710011	+	WP_000968542.1	myoglobin-dependent oxidoreductase	442.918185	1485751869	0.199910532	7.431972301	1.075e-13	3.716e-13	12.43062609
ABUW_RS01880	ABUW_1781	NZ_CP008706.1	1758355	1758993	-	WP_000332547.1	SCR response-associated peptidase family protein	561.7340635	1485245729	0.316316667	4.09019464	4.31e-05	7.225e-05	4.14162802
ABUW_RS1030	ABUW_2888	NZ_CP008706.1	2884635	2886239	-	WP_000214787.1	isocitrate lyase	10548.13305	1483294138	0.255544334	5.800927437	6.595e-10	1.845e-10	7.914797929
ABUW_RS12516	ABUW_2575	NZ_CP008706.1	2580876	2586074	-	WP_001180395.1	tsaG	369.6562697	1481822513	0.26218493	5.651821766	1.595e-08	3.575e-08	7.447731784
ABUW_RS11600	ABUW_2314	NZ_CP008706.1	2371396	2372862	-	WP_0001071065.1	MFS transporter	48.41210282	1478510062	0.288449235	5.125730574	2.965e-07	6.07e-07	6.21811009
ABUW_RS0116	ABUW_0228	NZ_CP008706.1	247853	248410	-	WP_000733355.1	NAD(P)H-dependent oxidoreductase	94.73352486	1478277277	0.19207959	7.695449372	1.41e-14	5.225e-14	1.82823295
ABUW_RS1345	ABUW_2128	NZ_CP008706.1	212686	212854	-	WP_0001925789.1	2-oxo-acid dehydrogenase subunit E2	734.8421235	1477100685	0.428036285	3.450877262	0.000558768	0.000484958	3.070563363
ABUW_RS20485	ABUW_4210	NZ_CP008707.1	6270	6410	+	WP_000691626.1		69.58426426	1475336308	0.4295107	3.434920336	0.000592728	0.000900151	3.045684632
ABUW_RS08275	ABUW_4699	NZ_CP008706.1	4695882	4697310	-	WP_0001055201.1	Y-family DNA polymerase	210.3581649	1472473076	0.204821897	7.189041284	6.525e-13	2.125e-12	11.67366144
ABUW_RS0545	ABUW_1663	NZ_CP008706.1	1655820	1655993	+	WP_001189332.1	hypothetical protein	37.25054944	1472014786	0.454699064	3.235417334	0.00124851	0.00178868	7.247487349
ABUW_RS19245	ABUW_4626	NZ_CP008707.1	15564	15797	+	WP_000241707.1	hypothetical protein	123.898658	146994051	0.31640178	4.67181330	2.995e-06	5.525e-06	1.000506022
ABUW_RS04840	ABUW_1328	NZ_CP008706.1	1340370	1340558	+	WP_001187568.1	hypothetical protein	138.7459871	1469146808	0.289901826	5.076332181	4.135e-07	8.145e-07	6.08937594
ABUW_RS06330	ABUW_0302	NZ_CP008706.1	118777	119245	+	WP_000534212.1	hypothetical protein	21.55605797	1469056765	0.405179705	3.62438109	0.000239978	0.000449406	3.34711594
ABUW_RS05160	ABUW_1551	NZ_CP008706.1	1560355	1561689	+	WP_001183836.1	hypothetical protein	369.3034937	1463415074	0.205182493	7.11910333	9.905e-13	3.176e-13	11.88914074
ABUW_RS04330	ABUW_1715	NZ_CP008706.1	1714895	1716298	-	WP_001076966.1	PLP-dependent aminotransferase family protein	878.5500148	146310221	0.18719136	12.31676933	7.455e-35	9.785e-34	33.0096616
ABUW_RS17370	ABUW_0969	NZ_CP008706.1	962366	9627236	-	WP_000929593.1	peptidoglycan hydrolase	126.972999	1460897055	0.245131701	5.959641484	2.5375e-09	6.095e-09	8.25382707
ABUW_RS0685	ABUW_1802	NZ_CP008706.1	188482	188510	-	WP_000168431.1	hypothetical protein	418.5955034	1460506859	0.230066064	3.648206399	2.185e-10	6.735e-10	9.241845378
ABUW_RS0590	ABUW_1501	NZ_CP008706.1	151	951	+	WP_001050343.1	repM	2709.803281	1460106299	0.23189343	3.615438562	2.695e-10	7.040e-10	9.542427341
ABUW_RS09135	ABUW_9317	NZ_CP008706.1	9317397	9318368	-	WP_001181838.1	SCR family oxidoreductase	180.077509	1459434774	0.382776873	3.827755832	0.000129317	0.000206753	3.6841584
ABUW_RS0660	ABUW_2163	NZ_CP008706.1	2179563	2179846	-	WP_001318961.1	acyl-CoA dehydrogenase family protein	300.2371846	1458920697	0.186750584	7.812135447	6.525e-15	2.181e-14	9.18716204
ABUW_RS1525	ABUW_2578	NZ_CP008706.1	2571422	2571825	-	WP_000653195.1	type VI secretion system tail subunit Hop	7035.970453	1455476987	0.243487756	5.977817796	2.265e-09	5.505e-09	8.25953731
ABUW_RS03895	ABUW_1738	NZ_CP008706.1	177380	1774208	+	WP_0002749311.1	helicase-helic domain-containing protein	2209.486695	1454880022	0.205968527	7.020626173	1.635e-12	5.11e-12	10.21915791
ABUW_RS01960	ABUW_2403	NZ_CP008706.1	2390433	2391820	-	WP_000941172.1	MFS transporter	122.9665987	1453438062	0.284443389	5.192283368	3.235e-07	6.605e-07	6.19054064
ABUW_RS0600	ABUW_2583	NZ_CP008706.1	2587021	2587761	-	WP_001090546.1	DUF B89 domain-containing protein	18.7058388	1453187683	0.38950917	7.323716816	0.000193386	0.000297597	3.523731551
ABUW_RS1414	ABUW_2142	NZ_CP008706.1	2189962	2192987	-	WP_000543590.1	YnfJ domain-containing protein	2458.612818	145295641	0.12018414	8.10947405	1.095e-33	1.345e-32	31.1872953
ABUW_RS0540	ABUW_3202	NZ_CP008706.1	3229841	3230866	-	WP_000592063.1	fatty acid desaturase	88.29481038	1452954782	0.227137804	6.391733329	1.645e-10	4.355e-10	9.36195743
ABUW_RS0335	ABUW_1921	NZ_CP008706.1	1918920	1920250	-	WP_0001785781.1	MFS transporter	234.8587641	145271704	0.21816909	6.68110594	6.51e-12	1.935e-11	10.71444269
ABUW_RS02870	ABUW_05													

ABUW_RS08690	ABUW_1784	NZ_CP008706.1	1781988	1782362	-	WP_012300584.1			DUF2750 domain-containing protein	602.0149776	1398202437	0.238174922	5.870485554	4.356e-09	1.036e-08	7.981782775
ABUW_RS08235	ABUW_691	NZ_CP008706.1	6187602	688839	-	WP_000754611			PeP5Y domain-containing protein	232.0987085	1397829686	0.88928405	7.398726956	1.376e-13	4.74e-13	0.32697909
ABUW_RS0990	ABUW_2675	NZ_CP008706.1	2667822	2668109	-	WP_001934729.1			hypothetical protein	3881.7100127	1396477079	0.248424707	5.632192987	1.886e-08	4.236e-08	7.73560363
ABUW_RS0950	ABUW_2591	NZ_CP008706.1	2582744	2586349	-	WP_000475282.1	ucb		uracil carboxylase	921.9258411	1396237268	0.210344876	6.606440197	3.946e-11	1.00e-10	9.958607319
ABUW_RS0910	ABUW_085	NZ_CP008706.1	98650	987016	-	WP_01022505.1			hypothetical protein	917.7267189	1396060424	0.206389447	6.764204475	1.346e-11	3.876e-11	0.41229093
ABUW_RS02840	ABUW_0578	NZ_CP008706.1	573882	574091	-	WP_000698474.1			tail protein X	37.2381185	1395400839	0.302437487	4.913848804	3.956e-06	7.246e-06	5.160261304
ABUW_RS09795	ABUW_2017	NZ_CP008706.1	2008958	2009176	-	WP_01093187.1			phage coat protein	810584746	1392994234	0.268688964	5.84029921	2.175e-07	4.466e-07	6.34773569
ABUW_RS02015	ABUW_1657	NZ_CP008706.1	1657107	1651608	+	WP_000161254.1			hypothetical protein	513.5381563	1390961125	0.610918167	2.2768371	0.022795955	0.023997177	153.855964
ABUW_RS03875	ABUW_0790	NZ_CP008706.1	770304	771401	+	WP_001028499.1			hypothetical protein	102.378447	1388895153	0.89523189	6.961622069	3.376e-12	1.026e-11	0.59159583
ABUW_RS02050	no	NZ_CP008706.1	2671685	2671830	+				hypothetical protein	169.4731092	1388870495	0.81109494	7.668678577	1.746e-14	6.386e-14	0.1937933
ABUW_RS18480	ABUW_3058	NZ_CP008706.1	3084083	3084958	-	WP_000992293.1			metal-dependent hydrolase	506.2555932	1387347604	0.260441553	5.326905739	9.996e-08	2.126e-07	6.673664139
ABUW_RS14335	ABUW_2993	NZ_CP008706.1	3101642	3101259	+	WP_000624780.1			hypothetical protein	95.37077849	1387219477	0.283162346	4.899194715	9.626e-07	1.876e-06	5.72818393
ABUW_RS0590	ABUW_3410	NZ_CP008706.1	3459303	3460073	+	WP_001072727.1	latC		trwA-arginine translocase subunit TrwA	45.2050497	1386938021	0.31886893	4.418409356	9.946e-06	1.766e-05	4.754818332
ABUW_RS08030	ABUW_1645	NZ_CP008706.1	1640257	1640811	+	WP_001103116.1			TetR-like family transcriptional regulator	10.2419457	1384542827	0.99216657	1.395473632	0.916270061	0.98851552	0.724657497
irRNA65	no	no	no	no	no	no	no	no	no	93.6197108	1383734367	0.345423523	0.4005906596	6.186e-05	0.000119104	3.992235158
ABUW_RS03845	ABUW_0785	NZ_CP008706.1	767868	768236	+	WP_000524234.1			hypothetical protein	18.80421461	1379867746	0.367815921	3.751506883	0.000157575	0.000277398	3.556896674
ABUW_RS1530	ABUW_2912	NZ_CP008706.1	2921493	2922116	+	WP_002019760.1			anylesterase	30.14891092	137676268	0.1952905	9.867140041	5.786e-23	3.712e-22	214.3062609
ABUW_RS160	ABUW_2401	NZ_CP008706.1	2387465	2388349	-	WP_000698343			lipocholesterol dehydrogenase	92.0770966	137673335	0.376148236	3.657423379	0.000254763	0.00039723	3.40095796
ABUW_RS0570	ABUW_1118	NZ_CP008706.1	79719	81011	+	WP_000662932.1			Y-family DNA polymerase	355.4777699	137500527	0.23594838	5.88637119	9.375e-09	9.375e-09	8.026360409
ABUW_RS0565	ABUW_2607	NZ_CP008706.1	2600772	2602025	-	WP_001897220.1			divalent metal cation transporter	3.64102445	137391951	0.402502303	3.419430187	0.000641606	0.000970587	3.01297197
ABUW_RS0730	ABUW_2623	NZ_CP008706.1	2619612	2620562	-	WP_000396495.1			3-hydroxyacyl-CoA dehydrogenase	448.3124468	1373708926	0.195980286	6.866571472	6.588e-12	1.956e-11	0.70996539
ABUW_RS14745	ABUW_2988	NZ_CP008706.1	3216372	3218296	+	WP_000470123.1			hypothetical protein	571.6702606	1373065252	0.242847238	5.654026869	1.576e-08	3.536e-08	7.428225295
ABUW_RS1080	ABUW_2482	NZ_CP008706.1	247847	2478001	+	WP_001057853.1			TGIR3364 family FAD-dependent oxidoreductase	24.71401846	1371074457	0.330095642	4.081470525	4.448e-05	7.496e-05	4.10551862
ABUW_RS14510	ABUW_2988	NZ_CP008706.1	3006055	3007395	-	WP_000491023.1			LyfR family transcriptional regulator	276.9057725	1371027004	0.22961297	5.972202656	2.340e-09	5.666e-09	8.247813669
ABUW_RS1050	ABUW_2810	NZ_CP008706.1	2809373	2810269	-	WP_000368993.1			ATP-binding protein	4.91430525	1371200531	0.814196652	8.154910686	6.556e-17	2.826e-15	0.15497088
ABUW_RS1085	ABUW_2612	NZ_CP008706.1	2604930	2605448	-	WP_000459778.1			hypothetical protein	234.8337672	1370583341	0.30389381	4.508655319	6.626e-06	1.976e-05	4.93181438
ABUW_RS0405	ABUW_013	NZ_CP008706.1	1025273	1025509	+	WP_000404324.1			hypothetical protein	548.9474671	1368977902	0.29551055	6.328175702	2.526e-10	6.596e-10	9.1114858
ABUW_RS1090	ABUW_2078	NZ_CP008706.1	2009405	2006097	-	WP_000971581.1	modB		molybdate ABC transporter permease subunit	68.9416177	1369330292	0.259371437	5.279418238	1.306e-07	2.736e-07	6.56837353
irRNA95	no	no	no	no	no	no	no	no	no	203.3597738	1369070824	0.262337901	5.218073504	1.806e-07	3.76e-07	6.425968732
ABUW_RS05650	ABUW_1684	NZ_CP008706.1	1695059	1695844	-	WP_000027937.1			helicase-helicase transcriptional regulator	1238.794836	1368666402	0.250434041	4.547899644	4.826e-08	1.046e-07	6.262966661
ABUW_RS1520	ABUW_3165	NZ_CP008706.1	3191885	3193064	+	WP_000707149.1			NAD(P)+FAD-dependent oxidoreductase	697.7179244	1366251262	0.21643443	4.81642665	2.275e-10	5.966e-10	9.2247334
ABUW_RS02020	no	NZ_CP008706.1	2606643	2606996	-				hypothetical protein	32.85499857	136621019	0.46792210	2.91972056	0.003603445	0.00466454	2.30377727
ABUW_RS04895	ABUW_0957	NZ_CP008706.1	1650534	1650921	+	WP_000206278.1			tyrosine recombinase	605.180034	1364600867	0.81058822	7.524364077	5.305e-14	1.886e-13	0.72584215
ABUW_RS10465	ABUW_2773	NZ_CP008706.1	2766768	2767844	+	WP_000470073.1			aromatic ring-hydroxylating dioxygenase subunit alpha	66.8419261	1363840406	0.26571048	5.1276626	2.866e-07	5.866e-07	6.23162284
ABUW_RS05465	ABUW_1983	NZ_CP008706.1	1989175	1989432	-	WP_001840585.1			hypothetical protein	1469.0841	136218232	0.25378413	5.763617389	8.56e-08	1.756e-07	6.56387353
ABUW_RS1075	ABUW_2339	NZ_CP008706.1	2330262	2332895	+	WP_001007363.1			MeG-NpA family ABC transporter substrate-binding protein	109.184285	1360865505	0.90929509	8.008408625	1.186e-15	4.606e-15	11.37214217
ABUW_RS0380	ABUW_0308	NZ_CP008706.1	1310064	1310161	+	WP_001288008.1			hypothetical protein	103.6764899	1359779303	0.203258838	6.689988923	2.236e-11	6.376e-11	0.16880507
ABUW_RS06310	ABUW_0294	NZ_CP008706.1	1315595	1316988	+	WP_000197963.1			minor capsid protein	99.0421659	1359773718	0.223921949	6.072473556	1.285e-09	3.18e-09	8.504455662
ABUW_RS0930	ABUW_2684	NZ_CP008706.1	2686881	2686980	-	WP_000651921			DUF2210 domain-containing protein	93.97368416	1359459809	0.272294512	5.926081893	5.966e-07	1.36e-06	5.943095149
ABUW_RS17325	ABUW_3660	NZ_CP008706.1	3617664	3619765	+	WP_001072475.1			H ₂ O ₂ family secretion protein	768.5044841	1359154716	0.81777035	8.954943165	3.404e-10	1.686e-10	1.77465027
ABUW_RS10585	ABUW_3667	NZ_CP008706.1	3725597	3726031	+	WP_001275666.1	ansC		aminate reductase (glutaredoxin)	442.2054857	1358446978	0.1983628	9.798638552	1.146e-22	7.186e-22	21.43871556
ABUW_RS03795	ABUW_0774	NZ_CP008706.1	760231	760746	+	WP_000729387.1			DUF2280 domain-containing protein	7.84483286	1357487738	0.535819348	2.530520447	0.010292315	0.01500045	182.108882
ABUW_RS1685	ABUW_0197	NZ_CP008706.1	1032732	1032659	-	WP_001084983.1			hypothetical protein	15.34859244	1355078862	0.471622389	2.93174297	0.004552046	0.00368103	2.965867671
ABUW_RS10910	ABUW_4033	NZ_CP008706.1	40653	20382	+	WP_000701903.1			hypothetical protein	162.863631	1353073412	0.269932994	5.02639685	5.376e-07	1.076e-06	5.970619223
ABUW_RS11235	ABUW_2308	NZ_CP008706.1	2293182	2293394	-	WP_000303093.1			hypothetical protein	0.16103497	1350418197	0.2558639197	6.58676464	2.036e-07	4.206e-07	6.718676071
ABUW_RS1185	ABUW_2097	NZ_CP008706.1	2079357	2079998	+	WP_000310583.1			CoA transferase subunit B	6393.216324	1348883999	0.340423457	3.962370901	7.426e-05	0.000107338	3.91647837
ABUW_RS0010	ABUW_1869	NZ_CP008706.1	1866737	1868224	+	WP_000005610.1			NAD-dependent phenylacetaldehyde dehydrogenase	93.6095839	1347053062	0.21222109	3.648958614	2.176e-10	5.716e-10	9.243363692
ABUW_RS1870	ABUW_3173	NZ_CP008706.1	3173335	3173326	-	WP_000273948.1			fatty acyl-AMP ligase	82.37734642	134704481	0.269393675	5.00023373	5.726e-07	1.146e-06	5.943095149
ABUW_RS02140	ABUW_0077	NZ_CP008706.1	1000570	1000695	-	WP_000854366.1			hypothetical protein	18.38830157	1346392094	0.434357445	3.099732968	0.00169592	0.00208197	2.551072429
ABUW_RS00115	ABUW_0223	NZ_CP008706.1	27176	27319	+	WP_000161030.1			methionine/importin import family NIS transporter small subunit	778.9216626	1344708107	0.19850858	6.774284735	1.256e-11	3.636e-11	0.440073637
ABUW_RS07085	ABUW_1454	NZ_CP008706.1	1445258	1446631	+	WP_000744443.1			hypothetical protein	427.0224091	1344680094	0.50658051	7.066537804	1.176e-12	5.316e-12	112.7490456
ABUW_RS18355	no	NZ_CP008706.1	39232	39516	+				hypothetical protein	21.4126008	1342912223	0.260036539	5.9783527	7.06e-11	1.966e-10	9.707743929
ABUW_RS19510	ABUW_3216	NZ_CP008706.1	3247773	3248948	-	WP_000843791.1			zinc-binding dehydrogenase	97.2610178	133818137	0.299408077	4.469210559	7.856e-06	1.406e-05	4.88371964
ABUW_RS1080	ABUW_2096	NZ_CP008706.1	2078651	2079355	+	WP_000194056.1			CoA transferase subunit A	2383.518861	1336827581	0.32778047	4.028347553	4.536e-05	7.586e-05	4.07302794
ABUW_RS02155	no	NZ_CP008706.1	1409716	141003	+				sulfite exporter TsaD/TsaE family protein	35.62498375	1336826041	0.385038415	4.37192006	0.000517433	0.000788008	3.43067313
ABUW_RS08940	ABUW_1837	NZ_CP008706.1	1833377	1833790	+	WP_000997505.1	ptaC		4-carboxymuconolactone decarboxylase	56.0196382	133513402	0.316666196	4.22975401	2.346e-05	3.996e-05	6.40027164
ABUW_RS08850	no	NZ_CP008706.1	1405709	1406449	+				hypothetical protein	59.72351029	1333434462	0.278625932	4.785751671	1.705e-06	3.246e-06	5.4894499
ABUW_RS0360	ABUW_0741															

ABLU_RS00050	ABLU_928	NZ_CP008706.1	0260744	128 568	+	WP_000545000.1		Aac family transcriptional regulator	287.9515966	1281618463	0.181631986	7.060037892	16065-12	5.96E-12	1128483264
ABLU_RS00845	ABLU_938	NZ_CP008706.1	019677	161237	-	WP_000505571.1		PaeR family transcriptional regulator	489.7101363	1281400648	0.20576103	6.227645509	47336-10	1.2E-09	819712463
ABLU_RS01045	ABLU_0254	NZ_CP008706.1	269194	267345	-	WP_000469967.1		GNA1 family acetyltransferase	123.5618885	1280998974	0.269245337	4.757737786	19665-06	3.700E-06	5.431798276
ABLU_RS01320	ABLU_0256	NZ_CP008706.1	0136234	119476	+	WP_000004363.1		hypothetical protein	65.4252818	1280330206	0.272538416	4.697697471	2.635E-06	4.900E-06	5.30980392
ABLU_RS01730	ABLU_0607	NZ_CP008706.1	1623439	1693752	+	WP_001905649.1		heavy metal sensor histidine kinase	164.9329031	1280100708	0.141924209	0.190004897	1.886E-19	9.455E-19	8.02456519
ABLU_RS01960	ABLU_0841	NZ_CP008706.1	1836086	1937351	-	WP_001639470.1		right-handed parallel beta-helix repeat-containing protein	95.7402116	1277168894	0.270279255	4.725154627	2.305E-06	4.33E-06	5.36552273
ABLU_RS01930	ABLU_3759	NZ_CP008706.1	1814620	1819210	-	WP_000717463.1		LysE family transporter	220.462723	1277074656	0.290274701	5.10269176	3.355E-07	6.81E-07	6.18658388
ABLU_RS01940	ABLU_1425	NZ_CP008706.1	145063	141623	+	WP_0002039465.1		hypothetical protein	14.2654385	1275449035	0.540657702	2.359008519	0.018320873	0.023888264	1.621815048
ABLU_RS03890	ABLU_0793	NZ_CP008706.1	773502	773861	+	WP_000335868.1		DUF4258 domain-containing protein	2287.031594	1274647257	0.187888909	6.784047355	1.17E-11	3.40E-11	0.14665108
ABLU_RS0820	ABLU_3459	NZ_CP008706.1	3505261	3505668	+	WP_002018070.1		hypothetical protein	289.656229	127427773	0.194085599	5.65551144	5.95E-11	1.44E-10	9.84375508
ABLU_RS08455	ABLU_1233	NZ_CP008706.1	134757	133820	+	WP_000598523.1		hypothetical protein	97.7897789	1272671964	0.267029408	4.760036717	1.885E-06	3.56E-06	5.448550002
ABLU_RS01950	ABLU_2710	NZ_CP008706.1	2693006	2693488	+	WP_010137401.1	benA	benzoate 1,2-dioxygenase large subunit	97.45225423	1272501646	0.29748297	4.277561741	1.895E-05	3.25E-05	4.48819639
ABLU_RS08150	ABLU_1755	NZ_CP008706.1	1750160	1750609	-	WP_001046785.1		LipA/C family transcriptional regulator	10.2310464	1270962967	0.291882305	4.357533688	1.325E-05	2.30E-05	4.638272164
ABLU_RS01930	ABLU_3767	NZ_CP008706.1	1818736	1820601	-	WP_000247733.1		alpha/beta fold hydrolase	419.4746414	1268720613	0.23145642	5.481473097	4.225E-08	9.21E-08	7.03754037
ABLU_RS01575	ABLU_1179	NZ_CP008706.1	107379	107321	-	WP_045887597.1	baeD	acinetobacter non-ribosomal peptide synthetase subunit BaeC	538.1236862	1268049791	0.4195569616	3.029483611	0.002449722	0.003519702	2.453864432
ABLU_RS01980	ABLU_0970	NZ_CP008706.1	1072190	1073215	+	WP_001013804.1		Aac family transcriptional regulator	168.5199445	1267463929	0.210956194	6.007929686	1.885E-09	4.59E-09	6.338187314
ABLU_RS01920	ABLU_0602	NZ_CP008706.1	1602188	1603495	-	WP_000849751.1		sorbose dehydrogenase family protein	1369.888758	1266859827	0.26325439	4.812302761	1.495E-06	2.86E-06	5.543633967
ABLU_RS01935	ABLU_1012	NZ_CP008706.1	3037626	3037994	+	WP_001644481.1		hypothetical protein	26.26884775	1266080511	0.30281931	4.181020702	2.90E-05	4.91E-05	4.306919508
ABLU_RS01930	ABLU_1432	NZ_CP008706.1	1412197	1418404	+	WP_000931282.1		hypothetical protein	18.38272332	1265777378	0.478019482	2.647891297	0.000809556	0.01098758	1.95097918
ABLU_RS01790	ABLU_2219	NZ_CP008706.1	2294512	2294930	+	WP_000979740.1		hypothetical protein	67.64746433	1260202064	0.318619881	4.02595855	5.67E-05	9.39E-05	4.027334028
ABLU_RS01440	ABLU_0845	NZ_CP008706.1	825585	825981	-	WP_001986352.1		phosphatase PAPZ family protein	5413.900718	1261457814	0.162204711	7.776949319	7.43E-16	2.17E-16	15.5543598
ABLU_RS01480	ABLU_1210	NZ_CP008706.1	1141671	1143767	+	WP_001966311.1		BapA-profilin-like domain-containing protein	4525.440516	1261075052	0.205128457	6.149160015	7.79E-10	1.97E-09	8.705633774
ABLU_RS01435	ABLU_1111	NZ_CP008706.1	1129545	1100975	-	WP_010183471.1		aldehyde dehydrogenase family protein	429.1319369	1260873532	0.2697162035	4.674554196	2.95E-06	5.46E-06	5.262807357
ABLU_RS01985	ABLU_2845	NZ_CP008706.1	286787	281619	-	WP_000797489.1		DMF family transporter	103.7823783	1260816277	0.187975497	6.700671808	2.00E-11	5.7E-11	9.24339081
ABLU_RS02025	ABLU_2439	NZ_CP008706.1	2493153	2496106	-	WP_000987218.1		alpha/beta hydrolase	70.19077252	1259349115	0.308531296	4.018754859	4.47E-05	7.48E-05	4.10609406
ABLU_RS01965	ABLU_1165	NZ_CP008706.1	1191330	1192016	-	WP_000995337.1		pinin family protein	345.7270503	125369618	0.25357119	4.944486069	7.65E-07	1.00E-06	5.823908741
ABLU_RS01555	ABLU_3205	NZ_CP008706.1	3233548	3234933	-	WP_001010249.1		hypothetical protein	78.33217242	1252225698	0.244592824	5.116633853	3.06E-07	6.26E-07	6.203425667
ABLU_RS01945	ABLU_1652	NZ_CP008706.1	1653073	1654659	+	WP_000841503.1		GHS auto-inducible promoter family protein	86.49374677	1252087015	0.25122258	4.983983194	6.23E-07	1.23E-06	5.910949889
ABLU_RS01555	ABLU_3235	NZ_CP008706.1	2318320	2319555	+	WP_001986597.1		Shb family sulfur activation oxidoreductase	10.3711742	1251886392	0.230942087	4.520780631	5.93E-08	1.28E-07	6.89279003
ABLU_RS01555	ABLU_3235	NZ_CP008706.1	3254195	3254215	-	WP_000312237.1		multidrug efflux SMR transporter	449.864991	1251945671	0.146461976	5.845091822	1.28E-17	5.75E-17	6.24032196
ABLU_RS01270	ABLU_0664	NZ_CP008706.1	670429	671253	-	WP_000734607.1		uniflagellarin family protein	431.9565547	1246717775	0.160883059	7.616496361	8.38E-15	3.15E-14	35.0445566
ABLU_RS01910	ABLU_0311	NZ_CP008706.1	1272825	1274039	-	WP_000916408.1		MFS transporter	815.9594626	1244740055	0.179417616	6.915968016	3.63E-12	1.09E-11	10.56257319
ABLU_RS01985	ABLU_0222	NZ_CP008706.1	244494	245465	+	WP_000792640.1		TerR/Acr family transcriptional regulator	10.81870043	1247107883	0.567063422	2.199238806	0.027800948	0.035621334	1.44828982
ABLU_RS01965	ABLU_2710	NZ_CP008706.1	2695995	2696780	+	WP_000071231.1		1,6-dihydroxyacetone-2,4-dienone-5-carboxylate dehydrogenase	74.49491774	1247105852	0.202088607	6.078501193	6.17E-10	1.73E-09	8.761953987
ABLU_RS01910	ABLU_0616	NZ_CP008706.1	282495	283370	-	WP_001073965.1		uracase-acyl donor family protein UrdE	67.33718625	1245983309	0.279772553	4.435508058	8.45E-06	1.50E-05	5.063908741
ABLU_RS04050	ABLU_0827	NZ_CP008706.1	801489	805158	-	WP_001891057.1		phosphoethanolamine-lyase A transferase	438.1037166	1245515711	0.142143606	6.762388986	19.1E-18	9.04E-18	7.01483197
ABLU_RS01920	ABLU_2507	NZ_CP008706.1	2502388	2503581	-	WP_000500378.1		CoA transferase	414.0866442	1244257582	0.207826611	5.987085957	2.14E-09	5.91E-09	8.284832642
ABLU_RS01935	ABLU_1915	NZ_CP008706.1	1916544	1919333	+	WP_0010257126.1		hypothetical protein	130.8599571	1241903187	0.234570315	5.290538092	1.22E-07	2.87E-07	6.590686877
ABLU_RS01930	ABLU_2104	NZ_CP008706.1	2105015	2121055	+	WP_001021414.1		iron-containing redox enzyme family protein	692.169185	1240196347	0.201605001	6.162447911	7.18E-10	1.62E-09	8.739928612
ABLU_RS01940	ABLU_0203	NZ_CP008707.1	12151	12154	+	WP_000724905.1		PaeK family protein	3454.018065	1240032334	0.199337943	6.220754151	4.95E-10	1.27E-09	8.89619271
ABLU_RS01970	ABLU_0239	NZ_CP008707.1	257178	257178	+	WP_000191634.1		hypothetical protein	37.26748227	1239504956	0.325895657	3.803369197	0.000227494	0.003430503	
ABLU_RS01585	ABLU_3412	NZ_CP008707.1	3458869	3459306	+	WP_000887761.1	taIB	anti-heparinase domain subunit TaIB	104.3906833	1239418197	0.24422436	5.074968745	3.88E-07	7.85E-07	6.105100343
ABLU_RS01735	ABLU_1512	NZ_CP008707.1	1497572	1498771	+	WP_000598017.1		class I SAM-dependent methyltransferase	112.1165013	1239329106	0.312009843	3.858316191	0.00014171	0.00093377	7.73708482
ABLU_RS01990	ABLU_1847	NZ_CP008707.1	1843497	1844363	+	WP_001197028.1		MBL fold metallo-hydrolase	316.535403	1238831596	0.241920562	5.177829959	2.83E-07	6.91E-07	6.21125128
ABLU_RS01990	ABLU_1849	NZ_CP008707.1	1848708	1849307	+	WP_0010581927.1		class I SAM-dependent methyltransferase	1106.371545	1238162278	0.439339381	2.818232978	0.004823878	0.008724422	2.17180387
ABLU_RS02130	ABLU_2533	NZ_CP008707.1	2524232	2524987	-	WP_001018799.1	paeC	phenylacetate-CoA oxygenase subunit PaeC	2868.519042	1236064423	0.581439982	2.158607809	0.033516285	0.042475323	117186331
ABLU_RS02010	ABLU_3241	NZ_CP008707.1	3206904	3217043	-	WP_005262485.1	HE	putative plus assembly protein HE	638.8774502	123599314	0.197294458	9.002496386	2.21E-19	1.10E-18	9.78660731
ABLU_RS01945	ABLU_3796	NZ_CP008707.1	3858304	3859005	-	WP_000424563.1		DUF 001 domain-containing protein	168.690774	1235273128	0.677984409	1.821951791	0.068462301	0.083333719	1.079197236
ABLU_RS01975	ABLU_2610	NZ_CP008707.1	2603566	2603883	-	WP_001038420.1		hypothetical protein	626.6208053	1233542591	0.216040588	5.709774231	1.01E-08	2.59E-08	7.586700216
ABLU_RS02170	ABLU_1461	NZ_CP008707.1	1450089	1450662	+		tRNA-Tip	60.0030261	1231908833	0.366262015	3.363403038	0.00157079	0.000236988		
ABLU_RS01795	ABLU_3574	NZ_CP008707.1	3633292	3633783	-	WP_001010121.1		hypothetical protein	788.0260994	1229989712	0.224531602	5.847081458	4.30E-08	9.38E-08	7.027797162
ABLU_RS01965	ABLU_3752	NZ_CP008707.1	3808158	3808441	-	WP_000805283.1		DUF3861 domain-containing protein	685.8297042	1229501099	0.127116562	7.134793255	9.10E-13	2.92E-12	1.51346715
ABLU_RS01930	ABLU_2121	NZ_CP008707.1	2105154	2105925	-	WP_000925661.1		sulfite exporter Tau/Saf family protein	88.98358887	1226064367	0.310884697	3.94376848	8.02E-05	0.00010263	1.881957414
ABLU_RS04050	ABLU_0921	NZ_CP008707.1	920632	927974	-	WP_001488511.1		glycylglycylphosphatidylphosphatase	312.3609433	122524107	0.15484408	7.931079805	2.17E-15	8.45E-15	4.0734329
ABLU_RS01945	ABLU_2089	NZ_CP008707.1	2069797	2071647	-	WP_000918647.1		denitrification hydrolase family protein	38.94643016	1223260744	0.36876973	3.171039452	0.000909442	0.001308599	2.860091709
ABLU_RS01790	ABLU_1895	NZ_CP008707.1	1891828	1892911	+	WP_000918647.1		iron transporter	986.412662	1223261955	0.338199885	8.851956189	6.60E-19	4.16E-18	9.73181915
ABLU_RS01960	ABLU_2456	NZ_CP008707.1	2444655	2444557	+	WP_001088910.1		hydroxymethylglutaryl-CoA lyase	1030.797706	1221899543	0.28899739	4.23151937	2.32E-05	3.96E-05	4.402300418
ABLU_RS01950	ABLU_1414	NZ_CP008707.1	143493	144920	+	WP_000692620.1		conjugate transfer protein TraH	319.1945206	1220264555	0.209404414	5.820730336	5.88E-09	1.37E-08	

ABUW_RS02420	ABUW_0544	NZ_CP008706.1	549097	549267	-	WP_001016076.1		hyptothetical protein	69.88054721	1.07739348	0.23029552	5.19423168	3.16E-07	6.44E-07	6.19194133
ABUW_RS05916	ABUW_0211	NZ_CP008706.1	925951	925051	-	WP_000082790.1		hyptothetical protein	86.02401453	1.07596247	0.293320338	4.00996364	6.09E-05	0.000100534	3.997687038
ABUW_RS0660	ABUW_2606	NZ_CP008706.1	2599973	2600737	-	WP_000496077.1		LandY/YcfA family protein	9423.9541	1.074938856	0.359893888	3.26386421	0.001099038	0.0062795	2.788358938
ABUW_RS1485	ABUW_4101	NZ_CP008707.1	6181	62497	+	WP_000063840.1		conjugal transfer protein TraH	507.5342784	1.072425726	0.148834609	7.87372987	3.34E-16	1.29E-14	13.88944229
ABUW_RS1490	ABUW_3072	NZ_CP008706.1	3094040	3003056	-	WP_000148428.1		oxido-reductase	290.9107419	1.072365657	0.168461753	6.95293393	3.42E-12	1.03E-11	10.9877827
ABUW_RS1945	ABUW_3891	NZ_CP008706.1	395987	3960153	-	WP_0000447690.1		Tac family protein	276.5896274	1.072231973	0.238468293	4.95672476	8.85E-07	1.72E-06	5.74447553
ABUW_RS1955	ABUW_3596	NZ_CP008706.1	3658566	3659106	-	WP_000653880.1	secE	glycoprotein translocase subunit SecE	8589.430001	1.069678628	0.253452455	4.049853233	3.93E-06	7.2E-06	5.142064735
ABUW_RS03740	ABUW_1076	NZ_CP008706.1	921060	920368	+	WP_001004151.1	bauB	siderophore-binding periplasmic lipoprotein BauB	239.2229561	1.0676555	0.3488806	3.3508129	0.000805747	0.00107722	2.918033022
ABUW_RS04840	ABUW_849	NZ_CP008706.1	949467	950528	+	WP_000370770.1		Hyd family secretion protein	48.72850593	1.07047409	0.238510899	4.89305693	9.93E-07	1.93E-06	5.74442691
ABUW_RS1625	ABUW_2805	NZ_CP008706.1	280338	280425	+	WP_000191916.1		POC sensor domain-containing protein	307.5839368	1.06760002	0.205637548	5.67192386	1.42E-08	3.22E-08	7.492441428
ABUW_RS03710	ABUW_0756	NZ_CP008706.1	752237	752802	+	WP_000080875.1		hyptothetical protein	32.19129161	1.06765018	0.303343105	3.844348165	0.000120874	0.000194025	3.71242308
ABUW_RS09210	ABUW_891	NZ_CP008706.1	892175	892867	+	WP_000044208.1		type 1 glutamine amidotransferase domain-containing protein	17.01050375	1.064960905	0.41071532	2.829270297	0.004665428	0.00651687	2.1859065
ABUW_RS00895	ABUW_961	NZ_CP008706.1	954682	955515	-	WP_001019442.1		universal stress protein	810.688663	1.063210309	0.279472695	4.16210851	3.16E-05	5.33E-05	4.273272791
ABUW_RS06810	ABUW_036	NZ_CP008706.1	1410252	1403272	-	WP_00051677.1		hyptothetical protein	22.40298108	1.063027808	0.385652819	3.019737864	0.002563548	0.003873021	4.743971689
ABUW_RS0190	ABUW_0223	NZ_CP008706.1	245520	245936	-	WP_000455807.1		carboxymuconolactone decarboxylase family protein	74.7639754	1.06221521	0.22992322	0.504824471	4.31E-07	8.68E-07	6.081480275
ABUW_RS0125	ABUW_0310	NZ_CP008706.1	334143	334421	-	WP_000350408.1	tpoZ	DNA-directed RNA polymerase subunit omega	9846155599	1.061819887	0.18448526	5.973796683	2.32E-09	5.62E-09	8.250263684
ABUW_RS02105	ABUW_0434	NZ_CP008706.1	447440	448612	-	WP_001805461		acyl-CoA dehydrogenase family protein	306.5560056	1.059955597	0.225015441	5.163404372	2.56E-07	5.27E-07	6.27189385
ABUW_RS1630	ABUW_2431	NZ_CP008706.1	2416678	2420298	-	WP_001014338.1	umuD	uvrA-lexA-uvrC-uvrD DNA polymerase V autotranspeptidic subunit	3715925264	1.068244042	0.189508103	6.5327363	8.33E-12	2.45E-11	6.01683392
ABUW_RS03535	ABUW_952	NZ_CP008706.1	974882	974918	+	WP_000325043.1		hyptothetical protein	214.249682	1.07423908	0.33202216	3.4859993	0.000498302	0.000714835	3.05450865
ABUW_RS05516	ABUW_1046	NZ_CP008706.1	1070995	1072293	-	WP_000701456.1		aminopeptidase P family protein	572.7794649	1.07336095	0.09384572	8.303619106	1.01E-16	4.23E-16	15.36754271
ABUW_RS02160	ABUW_0438	NZ_CP008706.1	450223	451508	+	WP_000049106.1		hyptothetical protein	2101.025999	1.07109585	0.254242162	4.551939476	5.33E-06	9.65E-06	5.016472687
ABUW_RS1404	ABUW_0242	NZ_CP008707.1	92628	94184	+	WP_000096600.1		ParB/RepB/SpaB family partition protein	41.028770355	1.055281339	0.205799382	5.106828198	4.82E-08	4.4E-08	7.35556111
ABUW_RS10710	ABUW_4009	NZ_CP008707.1	6056	6247	+	WP_000182323.1		hyptothetical protein	240.1185183	1.054310076	0.295271748	3.909324886	9.26E-05	0.000160243	3.823201293
ABUW_RS1005	ABUW_2677	NZ_CP008706.1	268877	2689240	-	WP_001020294.1		glutathione-dependent formaldehyde dehydrogenase	678.61762962	1.05892106	0.463719524	2.484019885	0.010990852	0.012728486	1.434973576
ABUW_RS05200	ABUW_959	NZ_CP008706.1	916477	916918	-	WP_000885360.1		VII family protein	515343877	1.05800305	0.28718764	4.008104445	6.15E-05	0.000100929	3.09988403
ABUW_RS04440	ABUW_938	NZ_CP008706.1	939480	939778	+	WP_000389445.1		MF3 transporter	234.2135197	1.06063923	0.331414207	3.6627194048	0.000245474	0.000318924	3.409733446
ABUW_RS00965	ABUW_1430	NZ_CP008706.1	1420598	1423465	+	WP_000073511.1		lytic transglycosylase domain-containing protein	413.2583791	1.05018348	0.162880541	6.295771952	3.08E-10	7.95E-10	9.009632871
ABUW_RS1305	ABUW_2647	NZ_CP008706.1	2691714	2692937	+	WP_000064049.1		MF3 transporter	107.87189748	1.04635989	0.28438044	4.03707857	5.55E-05	9.2E-05	4.03574037
ABUW_RS07090	ABUW_1455	NZ_CP008706.1	1447635	1447816	+	WP_000190818.1		ATP-binding protein	5316085258	1.046358307	0.20833959	5.500595687	3.78E-08	8.26E-08	7.08130953
ABUW_RS02430	ABUW_0683	NZ_CP008706.1	843547	843753	+	WP_000009358.1		hyptothetical protein	1052.330459	1.04180644	0.21095234	5.145279885	6.21E-08	1.34E-07	6.872592029
ABUW_RS1355	ABUW_2642	NZ_CP008706.1	253445	2534595	+	WP_000932294.1		aldehyde dehydrogenase (NAD(P)+)	85.93096006	1.04063908	0.29051628	3.54240626	8.62E-05	0.00010507	3.852301039
ABUW_RS00990	ABUW_3310	NZ_CP008706.1	3346077	3347131	-	WP_000394405.1		NAD(P)+:transhydrogenase (NifH-specific) subunit beta	857.780479	1.040169022	0.27101462	4.202488245	2.64E-05	4.48E-05	3.20026296
ABUW_RS07190	ABUW_0345	NZ_CP008706.1	388667	387299	+	WP_000339167.1		hyptothetical protein	107.089628	1.040202359	0.259067418	4.401880071	1.08E-05	1.90E-05	4.721046399
ABUW_RS1010	ABUW_2782	NZ_CP008706.1	2772759	2778509	+	WP_000041002.1		Osp family protein	102.4745452	1.03994913	0.34960875	3.26061954	0.001161525	0.001945236	2.783371796
ABUW_RS03660	ABUW_1710	NZ_CP008706.1	1717289	1717600	+	WP_001047539.1		TusD/CdcC/DicC family suA/suB relay protein	265.8802846	1.05256172	0.206307271	5.502747503	3.74E-08	8.19E-08	7.086719698
ABUW_RS00800	ABUW_939	NZ_CP008706.1	936387	936872	+	WP_010189197.1		LysR/AcrC family transcriptional regulator	208.7447355	1.04848861	0.237199053	4.72293944	1.82E-05	3.46E-06	5.460293901
ABUW_RS02510	ABUW_010	NZ_CP008706.1	52342	525315	-	WP_000450896.1		aldehyde dehydrogenase	1899.148846	1.01896305	0.162479803	1.005161025	3.28E-12	9.94E-12	1.060619582
ABUW_RS02455	ABUW_073	NZ_CP008706.1	102485	102658	+	WP_001001967.1		hyptothetical protein	14.1638105	1.01426639	0.527449062	2.145091976	0.031945511	0.04056365	1.931862973
ABUW_RS00925	ABUW_2644	NZ_CP008706.1	2604830	2605193	-	WP_001065929.1		hyptothetical protein	237.4927349	1.01072785	0.246371239	4.590928674	4.4E-06	8.06E-06	3.670636458
ABUW_RS02660	ABUW_0541	NZ_CP008706.1	547699	548436	+	WP_000125747.1		3'-5' exonuclease	323.7310552	1.00961439	0.63666774	6.91068821	4.84E-12	1.45E-11	10.838352
ABUW_RS10015	ABUW_0306	NZ_CP008706.1	330212	330676	+	WP_000187923.1	bfr	bacterioferritin	5792.399281	1.02986691	0.42918962	6.62384865	0.004665304	0.01461942	1.904741194
ABUW_RS06215	ABUW_074	NZ_CP008706.1	101955	101966	+	WP_000891871.1		hyptothetical protein	29.03894474	1.02869045	0.370658472	3.045091722	0.002326094	0.003349475	2.475023259
ABUW_RS16710	ABUW_3328	NZ_CP008706.1	3354319	3355366	+	WP_000190300.1		DUF392 domain-containing protein	90.8518953	1.02566403	0.21173959	5.137683311	1.05E-07	2.33E-07	3.671981105
ABUW_RS1605	ABUW_876	NZ_CP008706.1	869306	870190	+	WP_001097352.1		hyptothetical protein	503.748639	1.02583234	0.16513763	8.07865302	9.29E-02	2.74E-11	10.5673071
ABUW_RS16905	ABUW_3016	NZ_CP008706.1	3248732	3247479	+	WP_001014481.1		LysR family transcriptional regulator	89.2034214	1.02277181	0.327563445	4.728058739	2.29E-06	4.29E-06	3.778504708
ABUW_RS19395	ABUW_3778	NZ_CP008706.1	383835	3839280	+	WP_001010133.1		enoyl-CoA hydratase/isomerase family protein	1199.231808	1.01961045	0.243898067	4.588771275	4.46E-06	8.14E-06	5.089375595
ABUW_RS01995	ABUW_0324	NZ_CP008706.1	346371	347312	+	WP_000691958.1		tiacylglycerol lipase	406.5281956	1.0173226	0.26266661	4.250473699	2.18E-05	3.66E-05	4.436519815
ABUW_RS04390	ABUW_0895	NZ_CP008706.1	892682	893209	+	WP_001022880.1		Ena family transporter	161.910388	1.01765434	0.29160059	3.831510962	0.000127357	0.000203944	3.690480667
ABUW_RS01625	ABUW_0330	NZ_CP008706.1	319925	325209	+	WP_000098101.1		Ena family transporter	419.4087503	1.01649582	0.196633076	7.988752316	1.36E-15	5.37E-15	14.27002571
ABUW_RS01385	ABUW_0792	NZ_CP008706.1	772484	772999	+	WP_001018578.1		hyptothetical protein	41.08788804	1.00986362	0.257573188	4.350451085	1.67E-05	8.88E-06	1.000607512
ABUW_RS12295	ABUW_2529	NZ_CP008706.1	2521057	252148	+	WP_000386291.1		2-(12-epoxy-1,2-dihydrophenylacetyl)-CoA isomerase	1400.627279	1.008772186	0.418826822	2.647366432	0.00810214	0.01000946	1.958566702
ABUW_RS14445	ABUW_3384	NZ_CP008706.1	3422058	3423356	+	WP_000191191.1		glycosyltransferase family I protein	168.9548678	1.00864497	0.231512336	4.788647899	1.68E-06	3.20E-06	4.549458022
ABUW_RS00515	ABUW_014	NZ_CP008706.1	11610	116809	+	WP_000061878.1		alpha,beta fold hydrolase	928.8888229	1.00861577	0.174443729	6.355521242	2.08E-10	5.48E-10	9.261218443
ABUW_RS02420	ABUW_962	NZ_CP008706.1	969551	969103	+	WP_000043926.1		TcpR/AcrC family transcriptional regulator	225.6195557	1.00823763	0.293296786	3.778053718	0.000167742	0.000250531	9.2104932
ABUW_RS11660	ABUW_2397	NZ_CP008706.1	2348496	2350504	+	WP_000124516.1		malonate decarboxylase holo-ACP synthase	117.8555566	1.00814884	0.285550984	3.680710091	0.00019431	0.000180086	3.774464558
ABUW_RS12615	ABUW_2339	NZ_CP008706.1	2398219	23954107	+	WP_000371861.1		MF3 transporter	282.8430433	1.00781959	0.250462367	4.19621516	9.91E-06	1.76E-05	4.77961845
ABUW_RS14630	ABUW_3015	NZ_CP008706.1	3038780	3038965	-	WP_000190154.1		hyptothetical protein	5.8464248	1.00620428	0.520500896	2.0326361	0.033564208	0.043252516	137.953472
ABUW_RS07880	ABUW_8172	NZ_CP008706.1	1500275	1506145	+	WP_000701935.1		3-hydroxyacyl-CoA dehydrogenase	810.99322						

ABUW_RS0580	ABUW_198	NZ_CP008706.1	1232764	1233747	+	WP_00194227.1	xdhC	xanthine dehydrogenase accessory protein XdhC	292.0939764	1042737.9	0.173926002	5.99529212	2.03E-09	4.95E-09	8.305394801
ABUW_RS09920	ABUW_2043	NZ_CP008706.1	2024376	2024579	+	WP_000301960.1		hypothetical protein	236.4085257	104005794	0.234299124	4.439017623	9.04E-06	1.61E-05	4.793174124
ABUW_RS13440	ABUW_2768	NZ_CP008706.1	2760039	2760893	+	WP_000834590.1		SDR family oxidoreductase	47.0978535	103711091	0.352268275	2.943952429	0.003240498	0.004806904	2.336590938
ABUW_RS06120	ABUW_1252	NZ_CP008706.1	1291909	1292198	+	WP_000028947.1		hypothetical protein	55.71232066	103767767.6	0.263784471	3.930244298	8.49E-05	0.00018421	3.858798016
ABUW_RS02645	ABUW_0538	NZ_CP008706.1	546080	547147	-	WP_000107855.1		ske-specific integrase	814.873932	1035198004	0.833954339	5.644305066	1.66E-08	3.72E-08	7.42945706
ABUW_RS1505	ABUW_2781	NZ_CP008706.1	2776038	2777177	+	WP_001155439.1		acyl-CoA dehydrogenase family protein	158.856032	1034295588	0.343588067	3.0127797	0.002610087	0.003737044	2.427471789
ABUW_RS1820	ABUW_3865	NZ_CP008706.1	3933639	3934181	+	WP_000964180.1		NAD(P)H-dependent oxidoreductase	7815208805	1033780655	0.256674325	4.027596655	5.63E-05	9.33E-05	4.030181356
ABUW_RS11665	ABUW_2398	NZ_CP008706.1	2385495	2386322	-	WP_001017588.1	mdcE	biotin-independent malonate decarboxylase subunit gamma	319.6520009	1033520526	0.273436407	3.779747316	0.000156988	0.000249213	3.603429307
ABUW_RS06950	ABUW_1427	NZ_CP008706.1	1417703	1418155	+	WP_001918074.1		GNAT family N-acetyltransferase	6.777461437	1032504768	0.573325474	1.800905098	0.071717839	0.087085948	1060051916
ABUW_RS08840	ABUW_1817	NZ_CP008706.1	1812757	1819674	-	WP_001147215.1		alpha/beta hydrolase	273.2753721	1032261546	0.187709217	5.22109866	1.78E-07	3.70E-07	6.431798276
ABUW_RS10300	ABUW_2120	NZ_CP008706.1	2104020	2105024	-	WP_000822381.1		hypothetical protein	182.7061514	1032084327	0.188728675	5.468614276	4.54E-08	9.86E-08	7.006123085
ABUW_RS03705	ABUW_0755	NZ_CP008706.1	751584	752240	+	WP_000026377.1		hypothetical protein	612.5176621	1031896367	0.313200121	3.294686998	0.000985314	0.001465422	2.834037293
ABUW_RS18540	ABUW_3809	NZ_CP008706.1	3870143	3870853	-	WP_001153625.1		GntR family transcriptional regulator	430.4632464	1026020755	0.24188621	4.24174969	2.22E-05	3.80E-05	4.420216403
ABUW_RS18885	ABUW_3472	NZ_CP008706.1	3520481	3521158	+	WP_000232911.1		DUF345 domain-containing protein	394.3406979	1022842513	0.149375149	6.847474408	7.52E-12	2.22E-11	10.65364703
ABUW_RS17820	ABUW_3659	NZ_CP008706.1	3719660	3721147	+	WP_000492599.1		SuP family inorganic anion transporter	2512.464297	102215286	0.203243867	5.029194114	4.93E-07	9.86E-07	6.006123085
ABUW_RS11980	ABUW_2462	NZ_CP008706.1	2454076	2455293	-	WP_000418129.1		MFS transporter	25.30183278	1021995397	0.332899238	3.069984186	0.002140701	0.003091356	2.509805979
ABUW_RS10000	ABUW_2059	NZ_CP008706.1	2040335	2041498	+	WP_000040098.1		catalsae family protein	656.8886024	1021884208	0.236385309	4.322959877	1.54E-05	2.68E-05	4.571865206
ABUW_RS12450	ABUW_2563	NZ_CP008706.1	2552111	2552963	+	WP_000460161.1		LysR family transcriptional regulator	220.3046533	102191203	0.1545782	6.12294057	3.78E-11	1.06E-10	9.974619435
ABUW_RS11880	ABUW_2441	NZ_CP008706.1	2429496	2429717	-	WP_000498474.1		hypothetical protein	184.1222427	1019672439	0.427387261	2.385827759	0.01074073	0.022298506	1651724234
ABUW_RS15330	ABUW_2786	NZ_CP008706.1	2781831	2782094	-	WP_000092890.1		FadR family transcriptional regulator	1316.898821	1013962621	0.181956077	5.285019352	1.28E-07	2.65E-07	6.576754126
ABUW_RS00980	ABUW_0198	NZ_CP008706.1	2227671	223090	-	WP_000082174.1		AzD domain-containing protein	6144208597	1013743052	0.267539657	3.789131914	0.000151175	0.000240175	3.619472201
ABUW_RS15670	ABUW_3228	NZ_CP008706.1	3256431	3258365	-	WP_000019553.1		copper resistance system multicopper oxidase	860.7917636	102226217	0.203593425	4.971802095	6.63E-07	1.31E-06	5.882728704
ABUW_RS15985	ABUW_3291	NZ_CP008706.1	3324185	3325793	+	WP_000253062.1		acyl-CoA synthetase	358.5102198	101160718	0.317980827	3.18134843	0.001465912	0.002141464	2.669289222
ABUW_RS03955	ABUW_0808	NZ_CP008706.1	784652	788098	+	WP_000590487.1		hypothetical protein	257.2478141	1010396769	0.192381488	5.25204718	1.50E-07	3.15E-07	6.501819446
ABUW_RS15000	ABUW_3090	NZ_CP008706.1	3181448	3120157	+	WP_001088484.1		tetratricopeptide repeat protein	115.108418	100931079	0.16114927	6.263225506	3.77E-10	9.73E-10	9.0188716
ABUW_RS03970	ABUW_0811	NZ_CP008706.1	789307	789573	-	WP_000019121.1		hypothetical protein	370.389869	1009144393	0.23258825	4.338761457	1.43E-05	2.50E-05	4.602059991
ABUW_RS17500	ABUW_3595	NZ_CP008706.1	3658145	3658678	-	WP_000832994.1	nusG	transcription termination/antitermination protein NusG	19050.55783	1008946097	0.220491438	4.57589695	4.74E-06	8.83E-06	5.063989204
ABUW_RS07370	ABUW_1511	NZ_CP008706.1	1496784	1497575	+	WP_000092860.1		DUF1865 domain-containing protein	33.01958007	1007852598	0.3503269	2.876891839	0.004016132	0.005663632	2.246904731
ABUW_RS16665	ABUW_2194	NZ_CP008706.1	2179868	2181073	+	WP_001053251.1		acyl-CoA dehydrogenase family protein	377.0871456	1007574881	0.153891371	6.555832465	5.53E-11	1.53E-10	8.815030659
ABUW_RS11150	ABUW_2292	NZ_CP008706.1	2279239	2279829	+	WP_001878721.1		lecithin retinol acyltransferase family protein	438.235189	1006578873	0.294813709	3.41287873	0.00063949	0.000967883	3.014171158
ABUW_RS20440	ABUW_0779	NZ_CP008706.1	764737	764889	+	WP_001291449.1		hypothetical protein	3.937722768	100363109	0.103605793	0.973566368	0.330271892	0.384366225	4.038461687
ABUW_RS07245	ABUW_1486	NZ_CP008706.1	1473140	1473778	-	WP_000590096.1		TetR/AcrR family transcriptional regulator	44.50382304	1000262121	1.16564699	0.86113367	0.389164593	0.423786868	0.372871156

Table S12. RNA-seq data: Absolute and relative expression (ChI/MEP > 2-fold down)

ABUW_RS00105	ABUW_0021	NZ_CP008706.1	24363	25055	-	WP_000698067.1		TGR04219 family outer membrane beta-barrel protein	1783.929754	-1.000742811	0.171299175	-7.060914473	1.65E-12	5.16E-12	11.2873503
ABUW_RS15025	ABUW_3095	NZ_CP008706.1	3121789	3121863	+			IRNA-Gln	198.1736355	-1.004191892	0.324660441	-3.093052819	0.001891089	0.002868058	2.54241027
ABUW_RS02835	ABUW_0536	NZ_CP008706.1	544597	545634	-	WP_001177156.1	queA	meC4Q13-A adenosylmethionine ribosyltransferase-isomerase	1266.065852	-1.005710182	0.194154454	-5.170943065	2.22E-07	4.59E-07	6.338187934
ABUW_RS16905	ABUW_3476	NZ_CP008706.1	3523312	3524244	-	WP_001089412.1		Rua family pseudouridine synthase	1290.107879	-1.007693294	0.192304603	-5.22324929	1.75E-07	3.66E-07	6.136518915
ABUW_RS03735	ABUW_0781	NZ_CP008706.1	753990	754415	+	WP_000020651.1		VRR-NUC domain-containing protein	4144072463	-1.009064999	0.309026796	-3.265319325	0.001093428	0.001602236	2.790421722
ABUW_RS17525	ABUW_3600	NZ_CP008706.1	3660780	3660855	-			IRNA-Gly	3504.761008	-1.009666163	0.282884764	-3.567917046	0.000531983	0.000553131	3.257172001
ABUW_RS15920	ABUW_3278	NZ_CP008706.1	3311928	3321188	+	WP_000897689.1		hypothetical protein	20722.67108	-1.010348615	0.304594039	-2.966430709	0.003012782	0.004290739	2.368478902
ABUW_RS17255	ABUW_3546	NZ_CP008706.1	3604299	3604383	-			IRNA-Leu	530.895283	-1.012636804	0.34193288	-2.966974192	0.003007483	0.004284678	2.36808191
ABUW_RS09005	ABUW_1850	NZ_CP008706.1	1846320	1847564	+	WP_000462461.1		acyl-CoA dehydrogenase family protein	324.6193565	-1.013328625	0.153274622	-6.61196387	3.81E-11	1.07E-10	9.970161222
ABUW_RS18715	ABUW_3844	NZ_CP008706.1	3915358	3919996	+	WP_000027529.1		TetR family transcriptional regulator	1056.29137	-1.016079744	0.132713164	-7.656209763	1.92E-14	7.01E-14	13.15428198
ABUW_RS07545	ABUW_1546	NZ_CP008706.1	1532793	1533239	-	WP_000832591.1	tpil	50S ribosomal protein L9	15253.3301	-1.016933217	0.24819589	-4.098230435	4.16E-05	6.98E-05	4.156144577
ABUW_RS18730	ABUW_3847	NZ_CP008706.1	3916556	3918369	+	WP_000807591.1	unc160	3-demethylubiquitinone 3-O-methyltransferase(2-octaprenyl)-6-hydro	1287.85924	-1.017006078	0.202152278	-5.0313888	4.87E-07	9.76E-07	6.010550182
ABUW_RS05810	ABUW_1190	NZ_CP008706.1	1222449	1223322	+	WP_000209397.1		uroporphyrinogen decarboxylase	2208.172454	-1.018016781	0.156146271	-6.519654767	7.05E-11	1.93E-10	9.714442691
ABUW_RS03065	ABUW_0623	NZ_CP008706.1	624365	625261	+	WP_001071168.1		acyl-CoA carboxylase carboxyltransferase subunit beta	25246.91395	-1.018418712	0.214565175	-4.746430609	2.07E-06	3.90E-06	5.408935393
ABUW_RS03730	ABUW_0760	NZ_CP008706.1	753436	753993	+	WP_000360554.1		hypothetical protein	40.08596648	-1.019504757	0.318666121	-3.072036252	0.002126039	0.003072386	2.512542223
ABUW_RS17870	ABUW_3670	NZ_CP008706.1	3726897	3727940	+	WP_000668561.1	ansB	ACR3 family arsenite efflux transporter	108.843662	-1.019642045	0.304923199	-3.343931357	0.000286002	0.00123176	2.905757413
ABUW_RS14375	ABUW_2961	NZ_CP008706.1	2974867	2975148	-	WP_000627259.1		FKBP-type peptidyl-prolyl cis-trans isomerase	779.0648017	-1.02007109	0.221468324	-4.609845768	4.11E-06	7.51E-06	5.124360063
ABUW_RS00195	ABUW_0040	NZ_CP008706.1	47905	48558	+	WP_001036017.1		START domain-containing protein	542.624313	-1.020782435	0.146395028	-6.972657809	3.11E-12	9.45E-12	11.02456819
ABUW_RS10685	ABUW_2198	NZ_CP008706.1	2185585	2185857	-	WP_001043034.1		HU family DNA-binding protein	13183.52626	-1.021038696	0.190611953	-5.357150814	8.45E-08	1.81E-07	6.742321425
ABUW_RS17830	ABUW_3661	NZ_CP008706.1	3721548	3722837	-	WP_000137809.1		ISL3-like element ISPPu2 family transposase	707.8019556	-1.02193066	0.225280805	-4.454769189	8.40E-06	1.50E-05	4.823908741
ABUW_RS05195	ABUW_1158	NZ_CP008706.1	1067320	1068366	-	WP_000051193.1		nitronate monooxygenase	663.2602768	-1.022187008	0.223737962	-4.568679686	4.91E-06	8.91E-06	5.050122296
ABUW_RS15005	ABUW_3091	NZ_CP008706.1	3120182	3120740	+	WP_000039824.1	lobB	outer membrane lipoprotein LoB	753.7355776	-1.023565326	0.199242634	-6.427709088	1.30E-10	3.47E-10	4.949670525
ABUW_RS15875	ABUW_2854	NZ_CP008706.1	2865221	2866453	-	WP_000005666.1		FAD-dependent monooxygenase	1016.915951	-1.023690622	0.154171517	-6.839946473	3.14E-11	8.87E-11	10.05207638
ABUW_RS06615	ABUW_1556	NZ_CP008706.1	1586460	1589359	+	WP_001025741.1		thiamine phosphate synthase	472.4045985	-1.024071072	0.218994694	-4.678373216	2.89E-06	5.37E-06	5.270025714
ABUW_RS03275	ABUW_0665	NZ_CP008706.1	671436	672146	-	WP_000805047.1		DacC family protein	105.476979	-1.02573138	0.15535776	-2.50561679	152E-07	3.17E-07	4.698404738
ABUW_RS03100	ABUW_0630	NZ_CP008706.1	633178	633621	+	WP_000757174.1		hypothetical protein	1022.10062	-1.025967791	0.2825337	-3.726952522	0.00193809	0.003034309	3.95865203
ABUW_RS01630	ABUW_0311	NZ_CP008706.1	334494	335123	-	WP_000016937.1	gnrk	guanylate kinase	2869.207226	-1.029038384	0.158334531	-6.491496678	8.08E-11	2.20E-10	9.657577319
ABUW_RS03550	ABUW_0681	NZ_CP008706.1	681819	686888	+	WP_000050593.1		lysyl-acyl-accepting chemotaxis protein	870.172025	-1.030090721	0.203783405	-4.96077819	7.93E-06	1.42E-05	4.84711856
ABUW_RS15350	ABUW_3161	NZ_CP008706.1	318470	318802	+	WP_000542992.1	gigC	Methy-1 family transcriptional regulator G1C	4745.555461	-1.036844664	0.2103457	-4.494878779	9.35E-07	1.62E-06	5.739922864
sRNA102	no	no	no	no	no	no	no	no	875.922477	-1.03247727	0.280162878	-3.685319021	0.0022842	0.003056684	3.447431649
ABUW_RS14800	ABUW_3050	NZ_CP008706.1	3076085	3076357	+	WP_000896934.1	minE	cell division topological specificity factor MinE	7612.7179	-1.033409508	0.148094282	-6.97085182	2.99E-12	9.11E-12	11.03058282
ABUW_RS15925	ABUW_3279	NZ_CP008706.1	3312359	3312655	-	WP_001021616.1		integration host factor subunit alpha	6958.744437	-1.034847833	0.17841603	-4.416502233	2.03E-06	3.83E-06	5.48801226
ABUW_RS17510	ABUW_3597	NZ_CP008706.1	365052	3650627	-			IRNA-Tyr	400.0070699	-1.037435625	0.20711996	-3.885355463	9.90E-07	0.000195136	3.782188239
ABUW_RS16880	ABUW_3837	NZ_CP008706.1	3904548	3906027	-	WP_000810005.1	ampD	1,6-anhydro-D-N-acetylglucosamine 1-L-alanine amidase AmpD	225.3415709	-1.03898318	0.21639999	-3.733704501	1.00E-07	1.54E-06	4.82192729
ABUW_RS04955	ABUW_1310	NZ_CP008706.1	1022792	1023478	-	WP_001167858.1		diphthine - ammonium ligase	761182.917	-1.038912315	0.158243723	-8.101777335	5.45E-15	2.21E-15	14.65560773
ABUW_RS01630	ABUW_0327	NZ_CP008706.1	348537	350313	+	WP_000552222.1		TSUP family transporter	490.373132	-1.03918959	0.160826415	-6.416208714	1.04E-10	1.80E-10	9.552481969
ABUW_RS11005	ABUW_2283	NZ_CP008706.1	2247942	2248724	+	WP_000051721.1		Paik family protein	2370.247118	-1.040537959	0.19523505	-6.534603789	6.38E-11	7.954881332	
sRNA95	no	no	no	no	no	no	no	no	126.249262	-1.040989423	0.258350711	-4.02936354	5.59E-05	9.27E-05	4.032920266
ABUW_RS00590	ABUW_0119	NZ_CP008706.1	194102	194458	+	WP_000877633.1		hypothetical protein	307.8347092	-1.044028664	0.277073925	-3.78059022	0.0014528	0.00206874	3.5556569203
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001029065.1		hypothetical protein	845.1754442	-1.044978269	0.103474662	-10.05889034	5.59E-24	3.87E-23	22.41228903
ABUW_RS10925	ABUW_2247	NZ_CP008706.1	2235455	2236188	-	WP_001071527.1	ung	uracil-DNA glycosylase	362.17704	-1.045330932	0.12050605	-3.20989764	1.07E-10	5.89E-10	9.22988471
ABUW_RS04840	ABUW_1743	NZ_CP008706.1	1714967	1742767	+	WP_000868103.1	lpxd	JDP-3, C(3)-hydroxymethylglucosamine N-acyltransferase	6862.340315	-1.045615749	0.176257247	-8.249666166	16.0E-16	6.70E-16	15.7329251

ABUW_RS0470	ABUW_118	NZ_CP008706.1	109284	104186	+	WP_001091973.1		phosphate ABC transporter ATP-binding protein	1987.48507	-1.045926421	0.146753981	-7.127073591	1.03E-12	3.28E-12	11.48432616
ABUW_RS0935	ABUW_2249	NZ_CP008706.1	2227045	2238004	-	WP_000303478.1	gapK	type II secretion system minor pseudopilin GapK	307.9633049	-1.04605107	0.95501085	-6.32050194	2.61E-10	6.82E-10	9.96226525
ABUW_RS1705	ABUW_3636	NZ_CP008706.1	3716336	3718563	+	WP_000894500.1		accessory factor UbiK family protein	258.9054031	-1.04703644	0.24692611	-4.24028109	2.23E-05	3.81E-05	4.419070024
ABUW_RS1075	ABUW_3510	NZ_CP008706.1	355926	3557101	-	WP_001110871.1	gapF	type II secretion system inner membrane protein GapF	103.963004	-1.047546948	0.6434929	-6.3741919	1.84E-10	4.85E-10	9.314250621
ABUW_RS0670	ABUW_035	NZ_CP008706.1	148721	149488	+	WP_01025871.1		transporter	7096.692988	-1.04886345	0.18404084	-7.57285295	3.50E-14	1.25E-13	12.903039945
ABUW_RS1700	ABUW_3495	NZ_CP008706.1	354353	3544191	+	WP_010300756.1		SAM-dependent methyltransferase	440.0235929	-1.04893198	0.20180905	-5.98146094	2.01E-07	4.17E-07	6.37986386
ABUW_RS0995	ABUW_2179	NZ_CP008706.1	216924	216102	-	WP_000006691.1		hypothetical protein	35.26797341	-1.04934367	0.348664527	-3.009608347	0.002816848	0.003743961	2.42066864
ABUW_RS0345	ABUW_2582	NZ_CP008706.1	2573749	2578150	+	WP_000443350.1		hypothetical protein	10.2428868	-1.04979184	0.20551913	-5.108020738	3.26E-07	6.63E-07	6.17848471
ABUW_RS0310	ABUW_2742	NZ_CP008706.1	2730748	2731977	+	WP_001058805.1		NAADPH-dependent aldo-keto reductase	1034.332471	-1.050751077	0.267037052	-3.934851248	8.32E-05	0.000159902	3.866774162
ABUW_RS0285	ABUW_0587	NZ_CP008706.1	585663	585859	+	WP_001046506.1		branched-chain amino acid transaminase	8093.378342	-1.052050882	0.1289544	-7.913680584	2.45E-15	9.49E-15	10.02273379
ABUW_RS07470	ABUW_630	NZ_CP008706.1	151572	1516438	-	WP_000733779.1		hypothetical protein	4489.248461	-1.052661002	0.154132566	-6.829582001	8.52E-12	2.51E-11	10.60032628
ABUW_RS17045	ABUW_3504	NZ_CP008706.1	3551389	3551846	+	WP_000003406.1	tusA	sulfatransferase TusA	816.9225935	-1.052971964	0.221957803	-4.744019683	2.10E-06	3.95E-06	5.403402904
ABUW_RS16345	ABUW_3364	NZ_CP008706.1	3404638	3406032	+	WP_001088578.1	adeC	ΔAdeK/OprM family multidrug efflux complex outer membrane	725.3486923	-1.053370941	0.200442461	-5.038954075	4.68E-07	9.35E-07	6.027334408
ABUW_RS06675	ABUW_068	NZ_CP008706.1	1383405	1384865	+	WP_000195383.1		aminoacyl-histidine dipeptidase	930.403716	-1.056931654	0.167166108	-5.659119108	1.52E-08	3.44E-08	7.483411557
ABUW_RS07935	ABUW_626	NZ_CP008706.1	1622178	1622537	+	WP_010120884.1		5-carboxymethyl-2-hydroxymuconate Delta-isomerase	465.8750387	-1.05825219	0.142195527	-7.442218952	9.90E-14	3.44E-13	12.4634165
ABUW_RS05095	ABUW_838	NZ_CP008706.1	1047555	1048513	+	WP_000806001.1		SDR family oxidoreductase	194.632202	-1.059095813	0.170505793	-6.218494615	5.25E-10	1.34E-09	8.872892502
ABUW_RS1679	ABUW_3499	NZ_CP008706.1	3538855	3538955	+	WP_001096920.1		ABC transporter	9176.547017	-1.060100883	0.164229511	-5.397031654	6.78E-08	1.46E-07	6.835647144
ABUW_RS02225	ABUW_0453	NZ_CP008706.1	455765	456406	+	WP_000057682.1		fumarylglutamate hydrolase family protein	2571.25578	-1.060983284	0.154222242	-7.295881309	2.97E-13	9.90E-13	10.0434651
ABUW_RS1400	ABUW_2966	NZ_CP008706.1	2979602	2979577	+	WP_010146499.1		acyl-CoA thioesterase	855.3062636	-1.06177607	0.178503889	-5.944309498	2.78E-09	6.66E-09	8.176523771
ABUW_RS0495	ABUW_3087	NZ_CP008706.1	310198	3110555	+	WP_00056981.1		outer membrane protein assembly factor BamD	5719.466468	-1.064885912	0.132167611	-8.309803822	9.59E-17	4.49E-16	5.38933994
ABUW_RS02990	ABUW_0608	NZ_CP008706.1	608223	609881	+	WP_010300504.1	baeS	sensor histidine kinase efflux regulator BaeS	1287.317547	-1.065575506	0.110196003	-7.600610025	2.95E-14	1.06E-13	12.974694103
ABUW_RS17005	ABUW_677	NZ_CP008706.1	1566692	1566990	+	WP_000739363.1		AarF/ABCtUBX kinase family protein	3225.858773	-1.065911807	0.146195623	-6.431917875	8.57E-11	2.31E-10	9.63368802
ABUW_RS04035	ABUW_0824	NZ_CP008706.1	794957	800083	+	WP_000435847.1		1-acyl-L-glycyl-L-phenyl phosphate acyltransferase	4195.1285035	-1.066061783	0.195302028	-5.585495026	4.80E-08	1.04E-07	6.982996661
ABUW_RS04810	ABUW_0981	NZ_CP008706.1	992691	993761	-	WP_000071984.1	purM	phosphoribosyl-formylglycinamide cyclo-ligase	17016.62391	-1.066717392	0.186194544	-5.731911028	9.98E-09	2.29E-08	7.640194818
ABUW_RS01380	ABUW_0281	NZ_CP008706.1	298738	299661	+	WP_000100134E.1	ramH	16S rRNA (cytosine:U4021-N42)-methyltransferase RamH	1918.364976	-1.06688454	0.18186809	-5.730036468	1.00E-08	2.31E-08	7.16838802
ABUW_RS05625	ABUW_1029	NZ_CP008706.1	1189058	1191329	+	WP_000846423.1		hypothetical protein	175.7478276	-1.06734331	0.25296003	-4.19318817	2.45E-05	4.17E-05	4.379863945
ABUW_RS07505	ABUW_637	NZ_CP008706.1	1527590	1524670	+	WP_000559187.1	mmnG	uridine-5-carboxymethylammonium(54)-synthase enzyme	5273.390754	-1.06933575	0.19918853	-5.36812235	7.95E-08	1.76E-07	6.7001893
ABUW_RS16315	ABUW_0631	NZ_CP008706.1	1316868	134398	+	WP_000446411.1		MHS family MFS transporter	2834.82218	-1.069511001	0.15821434	-6.759882621	1.38E-11	3.98E-11	4.61011693
ABUW_RS02930	ABUW_0596	NZ_CP008706.1	554190	554963	+	WP_001089508.1		hypothetical protein	1106.355826	-1.070191295	0.259069633	-4.136890002	3.57E-05	6.07E-05	4.221125528
ABUW_RS0300	ABUW_0061	NZ_CP008706.1	61496	65889	-	WP_000193600.1		4-hydroxy-2-oxo-4-oxidipicolinate synthase	12140.54355	-1.071647599	0.172269304	-6.044744213	1.50E-09	3.70E-09	4.831793276
ABUW_RS16545	ABUW_3404	NZ_CP008706.1	3451944	3451944	+	WP_001984475.1		VAT-dependent diacylglycerase	758.4941698	-1.071863252	0.13197103	-8.043701605	8.37E-16	3.36E-15	4.473766072
ABUW_RS03030	ABUW_0006	NZ_CP008706.1	6870	7427	+	WP_001009022.1		FFT domain-containing protein	532.0191863	-1.072510646	0.185894447	-6.762039418	1.39E-11	3.91E-11	4.01072324
ABUW_RS03375	ABUW_0686	NZ_CP008706.1	694890	695823	-	WP_001016570.1	dapE	succinyl-diaminopimelate desuccinylase	4052.828914	-1.073056432	0.11771167	-9.102191875	6.88E-20	3.46E-19	18.4802239
ABUW_RS1200	ABUW_2486	NZ_CP008706.1	2482129	2482881	+	WP_000434318.1		UTRA domain-containing protein	320.3203416	-1.073320885	0.165258848	-6.058956998	7.73E-11	2.18E-10	9.673711545
ABUW_RS14895	ABUW_3028	NZ_CP008706.1	3052957	3054225	+	WP_002010751.1		exonuclease Sbc-D subunit D	400.8210532	-1.075472826	0.149544546	-7.191655305	6.40E-13	2.08E-12	11.68193767
ABUW_RS0460	ABUW_144	NZ_CP008706.1	1948355	1944602	+	WP_000195308.1		NADH hydrolase	8112.959289	-1.075690267	0.311663639	-3.452163822	0.000553369	0.000845008	3.07319197
ABUW_RS17335	ABUW_3602	NZ_CP008706.1	361033	366108	+			tRNA-Thr	4673.477769	-1.075804664	0.269650059	-3.98961326	6.62E-05	0.000188914	3.962919292
ABUW_RS05025	ABUW_624	NZ_CP008706.1	1035102	1035711	+	WP_000470769.1		dTMP kinase	10110.97837	-1.075943659	0.19838995	-7.69416039	1.42E-14	5.27E-14	13.2781983
ABUW_RS16780	ABUW_3646	NZ_CP008706.1	3672387	3673293	+	WP_000100966.1		acyltransferase	1489.824782	-1.077272335	0.1884468	-5.107487982	1.05E-08	2.57E-08	7.590066877
ABUW_RS07470	ABUW_0762	NZ_CP008706.1	754425	755099	+	WP_000524893.1		metallophosphoesterase	108.4559827	-1.076444663	0.228064222	-4.718919045	2.36E-06	4.41E-06	5.55556141
ABUW_RS00990	ABUW_0200	NZ_CP008706.1	223851	224399	+	WP_000081959.1		helicase-tum-helic transcriptional regulator	901.9146634	-1.075995916	0.12241766	-8.167831635	3.25E-16	1.34E-15	8.71289251
ABUW_RS16785	ABUW_0972	NZ_CP008706.1	982999	983494	+	WP_001985538.1		YnfY/YnfU family protein	782.853886	-1.080797746	0.1519443	-6.789168116	1.0E-11	3.29E-11	10.4820041
ABUW_RS15910	ABUW_3276	NZ_CP008706.1	3309597	3309923	+	WP_001276871.1	tnaA	threonine	11984.46586	-1.083546079	0.183297673	-5.92821089	3.18E-09	7.60E-09	8.119186408
ABUW_RS0880	ABUW_3471	NZ_CP008706.1	351919	3520318	+	WP_000432340.1	hcrA	DNA-binding transcriptional regulator HcrA	1260.19181	-1.08606686	0.201387508	-5.327170243	9.98E-08	2.12E-07	6.673664199
ABUW_RS16205	ABUW_0330	NZ_CP008706.1	418712	417717	+	WP_000203495.1	recG	ATP-dependent DNA helicase RecG	914.7188033	-1.088852494	0.14037911	-7.17418038	8.96E-09	3.32E-14	4.178861992
ABUW_RS1718	ABUW_3518	NZ_CP008706.1	3566252	3568339	-	WP_001985730.1	rep	polynucleotide nucleotidyltransferase	4103.41912	-1.088745399	0.182248771	-5.973191951	1.23E-09	5.61E-09	8.251037109
ABUW_RS1465	ABUW_0454	NZ_CP008706.1	2924100	2925167	+	WP_000107266.1		hypothetical protein	904.2019196	-1.089078917	0.199414272	-9.1812197	7.64E-20	3.95E-19	18.40349229
ABUW_RS02280	ABUW_094	NZ_CP008706.1	945662	947697	+	WP_000218111.1	msiA	A (N6-isopentenyl)adenosine(37)-C(2)-methylthiotransferase	1019.805016	-1.08946034	0.167199057	-5.959345411	1.85E-13	6.24E-13	12.20481541
ABUW_RS1370	ABUW_2837	NZ_CP008706.1	2847054	2848064	+	WP_000008620.1		ABC transporter permease	272.5101382	-1.089425345	0.167166988	-6.516988845	1.17E-11	1.96E-10	9.707743929
ABUW_RS14740	ABUW_2980	NZ_CP008706.1	2996925	2997365	+	WP_000305962.1		YnfA family protein	34.3136574	-1.089589234	0.388747417	-2.862082015	0.000505785	0.00705003	1.21904538
ABUW_RS05185	ABUW_056	NZ_CP008706.1	1064959	1066167	+	WP_001038857.1		DUF1815 domain-containing protein	1699.552764	-1.089714479	0.089250047	-5.21483367	2.59E-34	3.28E-33	32.48412618
ABUW_RS1325	ABUW_2745	NZ_CP008706.1	2733162	2734511	+	WP_000517792.1		adenosylsuccinate synthase	30542.30006	-1.090300445	0.163476737	-6.67000373	2.56E-11	7.28E-11	10.17886862
ABUW_RS01645	ABUW_0334	NZ_CP008706.1	356447	356761	+	WP_000950560.1		antibiotic biosynthesis monooxygenase	232.5366425	-1.090819998	0.167260658	-6.525695012	6.95E-11	1.91E-10	9.178666313
ABUW_RS1300	ABUW_3355	NZ_CP008706.1	339272	3393728	+	WP_001165443.1	hxC	ketol-acyl reductoisomerase	33596.40446	-1.094318322	0.1492552	-6.10836264	5.04E-16	2.05E-15	16.88824614
ABUW_RS03635	ABUW_089	NZ_CP008706.1	187814	188116	+	WP_000302149.1		helicase-tum-helic transcriptional regulator	1608.683356	-1.09600237	0.189730855	-5.77682463	7.62E-09	1.76E-08	7.754487332
ABUW_RS01650	ABUW_3785	NZ_CP008706.1	35196	36491	+	WP_000071454.1		pyrimidine permease	7152.0905083	-1.097124205	0.198369742	-5.53088223	3.18E-08	7.154281982	
ABUW_RS1610	ABUW_1102	NZ_CP008706.1	1103422	1104084	+	WP_000530441.1		elongation factor P hydrolase	2398.255909	-1.097236194	0.146213594	-7.504337632	6.17E-14	2.18E-13	12.66164351
ABUW_RS0430	ABUW_110	NZ_CP008706.1	107737	102699	+	WP_000227394									

ABUW_RS07460	ABUW_628	NZ_CP008706.1	519779	154474	-	WP_00205890.1		ABC transporter permease	2875.540059	-1102423141	0.176336404	-6.40605608	1456-10	3.86E-10	9.41042695
ABUW_RS04045	ABUW_931	NZ_CP008706.1	829051	163028	-	WP_00102628.1		MFS transporter	204.7727776	-100508967	0.2114691	-5.35448991	8.60E-08	1.94E-07	6.73582177
ABUW_RS04575	ABUW_0934	NZ_CP008706.1	60684	107530	-	WP_001030169.1	tsaA	cell envelope integrity protein TsaA	1321886563	-110101635	0.2029184	-5.573834587	2.48E-08	5.51E-08	7.25884041
ABUW_RS05955	ABUW_973	NZ_CP008706.1	971483	197500	-	WP_000455546.1	adeR	efflux system response regulator transcription factor AdeR	87.551999	-1103105838	0.16210397	-6.989052329	2.77E-12	8.47E-12	1.07216959
ABUW_RS10880	ABUW_2855	NZ_CP008706.1	286450	286768	-	WP_001187365.1		FAD-dependent monooxygenase	819.68849	-1104377237	0.17532327	-6.47683531	9.72E-11	2.63E-10	5.58004252
ABUW_RS10665	ABUW_0318	NZ_CP008706.1	343087	343659	+	WP_001946489.1		prepilin-type N-terminal cleavage/methylolation domain-containing pil	325.648921	-1105565897	0.16028193	-8.34801934	6.94E-17	2.98E-16	9.25607474
ABUW_RS07145	ABUW_927	NZ_CP008706.1	918899	919620	-	WP_001070556.1	glbB	hydroxyxylylglyoxylate hydrolase	876.4556012	-1106233982	0.181784344	-6.250450147	4.05E-10	1.05E-09	8.978810701
ABUW_RS04400	ABUW_0897	NZ_CP008706.1	893880	894203	-	WP_000729551.1	yhvY	ribosome assembly RNA-binding protein YhvY	3358.065065	-1106293363	0.13305373	-8.51023269	1.72E-17	7.72E-17	6.102827
ABUW_RS04680	ABUW_0954	NZ_CP008706.1	962644	963489	+	WP_000923484.1	dapF	diaminopimelate epimerase	2511272709	-1108377631	0.192419455	-5.916125422	3.30E-09	7.86E-09	8.104271454
sRNA K15	no	no	no	no	no	no	no	no	22.65063245	-1108394492	0.404348957	-2.81687977	0.00486452	0.006778367	2.36880855
ABUW_RS18005	ABUW_3903	NZ_CP008706.1	3699443	3971203	-	WP_0011818090.1	ycdC	membrane protein insertase YcdC	33583.20947	-1108973925	0.216872253	-5.251947148	15.1E-07	3.15E-07	6.501899446
ABUW_RS18285	ABUW_3148	NZ_CP008706.1	3174093	3176156	+	WP_001026776.1	metG	methionine--tRNA ligase	5176.31494	-1114119143	0.178089466	-6.40788051	1.68E-10	3.92E-10	9.406715933
ABUW_RS18033	ABUW_911	NZ_CP008706.1	9171540	9172025	+	WP_0010204147.1		methyltransferase C factor biosynthesis protein MsaE	560.9555076	-1114161916	0.21660839	-5.36916398	7.91E-08	1.70E-07	6.769551978
ABUW_RS04670	ABUW_0952	NZ_CP008706.1	961141	961365	+	WP_001055198.1		hypothetical protein	785.4073993	-1142532237	0.224972233	-5.078547791	3.80E-07	7.71E-07	6.102945622
ABUW_RS16680	ABUW_2230	NZ_CP008706.1	3258903	3259724	-	WP_000218423.1		HAD family hydrolase	913.1280686	-1143933255	0.142779767	-8.011872245	1.01E-15	4.48E-15	8.34897199
ABUW_RS00635	ABUW_0128	NZ_CP008706.1	143273	143998	-	WP_001076274.1		ion channel protein Tsa	2811272538	-1145490416	0.234390829	-4.887095709	1.02E-06	1.98E-06	5.70333481
ABUW_RS18585	ABUW_3818	NZ_CP008706.1	3882717	3883979	+	WP_000686120.1		UDP-glucose/GDP-mannose dehydrogenase family protein	5401.71626	-1145684327	0.1964849	-7.074422243	1.50E-12	4.72E-12	1.1326058
ABUW_RS00245	ABUW_0334	NZ_CP008706.1	542759	543335	-	WP_000147160.1		LamA family protein	1167.512676	-1146898102	0.19868393	-6.078234296	1.22E-09	3.02E-09	8.59993057
ABUW_RS00450	ABUW_0591	NZ_CP008706.1	103891	104405	-	WP_000380676.1		phosphatidylglycerophosphatase A	3233.266885	-1147740752	0.172499275	-6.65393754	2.86E-11	8.18E-11	9.09899045
ABUW_RS18930	ABUW_3461	NZ_CP008706.1	3506833	3507423	-	WP_001094507.1		hypothetical protein	3411822579	-1149042009	0.10714354	-8.378443672	5.35E-17	2.32E-16	6.53451002
ABUW_RS04700	ABUW_0958	NZ_CP008706.1	966358	967107	+	WP_000646180.1		electron transport flavoprotein subunit beta/Fxa family protein	24391.53267	-1149570797	0.180030471	-6.385423488	1.71E-10	4.52E-10	9.344861665
ABUW_RS08070	ABUW_1655	NZ_CP008706.1	1648022	165078	-	WP_001189921.1		TonB-dependent sensorphore receptor	35168175437	-11498716901	0.541555937	-0.04261487	0.033664446	0.042638809	1.37014961
ABUW_RS02420	ABUW_0493	NZ_CP008706.1	50590	505546	-	WP_000224786.1	ipsi	30S ribosomal protein S9	43603.8864	-1149910723	0.217103577	-5.296612426	1.91E-07	2.50E-07	6.062059991
ABUW_RS17980	ABUW_0166	NZ_CP008706.1	3926609	3927175	+	WP_001090743.1		5'-nucleotidase	4411943964	-115300143	0.15019629	-10.0244782	1.91E-23	8.91E-23	22.01951498
ABUW_RS10660	ABUW_2254	NZ_CP008706.1	2240285	2241058	-	WP_000497300.1		TadD family hydrolase	3090.423944	-115431463	0.127423542	-9.058880269	1.32E-19	6.67E-19	8.1587417
ABUW_RS11610	ABUW_1100	NZ_CP008706.1	2247446	2249378	-	WP_000553193.1	nmrG	16S rRNA (adenine(527)-N(7))-methyltransferase NmrG	1107.58547	-1154942081	0.156559924	-7.419641953	1.17E-13	4.04E-13	9.234361963
ABUW_RS13630	ABUW_3387	NZ_CP008706.1	3407929	3408495	-	WP_000099436.1	omn	oligonucleotase	2244.009604	-1155559148	0.109077752	-8.82727186	1.07E-18	5.18E-18	7.12898263
ABUW_RS1425	ABUW_3380	NZ_CP008706.1	341822	3420514	+	WP_000093084.1	tmn	23S rRNA (adenine(2553)-C(2))-methyltransferase Tmn	5509.00945	-1156247161	0.19103478	-6.386878607	1.69E-10	4.48E-10	9.348721866
ABUW_RS1720	ABUW_0238	NZ_CP008706.1	3265780	3266406	-	WP_000200136.1		CoA pyrophosphatase	8.716750529	-1157602125	0.2265549	-5.10664979	3.23E-07	6.58E-07	6.18177406
ABUW_RS10745	ABUW_1601	NZ_CP008706.1	165011	162723	+	WP_001026730.1	ftsA	cell division protein FtsA	9303.255008	-1158633536	0.180314633	-6.425563423	13.1E-10	3.15E-10	9.454698284
ABUW_RS10220	ABUW_2642	NZ_CP008706.1	2639887	2641477	-	WP_000003555.1		HydC family type I secretion periplasmic adaptor subunit	2921445768	-1160747673	0.17608314	-6.582032574	4.34E-11	1.21E-10	9.9172633
ABUW_RS10990	ABUW_3168	NZ_CP008706.1	3106635	3119189	-	WP_000191030.1	fabG	3-oxoacyl-ACP reductase FabG	41823.46471	-1160965148	0.20002166	-5.804210503	6.47E-09	1.91E-08	7.82103053
ABUW_RS14435	ABUW_2973	NZ_CP008706.1	2988890	2990530	+	WP_000714073.1	mcp	maleate dehydrogenase (quinone)	13328.92757	-1162197262	0.279431657	-4.159148215	3.19E-05	5.40E-05	4.20780024
ABUW_RS08990	ABUW_0160	NZ_CP008706.1	919734	919934	+	WP_001623261.1		response regulator transcription factor	1165.081904	-1162689173	0.141606443	-8.216710953	2.20E-16	9.14E-16	5.03905338
ABUW_RS10875	ABUW_0136	NZ_CP008706.1	1416517	1416531	+	WP_000733830.1	dsbD	protein--disulfide reductase DsbD	2528.45012	-1164464121	0.132928182	-8.716129536	1.93E-18	9.16E-18	17.04095861
ABUW_RS10950	ABUW_3284	NZ_CP008706.1	3371862	3372251	-	WP_000124858.1	gpiT	50S ribosomal protein L20	33645.3677	-116478149	0.25677391	-4.136226511	5.73E-06	1.04E-05	4.98296661
ABUW_RS16515	ABUW_3166	NZ_CP008706.1	3224910	3225401	-	WP_000249482.1		flavin reductase	1472.464774	-1165547483	0.13020275	-7.759584703	0.000170196	0.000269015	3.570232504
ABUW_RS10480	ABUW_0950	NZ_CP008706.1	957177	959105	-	WP_000448860.1	radA	DNA repair protein RadA	774.8793501	-1166093095	0.149410648	-7.804461688	5.59E-15	2.26E-14	6.341881956
ABUW_RS12980	ABUW_0606	NZ_CP008706.1	605676	607421	-	WP_001051747.1		acyl-CoA dehydrogenase C-terminal domain-containing protein	7167.935858	-1167281496	0.220986254	-5.282193986	1.28E-07	6.5704721	
ABUW_RS104160	ABUW_0848	NZ_CP008706.1	826962	829973	+	WP_000271409.1	rluU	50S ribosomal protein L21	54542.30376	-1171024655	0.21954339	-5.335059579	9.55E-08	2.03E-07	6.692503962
ABUW_RS102415	ABUW_0432	NZ_CP008706.1	504532	504899	-	WP_001019146.1		glutathione S-transferase N-terminal domain-containing protein	484.8102393	-117183392	0.1841956	-6.364879304	1.96E-10	5.16E-10	9.287350149
ABUW_RS1450	ABUW_0385	NZ_CP008706.1	3423495	3425768	-	WP_000778302.1		carboxyl terminal--processing peptidase	10534.41889	-1170288239	0.170102699	-7.464264043	8.33E-14	9.22E-13	12.534617
ABUW_RS10670	ABUW_0319	NZ_CP008706.1	343566	343991	+	WP_000788336.1		prepilin-type N-terminal cleavage/methylation domain-containing pil	305.5426715	-1172221744	0.163902654	-7.516681974	2.60E-14	9.30E-14	13.0248831
ABUW_RS12975	ABUW_0882	NZ_CP008706.1	869759	871797	+	WP_001300567.1	kdsB	potassium transporting ATPase subunit KdsB	246.7248029	-117258493	0.192726766	-6.084193084	1.17E-09	9.25E-09	8.534611497
ABUW_RS08295	ABUW_0589	NZ_CP008706.1	581750	588588	+	WP_000697143.1		glyoxylate dehydrogenase family protein	1322.489972	-1172691747	0.117368114	-9.991918676	1.66E-23	1.91E-22	21.95078198
ABUW_RS10435	ABUW_2147	NZ_CP008706.1	2152616	2153212	-	WP_000490551.1	recR	recombination protein RecR	17102.848889	-1174628723	0.138393745	-8.487585341	2.11E-17	9.37E-17	8.02826041
ABUW_RS10360	ABUW_1363	NZ_CP008706.1	1388651	1389844	-	WP_000806837.1		clock shock domain--containing protein	1272.654885	-1175866174	0.184000912	-6.101017198	1.35E-09	3.35E-09	8.474995193
ABUW_RS18555	ABUW_3812	NZ_CP008706.1	3874665	3875488	-	WP_000587286.1	ltd	FMN-dependent L-lactate dehydrogenase Ltd	2830.650457	-1177591004	0.339837787	-3.464941082	0.000530347	0.000808463	3.5092339851
ABUW_RS18575	ABUW_3815	NZ_CP008706.1	3880041	3881057	-	WP_001062902.1	galE	UDP-glucose-4-epimerase GalE	5116.33314	-1177730713	0.140042032	-8.409945432	4.10E-17	1.79E-16	6.71474697
ABUW_RS10665	ABUW_2235	NZ_CP008706.1	2224254	2225396	-	WP_000933587.1		cell division protein ZapE	55997.54974	-1178043086	0.147702766	-7.978205973	1.48E-15	6.83E-15	14.2343145
ABUW_RS16515	ABUW_1026	NZ_CP008706.1	1046468	104910	-	WP_001017199.1		gamma carboxyl aminohydrolase family protein	627.0749455	-1181959663	0.12545195	-9.41010366	4.59E-21	2.60E-20	18.50502665
ABUW_RS103260	ABUW_0629	NZ_CP008706.1	668299	669405	+	WP_000196163.1		NADH:flavin oxidoreductase NADH oxidase	3052.889033	-1181954035	0.248069278	-7.476294243	19.1E-06	6.44E-09	42.9491429
ABUW_RS10670	ABUW_0366	NZ_CP008706.1	220729	222093	+	WP_001986480.1		MFS transporter	2071190358	-118218903	0.14601968	-8.096093836	5.68E-16	2.30E-15	6.43827274
ABUW_RS10505	ABUW_0133	NZ_CP008706.1	944007	944260	+	WP_000457193.1		serine hydroxymethyltransferase	9066.1059	-1183710081	0.184477977	-6.410549539	1.39E-10	3.72E-10	4.12403409
ABUW_RS10470	ABUW_0905	NZ_CP008706.1	912652	913773	+	WP_001015189.1		bifunctional 3,4-dihydropyrimidin-2-butanone-4-phosphate synthase (GTP cycl	8709.719093	-1183725512	0.21947612	-5.24032654	1.87E-08	4.17E-08	7.37863945
ABUW_RS10580	ABUW_1040	NZ_CP008706.1	106063	106679	-	WP_000611679.1	eymB	EF-P beta-lysyl-tRNA synthetase EymB	1740.718242	-1183364456	0.116021969	-10.3824795	2.97E-25	2.13E-24	23.95161914
ABUW_RS10645	ABUW_0936	NZ_CP008706.1	934561	935466	+	WP_000271449.1	tsaA	rRNA-3-thiouridine(32)-synthetase TsaA	3018.47183	-1185041231	0.11800382	-7.018500091	2.37E-12	7.31E-12	11.9608262
ABUW_RS10810	ABUW_2223	NZ_CP0													

ABUW_RS05970	ABUW_0222	NZ_CP008706.1	1262895	1263617	-	WP_001078588.1		IS RNA (rncI(486)-N3)-methyltransferase	679.6216475	-1239207084	0.176817716	-7.008387564	2.41E-12	7.42E-12	11.02959609	
ABUW_RS08300	ABUW_0167	NZ_CP008706.1	186519	187614	-	WP_006640204.1	prfB	peptide chain release factor 2	81.04	137348	-1239366199	0.199725428	-8.870018566	7.31E-19	3.54E-18	17.45099674
ABUW_RS06030	ABUW_0234	NZ_CP008706.1	1272793	1278120	-	WP_001008491.1	map	type I methionyl aminopeptidase	32.13	46037	-1240364725	0.164783055	-8.297588199	1.00E-16	4.48E-16	9.34872799
ABUW_RS02920	ABUW_0594	NZ_CP008706.1	592066	592881	-	WP_000719071.1		glycoyltransferase family 25 protein	966.0493968	-1240441506	0.17079191	-7.26230763	3.79E-13	1.28E-12	11.90308999	
ABUW_RS05330	ABUW_1100	NZ_CP008706.1	1194332	1192199	-	WP_001923216.1	surE1	5'/3'-nucleotidase SurE1	823.5592353	-1241982931	0.186378908	-6.592972695	4.13E-11	1.20E-10	9.920818754	
ABUW_RS03300	ABUW_0617	NZ_CP008706.1	618482	619711	+	WP_000371732.1	tyjB	tyrophan synthase subunit beta	4563.874184	-1242396207	0.207186617	-5.99657808	2.03E-09	9.94E-09	8.30621305	
ABUW_RS03420	ABUW_0695	NZ_CP008706.1	698870	699946	+			RNA-Asp	530.4009822	-1245332627	0.290703588	-4.283869611	1.84E-05	3.17E-05	4.498940738	
ABUW_RS06830	ABUW_1400	NZ_CP008706.1	1410244	1404147	-	WP_000096816.1		helic-tum-helix domain-containing protein	348.231844	-1245433924	0.185218506	-6.724122227	1.77E-11	5.00E-11	10.29584948	
ABUW_RS00701	ABUW_1164	NZ_CP008706.1	3128065	3128739	-	WP_000985168.1		HAD-1A family hydrolase	968.0784691	-1250433053	0.122862746	-16.0774793	2.50E-24	1.77E-23	22.75202673	
ABUW_RS03170	ABUW_0644	NZ_CP008706.1	650510	650995	+	WP_000935247.1		DUF934 domain-containing protein	1421.350918	-1251061452	0.219284142	-5.760537516	1.65E-08	2.63E-08	7.580044252	
ABUW_RS19320	ABUW_2805	NZ_CP008706.1	2873287	2873726	+	WP_001028274.1	lon	endopeptidase La	55429.76005	-1252520238	0.223894234	-5.594249644	2.22E-08	4.92E-08	7.308034897	
ABUW_RS18655	ABUW_3832	NZ_CP008706.1	3899496	3899924	+	WP_001019772.1		low molecular weight phosphotyrosine protein phosphatase	2947.91356	-125503093	0.138667935	-9.050621559	1.42E-19	7.17E-19	16.1448084	
ABUW_RS14545	ABUW_3182	NZ_CP008706.1	3209555	3209761	-	WP_001043214.1		hypothetical protein	1637.327806	-1256127874	0.223887888	-5.6105218	2.02E-08	4.49E-08	7.347753659	
ABUW_RS00480	ABUW_0170	NZ_CP008706.1	181945	182033	+	WP_000819040.1		alkene reductase	913.5455979	-1256230236	0.175653795	-7.155406009	8.34E-13	2.89E-12	11.57024772	
ABUW_RS14655	ABUW_3020	NZ_CP008706.1	3045841	3046992	-	WP_000128703.1		EnmA/Enk family multidrug efflux transporter periplasmic adaptor	64.10100321	-1256297844	0.282179675	-4.45210242	8.50E-06	1.51E-05	4.821023053	
ABUW_RS19030	ABUW_2187	NZ_CP008706.1	2170722	2172161	-	WP_000442383.1		DHA2 family efflux MFS transporter permease subunit	947.7528411	-125883797	0.463619658	-2.782424395	0.006622720	0.00910033	2.04037057	
ABUW_RS17675	ABUW_3630	NZ_CP008706.1	3688743	3690089	-	WP_000908240.1		UDP-N-acetylmutamoyl-L-alanine--D-glutamate ligase	1003.643463	-1259919779	0.195912669	-6.426930991	1.30E-10	3.48E-10	9.458420654	
ABUW_RS02545	ABUW_0518	NZ_CP008706.1	526811	525233	+	WP_001287659.1		acyl-CoA thioesterase	1316.675374	-1259186728	0.127365184	-7.305344191	2.77E-13	9.29E-13	10.3381927	
ABUW_RS01420	ABUW_0379	NZ_CP008706.1	3849646	38419256	+	WP_001366899.1	prfH	type IV plus biogenesis/stability protein PrfH	2000.678642	-1262102889	0.134992076	-9.349533897	8.80E-21	4.89E-20	9.1363991	
ABUW_RS01695	ABUW_0322	NZ_CP008706.1	345003	345143	+	WP_000441695.1	tmrD	RNA (guanosine(37)-N)-methyltransferase TmrD	337.019309	-1262271487	0.253602058	-4.973078226	6.59E-07	1.30E-06	5.880595648	
ABUW_RS02185	ABUW_0593	NZ_CP008706.1	591614	592047	-	WP_000909270.1		hypothetical protein	640.510592	-1264638626	0.190737719	-7.424734557	1.01E-10	3.90E-10	12.40893595	
ABUW_RS17365	ABUW_3568	NZ_CP008706.1	3624773	3626572	-	WP_012307759.1	uvrC	endonuclease ABC subunit UvrC	704.888748	-1265394608	0.210456518	-6.012617815	1.83E-09	4.47E-09	13.896982477	
ABUW_RS02900	ABUW_0590	NZ_CP008706.1	588595	589330	+	WP_000989966.1		polysaccharide deacetylase family protein	568.091744	-1267817961	0.120733125	-10.50100574	8.50E-26	6.57E-25	24.1842631	
ABUW_RS19515	ABUW_0641	NZ_CP008706.1	648486	646128	+	WP_000201352.1		carbohydrate pin	16278.53208	-1268467217	0.10288752	-7.769054647	6.34E-15	2.39E-14	13.616021	
ABUW_RS17580	ABUW_3611	NZ_CP008706.1	3608941	3617005	+	WP_000681771.1		hypothetical protein	1047.17091	-126861263	0.139947817	-9.0504048	1.25E-19	6.34E-19	16.9179174	
ABUW_RS01340	ABUW_0113	NZ_CP008706.1	1712972	1714207	+	WP_000010073.1		methylotetrapyrrole methyltransferase MoeA	838.2878515	-126916656	0.10264721	-10.35005055	4.85E-20	3.90E-20	23.9504162	
ABUW_RS03005	ABUW_0602	NZ_CP008706.1	66219	66863	+	WP_001985076.1	pncA	bifunctional nicotinamide/pyrazinamidase	460.7007637	-1272755273	0.14384918	-8.847848383	8.82E-19	4.29E-18	17.36754271	
ABUW_RS03565	ABUW_0767	NZ_CP008706.1	1176584	1195379	-	WP_001102188.1		hypothetical protein	182.292752	-1273355773	0.226107089	-5.630450028	1.80E-08	4.03E-08	7.934984954	
ABUW_RS09995	ABUW_2261	NZ_CP008706.1	2246373	2247008	-	WP_000264044.1		MotA/TolA/EnvB protein channel family protein	104.525071	-1274030458	0.17157952	-7.419792289	1.16E-14	9.20E-14	12.81737194	
ABUW_RS01690	ABUW_3433	NZ_CP008706.1	3478521	34781799	-	WP_0002027403.1		hypothetical protein	2965.48817	-1276488801	0.134484348	-3.738057327	0.000155448	0.00029749	1.534906024	
ABUW_RS17650	no	NZ_CP008706.1	3654347	3654972	+			NLDX domain-containing protein	1800.77915	-1279407201	0.146016549	-8.762051942	1.92E-18	9.06E-18	17.0429718	
ABUW_RS13960	ABUW_2752	NZ_CP008706.1	2742408	2742387	-	WP_000735756.1		hypothetical protein	2995.543435	-1280051874	0.224168579	-6.269991987	3.61E-09	9.34E-09	12.6055124	
ABUW_RS00485	ABUW_0094	NZ_CP008706.1	105770	106240	-	WP_001007829.1	rBfE	6,7-dimethyl-8-ribitylmazine synthase	6860.276249	-128182071	0.192907204	-6.841442347	3.11E-11	8.80E-11	10.0551733	
ABUW_RS18200	ABUW_3101	NZ_CP008706.1	3194562	3195365	+	WP_000420180.1		sulfite oxidoreductase TauD/Bif family protein	401.6489636	-1283107905	0.173524482	-7.394574478	1.42E-13	4.85E-13	12.1142828	
ABUW_RS04665	ABUW_0951	NZ_CP008706.1	959594	961000	+	WP_000070815.1		amino acid permease	5173.80101	-128454333	0.17382427	-7.390017165	1.47E-13	5.01E-13	12.3006227	
ABUW_RS01760	ABUW_0799	NZ_CP008706.1	1791867	1792671	-	WP_000242666.1		adenosine kinase	2785.749359	-1285993193	0.132605166	-9.69723331	3.16E-22	1.88E-21	20.72584216	
ABUW_RS14660	ABUW_3021	NZ_CP008706.1	3047262	3047759	-	WP_000216614.1		thioesterase family protein	278.0189127	-1286276024	0.17711919	-7.262372823	3.80E-13	1.26E-12	10.89962945	
ABUW_RS01870	ABUW_0797	NZ_CP008706.1	1179078	1191916	+	WP_000753036.1		DUF1449 family protein	397.914051	-1288672264	0.149885209	-8.977278053	8.10E-18	3.73E-17	16.48291197	
ABUW_RS11055	ABUW_2273	NZ_CP008706.1	2258391	2258984	+	WP_000819686.1	maf	cuprum family protein Maf	768.448104	-1289810055	0.133007005	-9.675965774	3.81E-22	2.30E-21	20.63827216	
ABUW_RS04850	ABUW_0689	NZ_CP008706.1	101989	1020755	+	WP_000268346.1		RNA methyltransferase	12117776	-1291838393	0.189070464	-7.636095675	2.24E-14	8.16E-14	10.8830904	
ABUW_RS12615	ABUW_2148	NZ_CP008706.1	1626351	1638365	+	WP_001069201.1	mutB	UDP-N-acetylmuramate dehydrogenase	1265.344704	-1294319964	0.117780054	-10.9829673	4.30E-28	2.64E-28	14.943218	
ABUW_RS04715	ABUW_0096	NZ_CP008706.1	1197613	1198200	+	WP_001985281.1		hypothetical protein	41.8616178	-1297344666	0.10199993	-12.7203403	4.56E-37	6.63E-36	35.17844647	
ABUW_RS01425	ABUW_1109	NZ_CP008706.1	1195361	1197734	+	WP_000117543.1		diaminobutyrate--2-oxoglutarate transaminase	17067.29737	-1298043295	0.180375336	-7.196345829	6.18E-13	2.02E-12	11.64464863	
ABUW_RS19995	ABUW_3385	NZ_CP008706.1	3319233	3319427	+	WP_001996369.1	gmiI	5Ss ribosomal protein L35	15405.93484	-13000345073	0.234108299	-5.393047609	6.90E-08	1.49E-07	6.82087193	
ABUW_RS19885	ABUW_2826	NZ_CP008706.1	2867690	2868012	-	WP_000717547.1	pepP	Xaa-Pro aminopeptidase	2647.19781	-1310187787	0.159218685	-8.33640223	6.55E-24	23.4497785		
ABUW_RS17180	ABUW_3531	NZ_CP008706.1	3588334	3589167	+	WP_001068589.1	bifunctional phosphoribosyl-AMP cyclitoldehydrophosphoribosyl-ATP diphosphate	2095.742044	-13103597464	0.189538519	-6.877714271	6.08E-12	1.81E-11	10.74232143		
ABUW_RS17995	ABUW_3697	NZ_CP008706.1	3755681	3756972	+	WP_000919493.1	mdfD	multidrug transporter subunit MdfD	806.1914748	-1310392819	0.191532276	-6.142607178	9.47E-12	2.78E-11	10.5595552	
ABUW_RS00615	ABUW_0104	NZ_CP008706.1	103436	103231	+	WP_000105974.1	parE	DNA topoisomerase IV subunit B	2436.763635	-13105523665	0.162769587	-8.020734748	1.05E-15	4.16E-15	14.37775598	
ABUW_RS17310	ABUW_3557	NZ_CP008706.1	3613919	3615586	+	WP_000950426.1	recN	DNA repair protein RecN	2217.810703	-1310455971	0.147807141	-9.722919863	2.41E-22	1.48E-21	20.82973828	
ABUW_RS04965	ABUW_0102	NZ_CP008706.1	1023999	1024670	+	WP_000127870.1	queC	7-cyano-7'-deazaguanine synthase QueC	71.61697573	-1311702547	0.173750083	-7.54988716	4.4E-12	1.55E-13	12.8096863	
ABUW_RS11685	ABUW_2279	NZ_CP008706.1	2264149	2264715	+	WP_000240301.1		DUF2058 domain-containing protein	546.272617	-1312352775	0.250519205	-5.238657078	1.62E-07	3.37E-07	6.472370099	
ABUW_RS18440	ABUW_2148	NZ_CP008706.1	2193222	2193351	-	WP_001028697.1		YbaB/Ebc family nucleoid-associated protein	2580.891071	-1311601149	0.18886374	-10.788783355	6.85E-15	2.58E-14	13.88328028	
ABUW_RS19555	ABUW_2457	NZ_CP008706.1	2445809	2446750	-	WP_001230724.1		Lydr family transcriptional regulator	542.020606	-1316397003	0.175660005	-7.672831248	1.68E-14	6.19E-14	10.2803305	
ABUW_RS01785	ABUW_1654	NZ_CP008706.1	1519262	1540017	-	WP_001187811.1		RDD family protein	1656.146815	-1318450856	0.15381557	-8.57857555	1.02E-17	4.63E-17	16.33441901	
ABUW_RS07385	ABUW_1615	NZ_CP008706.1	1610807	1609814	+	WP_000380356.1		glutamine--RNA ligase/Arg-YagD domain fusion protein	7271.1483672	-1319101128	0.172870977	-7.360185051	2.34E-14	8.50E-14	10.0705107	
ABUW_RS02325	ABUW_0655	NZ_CP008706.1	651947	652982	-	WP_001280992.1	tyjA	translational O-Phease TyjA	37234.42002	-1319363757	0.233431778	-5.65203148	1.59E-08	3.76E-08	74.44731784	
ABUW_RS18300	ABUW_3361	NZ_CP008706.1	3400194	3401173	+	WP_000742831.1	hnsK	DNA polymerase II subunit delta	1694.519043	-1319815032	0.15382917	-8.57941454	9.82E-19	4.39E-17	16.35753548	
ABUW_RS19895	ABUW_2200	NZ_CP008706.1	2186693													

ABUW_RS0300	ABUW_0610	NZ_CP008706.1	610651	612093	-	WP_001802220.1	YdU family protein	1601585.65	-139.94889	0.9104968	-7.28718621	3.17e-13	1.05e-12	11.678107
ABUW_RS0370	ABUW_2794	NZ_CP008706.1	2794864	2793324	+	WP_000446079.1	conferylaldehyde dehydrogenase	726.222861	-139.40541	0.93846022	-7.1918152	6.39e-13	2.08e-12	11.693607
ABUW_RS0700	ABUW_3435	NZ_CP008706.1	3474966	3478855	-	WP_001813874.1	ASDCh domain-containing protein	962.960459	-139.9407947	0.93843236	-9.6974776	3.09e-22	1.88e-21	20.7258425
ABUW_RS0305	ABUW_0635	NZ_CP008706.1	637674	638434	-	WP_000219258.1	patatin family protein	1060.687583	-139.383088	0.9430419	-9.66973838	4.05e-22	2.43e-21	20.6139373
ABUW_RS0405	ABUW_3303	NZ_CP008706.1	333760	3337161	-	WP_000810373.1	rimD 23S rRNA [unc(E939: C)5] methyltransferase RimD	2977.711005	-139.679482	0.93380603	-10.45367261	14.1e-25	1.08e-24	23.9665724
ABUW_RS0575	ABUW_0402	NZ_CP008706.1	428231	428778	+	WP_000537193.1	DUF853 domain-containing protein	8887.728719	-139.705105	0.20069276	-6.982838408	2.85e-12	8.83e-12	11.054593
ABUW_RS0405	ABUW_1051	NZ_CP008706.1	1027791	103885	+	WP_001057073.1	acyl-CoA deuterases	8930.02931	-139.943006	0.27180451	-5.16197295	2.44e-17	5.04e-17	6.29756464
ABUW_RS7795	ABUW_3854	NZ_CP008706.1	374263	371660	-	WP_000738516.1	ammonium transporter	3737.422396	-140.125719	0.17263212	-8.11071917	4.78e-16	1.95e-16	14.70966539
ABUW_RS0620	ABUW_0587	NZ_CP008706.1	595381	595932	-	WP_000919439.1	tetracycline repeat protein	625.419618	-140.2378777	0.2350578	-5.566101856	2.43e-19	5.87e-19	8.23106189
ABUW_RS0770	ABUW_0591	NZ_CP008706.1	583219	581722	+	WP_000825208.1	translocation/assembly module TamB domain-containing protein	6799.971211	-140.0905108	0.93788521	-10.22623729	15.1e-24	1.09e-23	22.9625735
ABUW_RS1825	ABUW_3724	NZ_CP008706.1	378264	3783233	+	WP_000633612.1	threonylcarbamoyl AMP synthase	524.335862	-140.9127137	0.130476048	-10.79989194	3.45e-27	2.82e-26	25.54975089
ABUW_RS0480	ABUW_0979	NZ_CP008706.1	99191	992000	+	WP_001160711.1	alpha/beta hydrolase	2624.615581	-141.0084228	0.93472171	-9.1874373	4.00e-20	2.11e-19	18.67571754
ABUW_RS1475	ABUW_3049	NZ_CP008706.1	3075270	3076062	+	WP_001074362.1	memD septum site-determining protein MemD	17000.91287	-141.0322783	0.15060195	-9.336165454	9.99e-21	5.52e-20	19.25800092
ABUW_RS0825	ABUW_0614	NZ_CP008706.1	6108586	610862	+	WP_000952702.1	c1pA ATP-dependent GpI protease ATP-binding subunit C1pA	6141.16663	-141.0210216	0.17653851	-9.988889393	1.26e-15	4.95e-15	14.305348
ABUW_RS0325	ABUW_0915	NZ_CP008706.1	616567	617469	-	WP_000045364.1	TonB-dependent receptor	5104.836293	-141.834211	0.1914672	-10.19310084	2.03e-24	1.51e-23	22.82192305
ABUW_RS1045	ABUW_2781	NZ_CP008706.1	2751807	2752430	-	WP_000071490.1	TerR/RacR family transcriptional regulator	57.7599935	-141.8743325	0.302236355	-4.69415191	2.68e-06	4.98e-06	5.302770657
ABUW_RS0450	ABUW_3181	NZ_CP008706.1	3208842	3209558	-	WP_000076440.1	response regulator transcription factor BmrR	1212.02799	-142.318033	0.240387682	-5.920261893	3.21e-09	7.67e-09	11.81274631
ABUW_RS0400	ABUW_2067	NZ_CP008706.1	2046293	2049447	-	WP_001047424.1	pqqE pyrimidoquinone quinone biosynthesis protein PqqE	549.505051	-142.3783059	0.22091212	-6.445046603	1.16e-10	3.15e-10	9.50863366
ABUW_RS0920	ABUW_2246	NZ_CP008706.1	2234324	2235458	-	WP_001983908.1	enoyl-CoA hydratase/isomerase family protein	7394.673035	-142.4710396	0.942300036	-10.0101972	1.35e-23	9.15e-23	22.03857291
gM9A1	no	no	no	no	no	no	no	255.279932	-142.4947656	0.27768193	-6.542357634	8.05e-11	1.67e-10	9.77723529
ABUW_RS1465	ABUW_2357	NZ_CP008706.1	2338780	2340300	+	WP_000078700.1	pyridoxal phosphate-dependent aminotransferase	1496.85727	-142.8506792	0.244074625	-5.841683826	5.17e-19	1.21e-18	7.9127463
ABUW_RS0890	ABUW_3272	NZ_CP008706.1	3304809	3305545	+	WP_000591848.1	phosphine-5-C-carboxylate reductase	3432.24779	-142.878193	0.11971061	-12.7172585	2.36e-17	3.46e-16	35.4603669
ABUW_RS06705	ABUW_0914	NZ_CP008706.1	918859	918924	-	WP_000264715.1	DUF423 domain-containing protein	1530.170061	-142.9028504	0.188195071	-7.593356037	3.02e-14	1.12e-13	12.9507198
ABUW_RS0480	ABUW_0730	NZ_CP008706.1	908650	908650	-	WP_000214356.1	phosphoenolpyruvate carboxykinase (GTP)	31459.07384	-142.991869	0.202353064	-7.066433959	15.9e-12	4.98e-12	11.03027706
ABUW_RS0690	ABUW_0384	NZ_CP008706.1	215653	219237	-	WP_000899419.1	tenA thiaminase I	726.0604883	-142.9939609	0.156852996	-9.174927298	4.52e-20	2.37e-19	18.6528195
ABUW_RS0180	ABUW_0196	NZ_CP008706.1	401158	401206	-	WP_001066013.1	areI alkinate dehydrogenase	1233.98917	-143.0010974	0.244147263	-5.857185699	4.71e-19	1.18e-18	7.954071021
ABUW_RS0580	ABUW_3827	NZ_CP008706.1	3881505	3882720	-	WP_0000445111.1	glucose-6-phosphatase isomerase	8168.71094	-143.0270588	0.19870807	-10.45589697	1.38e-25	1.06e-24	30.27469419
ABUW_RS1020	ABUW_3739	NZ_CP008706.1	3781483	3782613	+	WP_000914251.1	dprA DNA-processing protein DprA	605.6564719	-143.1011476	0.15551237	-9.201917263	3.52e-20	1.86e-19	18.73048706
ABUW_RS0725	ABUW_2206	NZ_CP008706.1	2190589	2194248	+	WP_001186578.1	hscA Fe-S protein assembly chaperone HscA	5980.52609	-143.1993788	0.8314674	-7.180071672	3.56e-15	2.03e-14	19.62550396
ABUW_RS1445	ABUW_3584	NZ_CP008706.1	3642842	3644266	-	WP_000594934.1	TRAP transposon/lage permease subunit	3010.051945	-143.2463477	0.22803742	-6.281929879	3.35e-10	6.96e-10	9.261480275
ABUW_RS0140	ABUW_0245	NZ_CP008706.1	253125	253751	-	WP_000209082.1	superoxide dismutase	14005.40078	-143.2540352	0.253718961	-5.647746410	1.635e-08	4.73771706	
ABUW_RS0255	ABUW_0717	NZ_CP008706.1	27358	28038	-	WP_000376623.1	GNA1 family N-acetyltransferase	814.7079071	-143.4401792	0.249266406	-5.754493014	6.85e-19	2.05e-18	7.689700004
ABUW_RS0050	ABUW_2059	NZ_CP008706.1	2049729	2050483	-	WP_000195101.1	pqqG pyrimidoquinone-quinone synthase PqqG	1825.980252	-143.8807504	0.195284441	-7.364002131	1.78e-13	6.06e-13	12.2173738
ABUW_RS0125	ABUW_0770	NZ_CP008706.1	918195	918244	-	WP_000697907.1	D-alanyl-D-alanine carboxypeptidase PBP6B	3141.42213	-143.9994488	0.16495915	-8.720958656	2.57e-18	1.21e-17	19.1971463
ABUW_RS1090	ABUW_2718	NZ_CP008706.1	2702466	2706323	-	WP_000931918.1	hpaA ATP-dependent RNA helicase HpaA	5359.575327	-144.0280146	0.202637764	-7.07660431	1.18e-12	3.75e-12	11.425696673
ABUW_RS1540	ABUW_3603	NZ_CP008706.1	366107	3662700	-	WP_000209090.1	tpiE anthranilate synthase component I	2457.58762	-144.3271255	0.156477906	-9.2234266	2.88e-20	1.54e-19	18.8147829
ABUW_RS1425	ABUW_0293	NZ_CP008706.1	300623	310881	+	WP_000201406e.1	plus assembly protein PAM	4412.185578	-144.5971423	0.22335749	-6.473834492	9.55e-11	2.59e-10	9.586700236
ABUW_RS0260	ABUW_0521	NZ_CP008706.1	510383	510697	+	WP_000618820.1	sulfurtransferase	2343.500924	-144.6341495	0.22312781	-6.482102125	9.04e-11	2.46e-10	9.600604498
ABUW_RS0150	ABUW_104	NZ_CP008706.1	187108	189207	+	WP_000428308.1	MFS transporter	41.06180168	-144.8426602	0.146437546	-9.891987659	4.59e-23	2.93e-22	11.30042323
ABUW_RS0975	ABUW_2257	NZ_CP008706.1	2242421	2243192	-	WP_000860692.1	tdsB 3-deoxy-manno-oxolinonate cytidyltransferase	2396.503528	-144.9263408	0.090500363	-6.0189606	1.02e-17	5.02e-16	55.29929268
ABUW_RS0485	ABUW_0996	NZ_CP008706.1	907986	9080654	-	WP_000224630.1	tdoC YHL family 4-Fe-4S cluster ferredoxin	3025.860983	-144.9846273	0.21916031	-6.841602619	7.83e-12	2.31e-11	10.6383802
ABUW_RS0155	ABUW_0441	NZ_CP008706.1	516272	516535	-	WP_001186305.1	YHL family 4-Fe-4S cluster ferredoxin	132.2757823	-145.0583973	0.17961516	-3.82192219	0.000102416	0.00021639	3.874090553
ABUW_RS1475	ABUW_3584	NZ_CP008706.1	2997394	2997993	-	WP_0002003311.1	biuA2D-protein/lage permease subunit	78.14481981	-145.603361	0.358020355	-4.061441405	4.88e-05	8.15e-05	1.069449454
ABUW_RS0155	ABUW_2022	NZ_CP008706.1	272736	272840	-	WP_000216076.1	phosphoenolpyruvate sulfite reductase	2819.305928	-145.9324934	0.19391968	-10.89702536	1.19e-27	9.93e-27	26.30305795
ABUW_RS0990	ABUW_0757	NZ_CP008706.1	2036942	2038051	-	WP_000484218.1	S-(hydroxymethyl)glutathione dehydrogenase/class II alcohol dehydrog	1718.702606	-145.9931792	0.221654145	-6.584749974	4.56e-11	1.27e-10	9.886196279
ABUW_RS0345	ABUW_0698	NZ_CP008706.1	702126	702761	-	WP_000473052.1	PeptSY domain-containing protein	1695.183703	-146.0554268	0.331956056	-4.399842212	1.08e-05	1.19e-05	4.71866633
ABUW_RS0980	ABUW_0234	NZ_CP008706.1	926454	926926	-	WP_000994842.1	adenosylhomocysteine	124.141952	-146.1350722	0.18914197	-7.704231166	1.32e-14	4.88e-14	13.1168016
ABUW_RS07465	ABUW_1229	NZ_CP008706.1	117415	116496	-	WP_000614025.1	methionine ABC transporter ATP-binding protein	5552.75816	-146.0509094	0.18410002	-7.195671035	1.74e-15	6.90e-15	14.1105091
ABUW_RS0450	ABUW_0907	NZ_CP008706.1	901904	902252	+	WP_001239850.1	fold1/methylhydrofolate dehydrogenase/methylenetetrahydrofolate	2704.165964	-146.0511163	0.208890575	-7.01899165	2.37e-12	7.30e-12	11.13667714
ABUW_RS0455	ABUW_1943	NZ_CP008706.1	943281	943774	+	WP_000512982.1	nicotinate phosphoribosyltransferase	3526.543505	-146.0741788	0.39771933	-3.689459814	0.00024732	0.00031902	3.453576265
ABUW_RS1416	ABUW_3378	NZ_CP008706.1	3416784	3418475	-	WP_000405193.1	helic-tum-helic domain-containing protein	2185.549389	-147.0970487	0.13428807	-11.02438464	2.92e-28	2.44e-27	26.9559628
ABUW_RS0630	ABUW_3827	NZ_CP008706.1	3893093	3894316	-	WP_000088925.1	oligosaccharide fipase family protein	228.1262187	-147.3501165	0.20842806	-7.06900989	1.56e-12	4.89e-12	13.1169914
ABUW_RS1730	ABUW_3555	NZ_CP008706.1	361091	3612147	-	WP_000995685.1	pyrimidine nucleoside phosphorylase	2164.914021	-147.4102322	0.16550571	-9.55855667	6.49e-20	3.37e-19	18.4723701
ABUW_RS1716	ABUW_2203	NZ_CP008706.1	2189210	2189596	+	WP_000331712.1	hcuU Fe-S cluster assembly scaffold hcuU	9280.838752	-147.5659074	0.254293935	-5.802988888	6.15e-09	1.62e-08	7.81564521
ABUW_RS0590	ABUW_0307	NZ_CP008706.1	946817	947481	+	WP_000950506.1	rRNA-[mG20]58A'-hydroxylase	1863.314553	-147.6898078	0.129289094	-11.50914555	1.29e-30	1.29e-29	28.8894129
ABUW_RS0180	ABUW_0682	NZ_CP008706.1	179993	181459	+	WP_000566023.1	guaiB MP dehydrogenase	19335.60974	-147.81895644	0.92348797	-9.70731067	2.81e-22	1.72e-21	20.76447105
ABUW_RS0160	ABUW_0297	NZ_CP008706.1	316733	317608	+	WP_000219810.1	hypothetical protein	1083.848468	-148.0085447	0.19751474	-13.76634858	4.06e-43	8.16e-42	41.0993756
ABUW_RS0490	ABUW_0111	NZ_CP008706.1	923569	923985	-	WP_000771045.1	hypothetical protein	3004.248416	-148.0301731	0.20236644	-7.317103185	2.53e-13	8.49e-13	12.07102371
ABUW_RS0421	ABUW_0344	NZ_CP008706.1	938280	939464	-	WP_001198104.1	iron-containing alcohol dehydrogenase	2203.148378	-148.0597884					

ABUW_RS1440	ABUW_2668	NZ_CP008706.1	2980465	2982531	-	WP_000179784.1		choleine transferase	2564.085651	-153323774	0.20944458	-7.33099866	2.28E-10	7.68E-10	0.1463878
ABUW_RS0920	ABUW_086	NZ_CP008706.1	207347	20934	+	WP_001019472.1	betI	choleine BCGT transporter BetI	7935.009942	-1537228236	0.86030334	-9.25871918	2.07E-20	1.02E-19	8.95079168
ABUW_RS1745	ABUW_2210	NZ_CP008706.1	219502	2198473	+	WP_000487568.1	mfd	transcription-repair coupling factor	3075.17241	-1537508627	0.140819309	-9.91838582	9.42E-28	7.92E-27	26.1012482
ABUW_RS0550	ABUW_2583	NZ_CP008706.1	2576246	2577190	+	WP_000542531.1		ABC transporter permease	25193226219	-1537976727	0.219625642	-7.099698403	125E-12	3.66E-12	11.40230481
ABUW_RS0570	ABUW_1088	NZ_CP008706.1	191187	193305	-	WP_002017737.1		EA4 domain-containing protein	3168.7544	-1538230229	0.148907605	-9.30039652	5.55E-25	3.78E-24	23.4225802
ABUW_RS0445	ABUW_0888	NZ_CP008706.1	101215	100129	-	WP_000321932.1		RNA polymerase sigma factor	9873.148035	-1539923354	0.19657646	-8.19648952	4.68E-16	1.92E-15	11.7669887
ABUW_RS0940	ABUW_3098	NZ_CP008706.1	312116	312412	+	WP_001273422.1	rgpI	50S ribosomal protein L35	8014.32645	-1540194198	0.254119357	-5.831964933	5.49E-09	1.29E-08	7.88941029
ABUW_RS0280	ABUW_2116	NZ_CP008706.1	2100953	2101661	-	WP_000771649.1		NAD(P)H-dependent oxidoreductase	294.9407125	-15400594082	0.238106675	-6.470349034	9.78E-11	2.85E-10	9.576754108
ABUW_RS0750	ABUW_3445	NZ_CP008706.1	348890	3490820	+	WP_000323471.1		ATP-binding cassette domain-containing protein	2122.505855	-154343418	0.140019227	-11.02364581	2.94E-28	2.55E-27	26.59345882
ABUW_RS0480	ABUW_3052	NZ_CP008706.1	3089882	3090352	-	WP_001018055.1	rpsG	30S ribosomal protein S7	68711.16624	-1544092556	0.209757699	-7.361015283	1.82E-10	6.17E-10	12.20971484
ABUW_RS0490	ABUW_0999	NZ_CP008706.1	1010666	101870	-	WP_0010164002.1	nuvB	Holliday junction branch migration DNA helicase NuvB	1673.298355	-1545038051	0.173657182	-8.897057642	5.73E-19	2.79E-18	17.5543958
ABUW_RS0160	ABUW_0317	NZ_CP008706.1	3139222	3143076	+	WP_000708943.1		VWA domain-containing protein	3920.51719	-15451900227	0.154703809	-9.9880555	1.72E-23	1.95E-22	21.93300216
ABUW_RS1470	ABUW_3031	NZ_CP008706.1	3058852	3058889	+	WP_000335549.1		type IV pilus twitching motility protein PiliT	604.5524893	-1547039284	0.25143186	-6.15284216	7.61E-10	1.92E-09	87.16068771
ABUW_RS1745	ABUW_3578	NZ_CP008706.1	3636064	3636768	+	WP_001021850.1		DbaA family oxidoreductase	1001474801	-1548809181	0.148774085	-9.41476957	2.22E-25	1.68E-24	23.77465072
ABUW_RS1425	ABUW_2971	NZ_CP008706.1	2985152	2986624	+	WP_001028303.1	betB	betaine-aldehyde dehydrogenase	4266.030248	-1548847083	0.392649643	-3.144460310	7.99E-05	0.00010086	3.81913084
ABUW_RS0965	ABUW_0495	NZ_CP008706.1	219500	220582	+	WP_000680215.1		DUF475 domain-containing protein	5334.950811	-1549312348	0.193484122	-8.007439227	1.17E-15	4.44E-15	11.33348202
ABUW_RS1270	ABUW_0842	NZ_CP008706.1	473894	4743370	+	WP_000703572.1	ybaY	rRNA maturation RNase YbaY	1479.000886	-1549669027	0.53352351	-10.10528377	5.23E-24	3.64E-23	22.43389862
ABUW_RS0450	ABUW_0827	NZ_CP008706.1	935673	935606	+	WP_001109116.1		SCP2 zeta-like binding domain-containing protein	4108.045421	-1549718653	0.193502605	-8.931961872	4.15E-19	2.06E-18	17.6861027
ABUW_RS0410	ABUW_0852	NZ_CP008706.1	833230	833491	+	WP_000568942.1	serS	serine-RNA ligase	4697.70807	-1550560417	0.201094937	-7.70599632	1.45E-14	0.33254706	
ABUW_RS1645	ABUW_2271	NZ_CP008706.1	2256682	2257699	+	WP_001011933.1		phosphoglycerate kinase	4507.890302	-155167504	0.175423278	-8.845748176	9.09E-19	4.37E-18	17.36951855
ABUW_RS0700	ABUW_2616	NZ_CP008706.1	2607400	2608068	-	WP_000873472.1		hydropathic protein	777.8748284	-1554663111	0.334286504	-4.946454045	7.56E-07	1.48E-06	5.829736285
ABUW_RS0470	ABUW_0900	NZ_CP008706.1	918423	917107	+	WP_001184451.1	gynA	DNA gyrase subunit A	18935.58875	-1557831151	0.147412399	-10.56744328	4.20E-26	3.29E-25	11.50743021
ABUW_RS0430	ABUW_3381	NZ_CP008706.1	3420637	3423068	+	WP_000963851.1	ndk	nucleoside-diphosphate kinase	13627.87567	-1558172622	0.21024381	-7.383851073	1.54E-10	5.26E-10	12.2798407
ABUW_RS1010	ABUW_2143	NZ_CP008706.1	214316	2144184	+	WP_000422835.1		DUF2791 pilus twitching motility protein	1892.445785	-1561042214	0.233397474	-6.689627722	2.24E-11	0.38E-11	10.1951932
ABUW_RS1585	ABUW_3128	NZ_CP008706.1	3149119	3150156	+	WP_000405207.1		cell division protein Zpa	31904.010834	-1562007006	0.186194555	-8.388434401	4.88E-17	2.12E-16	16.5736144
ABUW_RS1410	ABUW_3397	NZ_CP008706.1	3441852	3443378	+	WP_002027467.1		fumarate hydratase	8764.720097	-156260818	0.188556252	-8.28725382	1.16E-16	4.90E-15	5.30902992
ABUW_RS0800	ABUW_3861	NZ_CP008706.1	3925858	3929599	+	WP_000771825.1	rbF	bifunctional riboflavin kinase/FAD synthetase	849.4024723	-1563748558	0.145253572	-10.76564617	5.00E-27	4.08E-26	25.38933804
ABUW_RS0205	ABUW_2391	NZ_CP008706.1	2379960	2380103	+	WP_000749814.1			256.479899	-1566169425	0.45883285	-3.765886922	0.000265999	0.000262833	3.58032108
ABUW_RS0485	ABUW_1742	NZ_CP008706.1	174189	174192	+	WP_001037943.1		Omptin family outer membrane protein	5896.748487	-1568029528	0.162195758	-9.319166552	1.20E-20	6.57E-20	19.8243651
ABUW_RS1020	ABUW_2286	NZ_CP008706.1	2250158	2251658	-	WP_001018031.1		phosphotransferase	1621.883874	-1569875585	0.152085355	-9.32233236	5.58E-25	4.09E-24	23.88227669
ABUW_RS0070	ABUW_0014	NZ_CP008706.1	5160	71392	+	WP_000335556.1		tyrosine-RNA ligase	3456.526666	-1570944473	0.19619794	-9.87861973	5.5E-23	3.3E-22	21.4017201
ABUW_RS0310	ABUW_0632	NZ_CP008706.1	635103	635774	-	WP_001889520.1		hemolysin B family protein	916.9142932	-1571144323	0.180900284	-8.865140210	3.73E-19	1.76E-17	16.75443731
ABUW_RS0730	ABUW_1655	NZ_CP008706.1	1540082	1542469	+	WP_000853480.1	ppsA	phosphoenolpyruvate synthase	5189.22276	-1571018784	0.144501841	-8.87402038	1.53E-27	1.27E-26	25.8919628
ABUW_RS1730	ABUW_3573	NZ_CP008706.1	3632075	3633247	+	WP_000210712.1	fadA	acetyl-CoA C-acyltransferase FadA	5429.800599	-1573373374	0.258104999	-6.095187192	1.09E-09	2.73E-09	8.56383753
ABUW_RS0295	ABUW_0610	NZ_CP008706.1	609901	610587	+	WP_000680574.1		response regulator	15118.08905	-1573785049	0.19219618	-9.99031621	2.46E-19	6.16E-18	16.32882176
ABUW_RS1780	ABUW_2421	NZ_CP008706.1	2408441	2409301	+	WP_000476792.1		transporter substrate-binding domain-containing protein	276.337033	-1575997817	0.210072228	-7.50210719	6.28E-14	2.21E-13	12.05560773
ABUW_RS1970	ABUW_3691	NZ_CP008706.1	3710599	3715116	+	WP_000366687.1		MFS transporter	942.4083812	-1576371732	0.17897051	-8.807718895	1.28E-18	6.06E-18	17.9238271
ABUW_RS1585	ABUW_3102	NZ_CP008706.1	367016	367454	+	WP_001032021.1		hydropathic protein	1000.522334	-1576932388	0.11114555	-14.10709171	1.0E-45	2.64E-44	43.87839607
ABUW_RS0490	ABUW_3492	NZ_CP008706.1	3248451	3249266	+	WP_000919641.1	cysE	serine O-acetyltransferase	1664.256811	-1576418333	0.14709095	-9.05710593	1.60E-26	1.29E-25	24.88941292
ABUW_RS0200	ABUW_0041	NZ_CP008706.1	45999	49789	+	WP_001007146.1		MFS transporter	339.7620582	-1576939974	0.232882804	-6.771088638	1.28E-11	3.69E-11	22.93297363
ABUW_RS1445	ABUW_0294	NZ_CP008706.1	310860	3105025	+	WP_001017040.1		type IV pilus secretase PiliQ family protein	3115.449195	-1577787257	0.16114738	-9.790536446	1.23E-22	7.72E-22	11.013827
ABUW_RS0400	ABUW_2925	NZ_CP008706.1	2935728	2937359	+	WP_001018741.1		inorganic phosphate transporter	8412.527363	-1578421565	0.170556226	-9.24555268	2.16E-20	1.9E-19	5.93554201
ABUW_RS1025	ABUW_2287	NZ_CP008706.1	2251289	2253727	+	WP_000680628.1		LiP-assembly binding protein LiPd	3685.775373	-1578472244	0.200468717	-7.878893639	3.30E-15	1.27E-14	11.89619628
ABUW_RS0745	ABUW_0832	NZ_CP008706.1	1194785	1195340	+	WP_001771595.1		histidine phosphatase family protein	677.3377328	-1581669091	0.131497233	-8.805740646	1.52E-37	2.26E-36	35.64581956
ABUW_RS0995	ABUW_3820	NZ_CP008706.1	3848494	3848658	-	WP_000772194.1		polysaccharide biosynthesis protein	2519.747234	-1581850883	0.20682692	-9.10733591	2.98E-39	4.80E-38	37.31971876
ABUW_RS1870	ABUW_3288	NZ_CP008706.1	3297518	3298435	+	WP_000785635.1		mechanosensitive ion channel family protein	1004.323744	-1586101336	0.2217943	-7.188092097	7.61E-10	2.46E-10	11.605906489
ABUW_RS0160	ABUW_0383	NZ_CP008706.1	385237	385521	+	WP_000631648.1		hydropathic protein	790.3352533	-1587366851	0.20309102	-7.816033298	5.43E-15	2.07E-14	11.04822965
ABUW_RS0545	ABUW_2170	NZ_CP008706.1	2191096	2192184	+	WP_0002120208.1		3-deoxy-7-phosphoheptulonate synthase	4506.74442	-158750972	0.102196184	-11.20250562	4.78E-20	1.24E-18	37.05574651
ABUW_RS1020	ABUW_3133	NZ_CP008706.1	3106183	3106897	+	WP_000839416.1		paraoxonase kinase	373.364275	-1587742499	0.174459952	-9.08854269	9.10E-20	4.69E-19	16.32882176
ABUW_RS0995	ABUW_3494	NZ_CP008706.1	3542358	3543563	+	WP_000824664.1		TGRO3862 family flavoprotein	345.0466804	-1588100419	0.159660244	-9.948749311	2.61E-23	1.72E-22	21.76447105
ABUW_RS0120	ABUW_0309	NZ_CP008706.1	313829	313934	+	WP_001171590.1	bifunctional (p/gpCopp synthetase/lysine-3'-5'-bisphosphate)3'-pyrophosphatase	4235.696217	-158850310	0.126866173	-12.52109285	5.72E-36	7.93E-35	14.10072851	
ABUW_RS0280	ABUW_3755	NZ_CP008706.1	3810167	381875	+	WP_0002021750.1	guaA	guanine- hydrolyzing GMP synthase	12269.3814	-1589964745	0.227958808	-6.974789703	3.08E-12	9.3E-12	10.70185032
ABUW_RS0455	ABUW_0296	NZ_CP008706.1	316553	316717	+	WP_001018997.1	anB	3-hydroxyketone synthase	3338.1954343	-1590354535	0.11243371	-14.16610577	1.17E-45	4.01E-44	43.39685563
ABUW_RS0170	ABUW_2876	NZ_CP008706.1	2883001	2887019	+	WP_000808164.1	mdA	penicillin-binding protein 2	977.5536938	-1591957141	0.174030384	-9.147581822	5.82E-20	3.03E-19	15.9855737
ABUW_RS0240	ABUW_0501	NZ_CP008706.1	516419	511823	+	WP_000454860.1	hix	GTPase HIX	692.6602995	-1592900085	0.17863141	-11.5542129	7.03E-31	7.17E-30	29.1444804
ABUW_RS0485	ABUW_0098	NZ_CP008706.1	104108	102848	+	WP_000325593.1		hydropathic protein	4800.004674	-1593243089	0.187316038	-8.07466071	6.77E-16	5.74E-15	16.96224844
ABUW_RS1050	ABUW_2334	NZ_CP008706.1	2317210	2317974	+	WP_001285603.1		glutathione S-transferase	3216.157447	-1597683952	0.177323281	-9.009549434	2.07E-19	1.03E-18	17.98718772
ABUW_RS0490	ABUW_2902	NZ_CP008706.1	2919332	2916496	+	WP_000706495.1		rubredoxin	2527.60329	-1599002217	0.172683661	-9.239724451	2.05E-20	1.11E-19	18.95487728
ABUW_RS14															

ABUW_RS1445	ABUW_2918	NZ_CP008706.1	292249	2922763	-	WP_00141692.1		carbonic anhydrase	14123.8559	-1.666564845	0.170204026	-9.791671234	1226.22	7.69622	21.1407766
ABUW_RS04735	ABUW_0892	NZ_CP008706.1	887420	887896	-	WP_001982024.1	greA	transcription elongation factor GreA	4756.033008	-1.667198364	0.264774051	-6.299670818	2.98610	9.18118279	
ABUW_RS00440	ABUW_0089	NZ_CP008706.1	100589	102497	-	WP_000334179.1	gndH	glutamine--succinate--6-phosphotransferase (isomerizing)	21667.44232	-1.668894301	0.161504477	-11.0245466	3.33628	2.87627	26.242181
ABUW_RS10476	ABUW_3498	NZ_CP008706.1	354519	3546164	-	WP_000007331.1	hemH	hemolysate	9467.805789	-1.67160373	0.95567295	-15.846661	14.6556	6.91655	54.20380395
ABUW_RS0245	ABUW_3748	NZ_CP008706.1	380577	3805803	+	WP_000467262.1		SPOR domain-containing protein	2085.38825	-1.673701003	0.9479248	-11.31478835	1.16219	1.03828	27.9674878
ABUW_RS04465	ABUW_0910	NZ_CP008706.1	903722	905053	-	WP_001866541.1		MPF transporter	34513.42625	-1.674142928	0.2368761	-7.06789046	15.8612	0.44612	13.9062705
ABUW_RS00705	ABUW_0142	NZ_CP008706.1	155897	156547	+	WP_000216100.1	pyrE	uracilate phosphoribosyltransferase	1411926369	-1.674292562	0.176804882	-9.464360733	2.95621	1.69620	9.7721703
ABUW_RS01005	ABUW_0266	NZ_CP008706.1	283580	284665	+	WP_00516306.1		TolC family protein	359.0277373	-1.680589004	0.24341957	-6.904299301	5.00512	1.95111	8.0228302
ABUW_RS00990	ABUW_2280	NZ_CP008706.1	2245929	2246357	+	WP_000665684.1		bicopolymer transporter EabD	188.363632	-1.68165791	0.14347277	-11.71700183	1.04621	1.12530	29.95078198
ABUW_RS10405	ABUW_2892	NZ_CP008706.1	2898920	290167	+	WP_000956799.1		CDM85 family transporter	3737.767202	-1.682176685	0.9309288	-8.71191084	2.99618	1.40617	6.85387196
ABUW_RS0550	ABUW_3405	NZ_CP008706.1	3452403	3454100	+	WP_000978841.1	leuA	2-isopropylmalate synthase	8761898879	-1.684853161	0.215846775	-7.805784719	5.91615	2.24614	13.6497819
ABUW_RS04855	ABUW_0990	NZ_CP008706.1	1002822	1003793	-	WP_0000617970.1		class I fructose-bisphosphatase	2627.275644	-1.684919441	0.90930073	-9.91639356	3.57623	2.31622	2.163638802
ABUW_RS03416	ABUW_0693	NZ_CP008706.1	696857	698733	+			RNAse Aap	675.0332709	-1.685521806	0.341728036	-4.932348613	8.92617	1.996106	5.798602876
ABUW_RS17735	ABUW_3642	NZ_CP008706.1	3702344	3730618	-	WP_000939109.1		peptidase S41	944.851007	-1.686617139	0.147638706	-11.42394961	3.97630	3.05629	28.5167010
ABUW_RS18216	ABUW_3741	NZ_CP008706.1	3727108	3797713	+	WP_000903118.1		transcriptional repressor	660.4077478	-1.68820984	0.16975005	-10.56781076	4.20626	3.29625	24.4828041
ABUW_RS15050	ABUW_3605	NZ_CP008706.1	3663543	3664172	-	WP_000218967.1		FHA domain-containing protein	2103.96051	-1.688576972	0.1506434	-11.20925354	3.67629	3.28628	27.8441061
ABUW_RS17575	ABUW_3610	NZ_CP008706.1	3668964	3669404	-	WP_000661609.1		acyl-CoA thioesterase	414.9718217	-1.689305382	0.19851439	-8.509737663	1.74617	7.80617	6.170904
ABUW_RS00345	ABUW_0088	NZ_CP008706.1	98290	99990	+	WP_001697241.1		thioesterase--homon	3027.300806	-1.690738562	0.938693809	-8.720535662	2.77518	1.30517	9.68460561
ABUW_RS00895	ABUW_0267	NZ_CP008706.1	1247247	1248662	+	WP_000061267.1	glaA	type I glutamate--ammonia ligase	16569.5293	-1.690784943	0.226956724	-7.449812081	9.35514	3.26512	12.4881664
ABUW_RS00495	ABUW_0744	NZ_CP008706.1	1742714	1743299	+	WP_000405623.1	fabZ	3-hydroxyacyl-ACP dehydratase FabZ	8307.39051	-1.692461391	0.163797102	-10.99775663	3.93528	3.36527	26.47366072
ABUW_RS18375	ABUW_3370	NZ_CP008706.1	3416204	3416461	+	WP_000729628.1	gncX	glutaredoxin 3	4240.510412	-1.692240705	0.21672039	-7.983320398	1.42618	6.60618	14.2519197
ABUW_RS00545	ABUW_3819	NZ_CP008706.1	3884097	3884792	-	WP_000591427.1	galU	UTP--glucose-1-phosphate uridylyltransferase GalU	7977.346234	-1.694789995	0.192570557	-13.08005483	4.28639	6.85538	37.5840363
ABUW_RS01880	ABUW_0341	NZ_CP008706.1	363864	364508	-	WP_000849451.1		Park family protein	2233.847142	-1.696818523	0.263834563	-6.431073146	1.26610	3.39610	9.469800302
ABUW_RS01745	ABUW_1372	NZ_CP008706.1	187849	188834	-	WP_001814366.1		thiazine synthase	2794.19984	-1.698226048	0.146966485	-11.5551967	6.95611	7.11630	29.148104
ABUW_RS0270	ABUW_0462	NZ_CP008706.1	454626	455105	-	WP_000745523.1		YheV family putative metal-binding protein	1766.887067	-1.699263651	0.207437451	-8.1955752	2.58816	1.07619	14.9706122
ABUW_RS0100	ABUW_2242	NZ_CP008706.1	2247058	2247945	-	WP_000023429.1		Park/RagB/SpdD family partition protein	2035.152311	-1.701197813	0.147491914	-11.51091617	1.02630	1.91629	28.5050789
ABUW_RS01860	ABUW_0399	NZ_CP008706.1	425910	426689	-	WP_001254461.1		YfhA family ribosome hibernation GTP-binding protein	987.9190807	-1.702007274	0.155979431	-12.5168522	6.00636	8.34635	30.47883395
ABUW_RS10545	ABUW_0314	NZ_CP008706.1	336833	337393	+	WP_001245718.1	pilV	type IV pilus modification protein PilV	167.2063096	-1.702880912	0.304934957	-5.584407009	2.346108	5.02618	27.98399656
ABUW_RS16885	ABUW_3838	NZ_CP008706.1	3906199	3907404	+	WP_000269261.1		carboxylating nicotinate-nucleotide diphosphorylase	951.7837611	-1.703097328	0.233885919	-7.281743936	3.306119	1.81612	11.99860731
ABUW_RS00530	ABUW_0320	NZ_CP008706.1	1642206	1643033	-	WP_000344900.1	lcpB	signal peptidase	3767.850848	-1.703306064	0.14107814	-12.07080055	1.505133	1.94512	31.7351828
ABUW_RS10705	ABUW_2820	NZ_CP008706.1	2824689	2825750	-	WP_000732661.1		ribitol dehydrogenase	3284.280267	-1.704063188	0.28355969	-13.27607277	3.95409	6.42529	38.2660071
ABUW_RS18185	ABUW_0643	NZ_CP008706.1	648874	650517	+	WP_000281764.1		ribitol dehydrogenase	3884.423421	-1.710770938	0.244165141	-7.011946481	2.35512	9.111272747	
ABUW_RS10305	ABUW_2741	NZ_CP008706.1	2729880	2730587	+	WP_000203217.1	cap	cAMP-activated global transcriptional regulator CAP	8603.188988	-1.711837554	0.147652635	-11.5943583	4.40611	4.54630	29.34204416
ABUW_RS01680	ABUW_0321	NZ_CP008706.1	3414409	3414957	-	WP_000189236.1	renM	ribosome maturation factor RenM	50620.40733	-1.712351534	0.26237649	-6.526462732	6.733611	1.85510	9.732826272
ABUW_RS10450	ABUW_2160	NZ_CP008706.1	2142311	215418	-	WP_001071038.1		O-succinylhomoserine sulphydrylase	2196.104210	-1.71260226	0.123679596	-13.4670881	1.326143	1.86612	11.546066731
ABUW_RS00575	ABUW_0324	NZ_CP008706.1	1045148	1045348	-	WP_001895517.1		MG38184 family lipoprotein	1573.606957	-1.71396862	0.160718045	-8.987282005	2.533619	1.26618	17.89062645
ABUW_RS10055	ABUW_2070	NZ_CP008706.1	2001492	2001403	-	WP_000548467.1	pcqB	pyrimidoquinoline quinoxaline biosynthesis protein PqB	158.533988	-1.717823925	0.17778426	-9.662407253	4.36622	2.60621	20.58052065
ABUW_RS1030	ABUW_2268	NZ_CP008706.1	2253277	2255307	-	WP_000850091.1		pyruvate/oxaloisomerase	4427.033963	-1.718145329	0.13210946	-13.00253695	1.98138	1.83637	36.73754891
ABUW_RS08170	ABUW_0802	NZ_CP008706.1	976260	978989	+	WP_000216290.1		insulin-like family protein	10067.57102	-1.720632477	0.18008973	-13.16378014	1.62519	2.64638	37.57839607
ABUW_RS17195	ABUW_3534	NZ_CP008706.1	3592340	3595989	+	WP_000381500.1		monovalent cation/H ⁺ antiporter subunit A	6513.576647	-1.7208963	0.16208888	-10.6703703	2.48626	1.98625	24.70333441
ABUW_RS10375	ABUW_2755	NZ_CP008706.1	2744837	2746166	-	WP_000729980.1		NC23 family permease	1374.321645	-1.721043491	0.188900439	-11.913030578	8.14620	9.36767071	
ABUW_RS17725	ABUW_3640	NZ_CP008706.1	3699416	3700984	-	WP_00160337.1		PAS domain-containing sensor histidine kinase	917.5506069	-1.721884527	0.202269233	-8.512634627	1.70617	7.42617	6.11804033
ABUW_RS02580	ABUW_0525	NZ_CP008706.1	533465	534079	-	WP_000645707.1		separation protein lepZ	1089.803164	-1.72488902	0.134278195	-12.84266635	9.466138	1.62536	35.8477166
ABUW_RS00590	ABUW_1142	NZ_CP008706.1	1168889	1188985	+	WP_000380475.1		carbon starvation protein	4232.634448	-1.730193336	0.233553034	-5.347308016	8.83638	1.91607	6.71966663
ABUW_RS02725	ABUW_0165	NZ_CP008706.1	161872	161869	+	WP_000123435.1	murG	4(β-phospho-muramyl)glucosyl transferase MurG	1302.390056	-1.730193336	0.199922263	-14.42720171	3.406147	9.078146	45.4232971
ABUW_RS02055	ABUW_0418	NZ_CP008706.1	437990	438526	+	WP_00010187.1	rplE	50S ribosomal protein L5	241090.0444	-1.732012752	0.263803935	-6.565530398	5.95111	1.44610	9.841837508
ABUW_RS04260	ABUW_0868	NZ_CP008706.1	841804	8418705	+	WP_00184863.1	sdhC	succinate dehydrogenase, cytochrome b556 subunit	10014.04957	-1.733597947	0.192449438	-9.674332362	3.99622	2.34612	20.6262021
ABUW_RS07485	ABUW_1533	NZ_CP008706.1	1519763	1520032	-	WP_000186304.1		DNA-binding transcriptional regulator Fis	98.08175505	-1.734634032	0.214308008	-8.09418741	5.77616	2.39615	14.63078144
ABUW_RS18905	no	NZ_CP008706.1	287012	2870896	+		serS	6S RNA	10217.1306	-1.737739936	0.246074601	-7.061841933	1.64612	5.1012	11.89882663
	srRNA4	no	no	no	no	no	no	no	10212.8865	-1.74010849	0.246056471	-7.057646803	1.69612	6.28812	11.27736068
ABUW_RS01075	ABUW_0036	NZ_CP008706.1	44788	45165	+	WP_000529425.1		hydrothermal protein	935.8497236	-1.743624527	0.20326336	-8.573966994	1.00617	4.55617	6.1184168
ABUW_RS19740	ABUW_3685	NZ_CP008706.1	3742844	3744160	+	WP_000910004.1		OptD family outer membrane porin	6457.852532	-1.744106044	0.233362551	-7.747380047	7.79614	2.73613	12.56383735
ABUW_RS17595	ABUW_3614	NZ_CP008706.1	3672235	3673152	-	WP_001394408.1	hemC	hydroxymethylbilane synthase	1233.302183	-1.744646147	0.181663129	-9.910057337	6.64622	3.92621	20.4067193
ABUW_RS01890	ABUW_3627	NZ_CP008706.1	362187	3624456	-	WP_000078452.1	eno	phosphoenolpyruvate hydratase	24287.51993	-1.747818909	0.156175108	-11.93707802	4.38629	3.89628	27.4100004
ABUW_RS16020	ABUW_3298	NZ_CP008706.1	3329720	3331193	-	WP_001814201.1	pcrB	polynucleotide adenyltransferase PcrB	2961103673	-1.748328013	0.195817363	-9.735205768	2.10622	1.29017	20.8827287
ABUW_RS18185	ABUW_0441	NZ_CP008706.1	454483	454914	-	WP_001030889.1		polyketide synthase	651.103046	-1.751257756	0.21800958	-8.033244228	9.40616	1.37616	14.42136079
ABUW_RS11435	ABUW_2351	NZ_CP008706.1	2332270	2334933	+	WP_000611078.1	phD	[protein-P] uridylyltransferase	3323.232678	-1.753208081	0.197854053	-14.87609496	4.716150	1.465148	47.83564714
ABUW_RS02740	ABUW_0557	NZ_CP008706.1	557519	558822	-	WP_000448306.1		primase	488.2440838	-1.753909971	0.196664749	-10.33750373	4.77625	3.52624	23.3453074
ABUW_RS18705	ABUW_3436	NZ_CP008706.1	3479863	3480162</											

ABUW_RS0030	ABUW_0026	NZ_CP008706.1	29975	3804	+	WP_001113590.1	hld	dihydroxy-acyl dehydrogenase	10375.92363	-1.847377118	0.178357432	-0.35772437	3.86E-25	2.86E-24	23.54363397
ABUW_RS0320	ABUW_0675	NZ_CP008706.1	678.84	68.632	-	WP_001985939.1		efflux RND transporter permease subunit	2.85.32371	-1.848000925	0.143578866	-0.87098944	6.56E-38	9.93E-37	36.00305705
ABUW_RS1715	ABUW_3598	NZ_CP008706.1	365938	3660528	-	WP_00192960.1	tuf	elongation factor Tu	18728.8966	-1.84819302	0.22018532	-8.393958751	4.70E-17	2.05E-16	55.6882404
ABUW_RS0605	ABUW_0746	NZ_CP008706.1	174400	744884	-	WP_00171008.1		tetranucleotide repeat protein	9288.52844	-1.84865872	0.259697049	-7.180520904	1.09E-12	3.47E-11	14.9567053
ABUW_RS1905	ABUW_3275	NZ_CP008706.1	3307787	3309317	-	WP_001279275.1	ggsA	enoylphosphatase	3047.56339	-1.850500086	0.113090994	-5.25955637	19.5E-59	1.07E-57	56.5706782
ABUW_RS0655	ABUW_0352	NZ_CP008706.1	636662	656961	-	WP_000783090.1		NbD/YgrL/Ysa family stress tolerance protein	5721.84086	-1.851941969	0.30235962	-6.12866892	9.24E-10	2.33E-09	8.632644079
ABUW_RS0595	ABUW_8332	NZ_CP008706.1	834303	844095	+	WP_00080699.1	mc	rbcu succinate II	2696.93939	-1.852482024	0.81946445	-8.84556579	7.85E-23	4.57E-22	21.3403638
ABUW_RS0230	ABUW_0047	NZ_CP008706.1	54563	55523	-	WP_000857011.1		DNA-3-methyladenine glycosylase I	278.1901954	-1.85658225	0.9393887	-9.573028104	1.04E-21	6.09E-21	20.1538271
ABUW_RS0215	ABUW_0432	NZ_CP008706.1	445342	445719	+	WP_001216380.1	tpd	50S ribosomal protein L17	87978.97395	-1.859203819	0.2507572	-7.288930993	3.10E-13	1.04E-12	119.629666
ABUW_RS0205	ABUW_0408	NZ_CP008706.1	433778	434098	-	WP_001058538.1	tpW	50S ribosomal protein L23	57055.1086	-1.859470474	0.29556102	-6.29159194	3.10E-10	8.17E-10	9.087777943
ABUW_RS0600	ABUW_0229	NZ_CP008706.1	127189	1272581	+	WP_001137505.1	shA	Si-specific NAD(P)+ transhydrogenase	7469.586491	-1.860304304	0.154822445	-13.79819505	2.61E-43	5.27E-42	41.27189338
ABUW_RS1670	ABUW_1345	NZ_CP008706.1	31709.0	3171785	-	WP_001659880.1		5'-methylthioadenine S-adenosylhomocysteine nucleotidase	878.172599	-1.860963759	0.96050395	-9.517776079	1.17E-21	1.03E-20	9.98716278
ABUW_RS0835	ABUW_646	NZ_CP008706.1	1640874	1643144	-	WP_00052708.1		TonB-dependent receptor	2039.817431	-1.869968032	0.376290331	-4.96848202	6.17E-07	1.32E-06	5.879420069
ABUW_RS1485	ABUW_3061	NZ_CP008706.1	3087565	3089703	-	WP_00110824.1	fusA	elongation factor G	481659.9235	-1.871972289	0.248952732	-7.51898673	5.52E-14	1.95E-13	12.70996539
ABUW_RS0900	ABUW_0182	NZ_CP008706.1	200589	204086	-	WP_001089740.1		hybrid sensor histidine kinase/response regulator	9255.530751	-1.872387239	0.141892037	-7.51898673	9.27E-10	1.52E-08	37.81815641
ABUW_RS0570	ABUW_8333	NZ_CP008706.1	104487	1045129	-	WP_00198558.1	ena	GTPase Ena	7341.334810	-1.874645568	0.619429327	-11.40994066	3.73E-30	3.57E-29	28.44733178
ABUW_RS0350	ABUW_0786	NZ_CP008706.1	768298	768828	+	WP_000443392.1		hypothetical protein	384.7616428	-1.874873117	0.258501015	-7.25203847	4.10E-10	1.35E-12	11.86966623
ABUW_RS0420	ABUW_3054	NZ_CP008706.1	3008082	3018719	+	WP_001278144.1	tsbB	thioredoxin disulfide reductase	5187.262095	-1.876840971	0.75326263	-13.70484788	9.66E-27	7.81E-26	25.9734597
ABUW_RS0965	ABUW_2255	NZ_CP008706.1	2241076	2241917	-	WP_001913027.1		PLZ domain-containing protein	353.9904428	-1.877584201	0.176370477	-10.64456831	1.83E-36	1.46E-25	24.3366474
ABUW_RS0430	ABUW_0000	NZ_CP008706.1	2241076	2241917	-	WP_001913027.1		PLZ domain-containing protein	6.596721655	-1.879302357	0.666194746	-2.89532712	0.004093962	0.00717794	2.179192029
ABUW_RS1620	ABUW_0745	NZ_CP008706.1	3800074	3800994	+	WP_000126887.1		Dhp-type peroxidase	2600.19644	-1.879304687	0.123388905	-0.23073927	2.21E-52	7.88E-51	50.10347378
ABUW_RS0470	ABUW_4087	NZ_CP008706.1	53507	54286	+	WP_000422638.1		APH(3)-Y family aminoglycoside O-phosphotransferase	1897.59792	-1.880795272	0.158442598	-11.87051624	1.68E-32	1.68E-31	30.719287
ABUW_RS1610	ABUW_3377	NZ_CP008706.1	3416547	3417662	+	WP_000572095.1	hspG	-dependent (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate	5804.401256	-1.88159191	0.91889215	-11.40268478	7.96E-29	7.02E-28	27.5368289
ABUW_RS0287	ABUW_0287	NZ_CP008706.1	305929	306261	+	WP_000198598.1		hypothetical protein	874.7885375	-1.884597071	0.12706442	-13.8182367	9.19E-50	2.72E-48	47.5654311
ABUW_RS1615	ABUW_3124	NZ_CP008706.1	3189533	3189744	-	WP_001024267.1		signal transduction family 4 protein	10364.74478	-1.885351772	0.18212403	-11.6278197	2.93E-31	3.06E-30	29.15427857
ABUW_RS1625	ABUW_3084	NZ_CP008706.1	3189533	3189744	-	WP_001024267.1	flh	glycyl-recognition pattern protein	6817.362227	-1.88929195	0.90218544	-11.81493339	3.28E-32	3.72E-31	30.42947058
ABUW_RS0295	ABUW_0426	NZ_CP008706.1	414333	424652	+	WP_002000592.1	secY	proteolipid translocase subunit SecY	174538.7486	-1.890487209	0.249705446	-7.99809259	3.18E-14	1.66E-13	40.3430915
ABUW_RS1610	ABUW_3028	NZ_CP008706.1	3199984	3194264	-	WP_001031442.1	bioA	adenosylmethionine-S-adenosyl-L-homocysteine transaminase	3760.010881	-1.896073804	0.82645894	-11.6420258	2.52E-31	2.66E-30	29.57191836
ABUW_RS0410	ABUW_0841	NZ_CP008706.1	818977	819337	-	WP_000927245.1		YnfJ family protein	176.2087859	-1.896958436	0.1648763	-9.654340276	4.17E-22	2.80E-21	20.5528197
ABUW_RS0575	ABUW_3634	NZ_CP008706.1	3754422	3754422	-	WP_000575778.1		Tec family protein	8412.66628	-1.900206303	0.153718453	-12.36101978	3.22E-35	5.64E-34	33.2487209
ABUW_RS0555	ABUW_3606	NZ_CP008706.1	3664210	3666489	-	WP_001984624.1	gspD	type 3 secretion system secretin GspD	4746.349102	-1.90162246	0.50559068	-0.6294027	1.51E-36	2.14E-35	34.69369263
ABUW_RS0535	ABUW_0714	NZ_CP008706.1	720871	721165	-	WP_000167699.1	galC	Agp-IRNA(hen)/Glu-IRNA(Gln) amidotransferase subunit GalC	1794.461968	-1.907445192	0.816225719	-11.47930136	1.75E-30	28.76447185	
ABUW_RS1770	ABUW_3635	NZ_CP008706.1	3693846	3694861	+	WP_00011968.1		DnaC family protein	2029.563285	-1.910418781	0.151644723	-12.99799051	2.17E-36	3.05E-35	34.1571018
ABUW_RS1710	ABUW_3589	NZ_CP008706.1	3646995	365188	-	WP_000653927.1	tpoC	DNA-directed RNA polymerase subunit beta'	93338.8346	-1.91889197	0.19102293	-9.994074634	1.62E-23	1.09E-22	21.9429735
ABUW_RS1670	ABUW_3369	NZ_CP008706.1	3409776	3410192	+	WP_000443306.1		rhodanese-like domain-containing protein	6029.58995	-1.919294784	0.95506994	-13.84431468	1.13E-22	8.22E-22	21.08544318
ABUW_RS0735	ABUW_0444	NZ_CP008706.1	513044	513194	-	WP_001024173.1	alr	alanine racemase	578.361621	-1.91980232	0.166840273	-13.03413659	7.79E-39	1.23E-37	36.1900489
ABUW_RS0210	ABUW_0444	NZ_CP008706.1	4573564	459781	-	WP_000195350.1	nrp	rbcu succinate I	5030.403583	-1.919451975	0.19405643	-7.347720779	2.32E-67	2.03E-66	64.89250396
ABUW_RS0380	ABUW_0782	NZ_CP008706.1	768103	767983	+	WP_000502910.1		hypothetical protein	375.4588938	-1.918409972	0.280577534	-11.64230621	8.82E-12	2.59E-11	10.58670204
ABUW_RS1780	ABUW_3651	NZ_CP008706.1	3710256	3710548	+	WP_001083669.1		DNA adenine methylase	2614.930892	-1.91618757	0.82246994	-11.80403229	3.72E-32	4.19E-31	30.73771698
ABUW_RS0675	ABUW_0448	NZ_CP008706.1	510505	510604	-	WP_000718711.1		methionine-NADP reductase	210.862495	-1.919974616	0.191511869	-10.04450588	1.46E-23	9.86E-23	22.00612903
ABUW_RS0240	ABUW_0049	NZ_CP008706.1	504549	505545	-	WP_0010252461.1		M23 family metallopeptidase	381129.0773	-1.920604439	0.86822856	-9.28035051	6.84E-25	6.30E-24	23.20063945
ABUW_RS0255	ABUW_0052	NZ_CP008706.1	51778	58452	-	WP_000190767.1		denitrification hydrogenase family protein	902.252445	-1.92117051	0.25938409	-7.40640563	1.30E-10	1.44E-12	12.3626103
ABUW_RS1675	ABUW_3042	NZ_CP008706.1	308959	3089211	-	WP_00068192.1	dut	dUTP diphosphatase	803.3596108	-1.927187992	0.174187991	-11.06495922	1.85E-28	1.62E-27	26.7044949
ABUW_RS0980	ABUW_3270	NZ_CP008706.1	3301387	3304158	+	WP_001934663.1	pskA	DNA polymerase I	4660.07195	-1.932285677	0.093064039	-20.76294378	9.36E-96	3.16E-93	92.5030750
ABUW_RS1930	ABUW_2319	NZ_CP008706.1	2304119	2304616	-	WP_00191759.1		PAACE efflux transporter	486.7408237	-1.93375610	0.533937511	-3.632189976	0.000453649	0.000435796	3.343375786
ABUW_RS0045	ABUW_0090	NZ_CP008706.1	102519	103174	-	WP_000188585.1	hglU	tylglycosamine diphosphorylase/glycosamine-1-phosphate N	1918.48632	-1.937218064	0.178850742	-10.83147367	2.44E-27	2.00E-26	25.68897
ABUW_RS1045	ABUW_2088	NZ_CP008706.1	2048444	2049728	-	WP_001931963.1	pqqD	tylglycosamine diphosphorylase/glycosamine-1-phosphate N	314.5377947	-1.94085936	0.84418537	-12.52038763	6.96E-26	5.40E-25	24.2670624
ABUW_RS1605	ABUW_0382	NZ_CP008706.1	388820	388930	-	WP_000177818.1		acetyltransferase	914.793257	-1.941938421	0.129804735	-11.96049902	1.33E-24	4.22E-49	48.3748755
ABUW_RS0435	ABUW_0636	NZ_CP008706.1	819329	819385	-	WP_000179363.1		DOMON-like domain-containing protein	886.3264542	-1.942186092	0.171667286	-11.13120693	1.01E-29	1.04E-28	27.9829666
ABUW_RS0180	ABUW_0642	NZ_CP008706.1	646302	648707	+	WP_001075596.1		glucose/succinate family membrane-bound PQOQ-dependent dehydratase	3845.73592	-1.943597992	0.17361009	-10.37353461	3.27E-25	2.45E-24	28.0293922
ABUW_RS0445	ABUW_0734	NZ_CP008706.1	1731685	1732028	+	WP_000856681.1	rnoD	30S ribosomal protein S2 methyltransferase RnoD	3784.765729	-1.945962584	0.154664659	-11.47140252	7.37E-29	6.5E-28	27.9641901
ABUW_RS1765	ABUW_3528	NZ_CP008706.1	3584433	3585101	+	WP_000268703.1		hypothetical protein	2248.580894	-1.947227679	0.176864425	-11.00971934	3.43E-28	2.95E-27	26.5307788
ABUW_RS1760	ABUW_0647	NZ_CP008706.1	3709062	3709469	+	WP_001151590.1		DNA polymerase beta subunit chi	108.43168	-1.952104422	0.11073627	-10.80837761	2.27E-43	4.59E-42	41.31387191
ABUW_RS0945	ABUW_0386	NZ_CP008706.1	818464	818433	-	WP_000108717.1		valine-IRNA ligase	17885.59965	-1.958312463	0.93061024	-10.16437369	3.54E-24	2.49E-23	22.60380055
ABUW_RS1780	ABUW_3684	NZ_CP008706.1	3723775	3724271	+	WP_000041581.1		cation transporter	432.966502	-1.960209332	0.320403737	-6.119935301	9.48E-10	2.38E-09	18.23243043
ABUW_RS1705	ABUW_3636	NZ_CP008706.1	3694906	3696207	+	WP_000805827.1		homoserine dehydrogenase	5102.586541	-1.96210345	0.225207922	-8.7245348	2.97E-18	1.39E-17	9.5618552
ABUW_RS0570	ABUW_0116	NZ_CP008706.1	127874	128339	+	WP_001240041.1		disulfide bond formation protein B	864.3054077	-1.964123081	0.17364888	-11.37666004	5.46E-30	5.86E-29	28.28439264
ABUW_RS0320	ABUW_0614	NZ_CP008706.1	619333	619511	-	WP_00050									

ABUW_RS1620	ABUW_2389	NZ_CP008706.1	237752	2378957	+	WP_00052002.1		cytochrome oxidase subunit I	2322.982851	-2.054747543	0.397058558	-5.174923203	2.285-07	4.71E-07	6.326979093
ABUW_RS0935	ABUW_089	NZ_CP008706.1	210987	21821	-	WP_00008335.1	uvrA	excinuclease ABC subunit UvrA	2759.199504	-2.050460691	0.22508558	-9.129541336	6.88E-20	3.57E-19	9.447378178
ABUW_RS0230	ABUW_0472	NZ_CP008706.1	483782	44845	+	WP_00010209.1	psaA	CDP-diacylglycerol- serine O-phosphatidyltransferase	1061441059	-2.057836873	0.10286849	-15.57942282	1.00E-54	4.01E-53	52.36985631
ABUW_RS0240	ABUW_0431	NZ_CP008706.1	44439	44533	+	WP_00019663.1	tpoA	DNA-directed RNA polymerase subunit alpha	3172918397	-2.058633451	0.284725853	-7.230230157	4.82E-13	1.59E-12	117.9680288
ABUW_RS1785	ABUW_824	NZ_CP008706.1	918883	920371	-	WP_00128453.1		hyothetical protein	6328.236387	-2.06026182	0.92973878	-12.6416896	1.24E-36	1.78E-35	34.74958
ABUW_RS1070	ABUW_3509	NZ_CP008706.1	3555321	3559592	-	WP_00086530.1	gspG	type I secretion system major pseudopilin GspG	1642.303607	-2.055465438	0.146374235	-14.0834514	4.80E-45	1.07E-43	47.7670822
ABUW_RS1025	ABUW_2102	NZ_CP008706.1	3185396	316148	+	WP_00032587.1		biotin- [acetyl-CoA: carboxylase] ligase	1029.429257	-2.062239496	0.12803507	-15.52859181	2.23E-54	8.46E-53	52.0726964
ABUW_RS03475	ABUW_0706	NZ_CP008706.1	71193	71028	-	WP_00061959.1		theonine ammonia- lyase	1504.432457	-2.064475269	0.13743484	-15.034781	4.57E-51	1.47E-49	48.83268267
ABUW_RS0605	ABUW_2182	NZ_CP008706.1	21831	2165479	-	WP_00041099.1		TbRn-dependent receptor	7183.270963	-2.065304727	0.340031615	-6.073860891	1.25E-09	3.10E-09	8.506838306
ABUW_RS0450	ABUW_0295	NZ_CP008706.1	315037	31606	+	WP_000643712.1	acK	shikimate kinase AcK	1559.021592	-2.065955232	0.13491161	-15.1338127	6.22E-53	2.26E-51	50.6489106
ABUW_RS17385	ABUW_3572	NZ_CP008706.1	3629909	3632602	+	WP_000858042.1	fadB	fatty acid oxidation complex subunit alpha FadB	10697.51077	-2.068863817	0.283728993	-7.291689857	3.00E-13	1.02E-12	119.1392983
ABUW_RS04795	ABUW_0978	NZ_CP008706.1	990156	991172	+	WP_001286615.1	sppA	signal peptide peptidase SppA	5972.536788	-2.06972429	0.17383934	-11.9234784	8.93E-33	1.04E-31	30.98296666
ABUW_RS10345	ABUW_2749	NZ_CP008706.1	2744005	2741295	+	WP_001815176.1		aspartate kinase	6566.554875	-2.072241024	0.231456875	-8.953033361	3.46E-19	1.7E-18	17.76700389
ABUW_RS05135	ABUW_0446	NZ_CP008706.1	1053802	1054593	-	WP_000222202.1		hyothetical protein	1886.800247	-2.073549193	0.258736385	-8.01408215	1.19E-15	4.42E-15	14.35457773
ABUW_RS8325	ABUW_3764	NZ_CP008706.1	3817685	3817760	+			tRNA- Gly	465.062382	-2.078419643	0.363684157	-5.714902899	1.10E-08	8.25E-08	7.589599449
ABUW_RS10575	ABUW_2379	NZ_CP008706.1	2366107	2366988	-	WP_001095252.1	tauD	taurine diacylglycerol	573.8570798	-2.080878967	0.233112224	-8.92651071	4.40E-19	2.16E-18	17.66554265
ABUW_RS07880	ABUW_1614	NZ_CP008706.1	807409	8071918	-	WP_000059660.1		peptidyl- prolyl cis- trans isomerase	19065.265	-2.081099018	0.220381589	-9.44588443	3.52E-21	2.01E-20	9.69680394
ABUW_RS01720	ABUW_0445	NZ_CP008706.1	15330	15334	+	WP_001254941.1	gabB	glutathione synthase	1141205665	-2.08107598	0.93554069	-12.7274478	4.15E-37	6.04E-36	52.31896306
ABUW_RS01355	ABUW_0682	NZ_CP008706.1	687035	69055	-	WP_000658992.1		Hsp domain- containing protein	6581.191979	-2.084775689	0.202988652	-10.2704181	9.58E-25	9.95E-24	23.1580152
ABUW_RS01005	ABUW_0246	NZ_CP008706.1	262407	263108	-	WP_000955638.1	haaA	5-[[5-phosphoribosylamino]methyl]furanamido]imidazole-4- c	3207.41821	-2.085231207	0.177492365	-11.74825023	7.21E-32	7.85E-31	30.1510034
ABUW_RS04045	ABUW_0092	NZ_CP008706.1	104384	105301	-	WP_000807403.1	thlA	thiamine- phosphate kinase	5439.594303	-2.089542876	0.18572192	-14.04714531	8.02E-45	1.77E-43	47.5202073
ABUW_RS03440	ABUW_0699	NZ_CP008706.1	70299	703494	-	WP_000125649.1		Sdp1 family protein	3866.894541	-2.096147066	0.100727229	-15.03451467	7.34E-58	6.65E-56	55.43770714
ABUW_RS00710	ABUW_1275	NZ_CP008706.1	1589336	1590202	-	WP_001285359.1	rgpH	RNA polymerase sigma factor RgpH	4537.974002	-2.10288451	0.16184331	-13.46543396	2.48E-41	4.51E-40	39.34982346
ABUW_RS10985	ABUW_2349	NZ_CP008706.1	224405	2245932	-	WP_001870729.1	mbaA	Ispid A export permease/ATP-binding protein MbaA	5249.734235	-2.110321787	0.14010426	-15.06609231	2.71E-51	0.99E-50	49.04343612
ABUW_RS10095	ABUW_2903	NZ_CP008706.1	2915889	2919170	-	WP_000553407.1		FAD-dependent oxidoreductase	1451188933	-2.111728895	0.99760602	-15.07529823	4.05E-26	3.19E-25	24.49620392
ABUW_RS04665	ABUW_1157	NZ_CP008706.1	1137873	1139127	+	WP_000167954.1	psfA	phosphate ABC transporter permease PsfA	538.9252746	-2.11006748	0.240740833	-8.77733878	16.7E-18	7.95E-18	17.09963287
ABUW_RS101510	ABUW_0307	NZ_CP008706.1	330921	331115	-	WP_000289091.1		bacterioferritin-associated ferredoxin	600.6857499	-2.114781978	0.732432842	-2.887248992	0.003886266	0.0054901	2.260419745
ABUW_RS04505	ABUW_0918	NZ_CP008706.1	925335	925169	+	WP_001274623.1	groL	chaperonin GroEL	52679.22472	-2.11480564	0.300488886	-7.03783056	1.95E-12	6.06E-12	112.9715738
ABUW_RS16665	ABUW_0834	NZ_CP008706.1	3902322	3903404	+	WP_000304043.1		FKBP- type peptidyl- prolyl cis- trans isomerase	3588.460895	-2.116782447	0.132463444	-15.87871721	8.90E-57	4.33E-55	54.349646495
ABUW_RS01665	ABUW_0104	NZ_CP008706.1	196378	194708	+	WP_000558427.1		acylhydropyrimidinone- containing protein	912.025264	-2.118416771	0.118423578	-18.67704033	7.61E-78	1.02E-75	74.91008489
ABUW_RS01690	ABUW_0220	NZ_CP008706.1	1274740	1259674	-	WP_000342684.1		NADP-dependent malic enzyme	28718.8283	-2.115685907	0.578783717	-13.42567526	4.26E-41	7.60E-40	39.1918641
ABUW_RS11440	ABUW_2352	NZ_CP008706.1	2334959	2339108	+	WP_001091103.1	dapC	succinylglutamate-glyoxylate transaminase	1670.854349	-2.12164163	0.118877914	-8.63084117	18.1E-17	2.80E-15	74.55284197
ABUW_RS18195	ABUW_3738	NZ_CP008706.1	3794701	3795578	-	WP_000718586.1	atpB	RF1/ATP synthase subunit A	81915.89338	-2.125947233	0.273170086	-7.780322942	7.24E-15	2.72E-14	91.5643111
ABUW_RS0340	ABUW_3363	NZ_CP008706.1	3342621	3344015	+	WP_000159505.1		MacB family efflux pump subunit	826.447942	-2.10085603	0.210797443	-10.9053827	5.06E-24	3.53E-23	22.45272529
ABUW_RS11625	ABUW_2370	NZ_CP008706.1	2378950	2379951	-	WP_000556431.1	cydB	cytochrome b ubiquinol oxidase subunit I	14.18.1735	-2.108728895	0.434574303	-4.197183492	8.78E-07	1.78E-06	5.76730091
ABUW_RS00235	ABUW_0248	NZ_CP008706.1	55154	55391	-	WP_001287365.1		hyothetical protein	398.987744	-2.119616275	0.162846926	-13.99844494	1.59E-44	3.45E-43	42.4621809
ABUW_RS01005	ABUW_0043	NZ_CP008706.1	227864	229166	+	WP_000369688.1	gabT	4- aminobutyrate- 2- oxoglutarate transaminase	19102.526494	-2.144404196	0.364843095	-5.875996073	4.20E-09	9.95E-09	8.002170919
ABUW_RS10110	ABUW_3617	NZ_CP008706.1	3675184	3676617	+	WP_000210742.1	argH	argininosuccinate lyase	9382.286841	-2.154730508	0.159373704	-15.85004747	1.38E-56	6.19E-55	54.20830395
ABUW_RS01605	ABUW_0975	NZ_CP008706.1	979269	980039	+	WP_000897602.1	adeB	multidrug efflux ABC transporter permease subunit AdeB	5514.271404	-2.167384053	0.292762186	-7.369066628	1.72E-13	5.84E-13	62.233871
ABUW_RS8330	ABUW_0765	NZ_CP008706.1	387806	3817881	+			tRNA- Gly	462.2082828	-2.168945401	0.35892311	-6.190653785	1.80E-09	4.40E-09	6.356547324
ABUW_RS03465	ABUW_3740	NZ_CP008706.1	709880	710455	+	WP_00100537.1		alanine: cation symporter family protein	7592.184518	-2.169375293	0.259240729	-8.329614346	8.11E-17	3.48E-16	15.84062609
ABUW_RS1785	ABUW_3858	NZ_CP008706.1	3925954	3926574	+	WP_00186827.1		TetR/RsaR family transcriptional regulator	386.9665303	-2.183565683	0.58268994	-13.67047077	1.52E-42	1.94E-41	45.75185267
ABUW_RS10515	ABUW_14913	NZ_CP008706.1	14913	150261	-	WP_001917255.1	dacC	D- alanine- D- alanine carboxypeptidase PBP5/6	2881057605	-2.16571186	0.98702603	-11.47684182	1.72E-30	2.96E-29	28.7231963
ABUW_RS11075	ABUW_2277	NZ_CP008706.1	2262827	2263489	+	WP_000889099.1	satT	antimethanogenic transporter SatT	4686.714791	-2.169174609	0.92102834	-11.89974113	1.47E-29	1.35E-28	27.89666623
ABUW_RS16445	ABUW_3424	NZ_CP008706.1	3476646	3471650	-	WP_000885431.1		hemolysin transporter HsdD	2704.455038	-2.175189368	0.191873841	-7.2372255	5.48E-13	1.80E-12	17.414472749
ABUW_RS04470	ABUW_0739	NZ_CP008706.1	973631	973727	+	WP_000164643.1		1-deoxy- D- xylulose- 5- phosphate reductoisomerase	5527.04313	-2.179503088	0.165959307	-13.1616977	1.46E-39	2.39E-38	37.6216021
ABUW_RS17205	ABUW_3536	NZ_CP008706.1	3595554	3597365	+	WP_000458267.1		monovalent cation/antiporter subunit F	2672.923597	-2.180110493	0.224736172	-10.705757361	2.99E-22	1.82E-21	20.73992861
ABUW_RS04901	ABUW_1022	NZ_CP008706.1	1144531	1145919	-	WP_000093084.1	purH	adenylyltransferase	9530.797367	-2.180363536	0.153262188	-14.22636311	6.29E-46	1.64E-44	43.10471928
ABUW_RS02605	ABUW_0530	NZ_CP008706.1	530995	530900	-	WP_001985897.1	secF	protein translocase subunit SecF	1216133325	-2.185236977	0.207565861	-10.52935457	6.39E-26	4.97E-25	24.30384361
ABUW_RS01500	ABUW_0161	NZ_CP008706.1	10233	103547	-	WP_000007455.1	picB	nicotinate phosphoribosyltransferase	1536.045133	-2.187481878	0.18727147	-14.78002016	5.73E-49	1.62E-47	46.79044949
ABUW_RS01825	ABUW_0025	NZ_CP008706.1	28664	28626	-	WP_000691200.1	fnt	methylgly- RNA formyltransferase	1885.21028	-2.188374666	0.12092195	-17.92358608	7.67E-72	9.09E-70	69.0414734
ABUW_RS01166	ABUW_0430	NZ_CP008706.1	443672	444298	+	WP_00151204.1	rgpD	30S ribosomal protein S4	143627.8745	-2.189274371	0.272423366	-8.036294392	9.26E-16	3.7E-15	14.03460609
ABUW_RS1490	ABUW_3383	NZ_CP008706.1	3344980	3343560	+	WP_000034283.1	eda	isocy- 2- oxoglutarate aldolase/2- dehydro- 3- deoxy- phosphog	3031339621	-2.202839227	0.293768057	-9.187375727	4.03E-20	2.12E-19	87.3676414
ABUW_RS10900	ABUW_2242	NZ_CP008706.1	2230839	2232512	-	WP_000140309.1	rgpA	30S ribosomal protein S1	206336.9575	-2.209749194	0.16195487	-13.64397679	2.91E-42	4.17E-41	403.78693935
ABUW_RS11726	ABUW_3538	NZ_CP008706.1	3597892	3598187	+	WP_00154076.1		monovalent cation/antiporter subunit F	211.7020229	-2.211474884	0.314689819	-7.027475175	2.10E-12	6.52E-12	11.857524
ABUW_RS10275	ABUW_0282	NZ_CP008706.1	104303	1054057	+	WP_000104537.1		hyothetical protein	20517186042	-2.216324038	0.241932949	-9.176515328	4.44E-20	2.36E-19	82.07088
ABUW_RS04405	ABUW_0888	NZ_CP008706.1	894403	895953	+	WP_000335573.1	tniE	23S rRNA [inter(25S)] 2'- O- methyltransferase RniE	23062.03341	-2.218435325	0.221867462	-9.980089512	1.86E-23	1.25E-22	2.1903

ABUW_RS02090	ABUW_0425	NZ_CP008706.1	440847	442827	+	WP_000175340.1	tpiO	50S ribosomal protein L15	81988.17951	-2.34756918	0.264771853	-8.866391634	7.56E-10	3.65E-18	17.43770714
ABUW_RS14880	ABUW_3066	NZ_CP008706.1	3093957	3094409	-	WP_000330889.1	hemJ	protoporphyrinogen oxidase HemJ	5813.89055	-2.34862262	0.8880049	-1.90939849	5.55E-44	1.17E-42	419318114
ABUW_RS16655	ABUW_3236	NZ_CP008706.1	3471715	3472401	-	WP_000083586.1		energy transducer TonB	561220189	-2.351932604	0.428385879	-5.489285988	0.04E-08	8.81E-08	7.055024092
ABUW_RS00420	ABUW_0299	NZ_CP008706.1	307165	309661	-	WP_000373662.1	penA	penicillin-binding protein PBP1a	4182247066	-2.3549477	0.82437674	-8.33570084	4.29E-75	6.41E-73	72193187
ABUW_RS04505	ABUW_1735	NZ_CP008706.1	1737080	1737808	-	WP_000852257.1	pyrH	UMP kinase	6480.819324	-2.363597655	0.87283726	-14.0527433	2.51E-45	5.67E-44	43.24641934
ABUW_RS16116	ABUW_2387	NZ_CP008706.1	2376640	2376858	-	WP_000479320.1		hypothetical protein	610.4546051	-2.380891768	0.30064269	-6.78779805	1.16E-11	3.32E-11	10.7681922
ABUW_RS04255	ABUW_0867	NZ_CP008706.1	846075	847349	-	WP_001281579.1	gltA	citrate (5S)- synthase	34759.78554	-2.380883497	0.228565955	-10.41618047	2.09E-25	1.59E-24	23.7960289
ABUW_RS06665	ABUW_1846	NZ_CP008706.1	1380477	1382723	-	WP_000082052.1	bfunctional	phenylate dehydrogenase3-phosphohikimate 1-carboxyl	4200.558492	-2.383520916	0.16527410	-10.04674097	3.63E-51	1.20E-49	48.9281875
ABUW_RS18805	ABUW_3862	NZ_CP008706.1	3929661	3932498	-	WP_001230461.1	leS	isoleucine - tRNA ligase	2146164893	-2.388714347	0.15148262	-10.77581195	4.56E-56	1.94E-54	53.7121827
ABUW_RS00740	ABUW_0149	NZ_CP008706.1	164096	164900	-	WP_000057904.1		cell division protein FtsQ/Dvb	2277.398777	-2.393107039	0.164588533	-10.48050991	4.69E-54	1.75E-52	51.75696195
ABUW_RS14850	ABUW_3060	NZ_CP008706.1	3086280	3087470	-	WP_001022961.1	tuf	elongation factor Tu	23118.7247	-2.393303479	0.211458614	-11.31807038	1.07E-29	9.94E-29	28.00261362
ABUW_RS16216	ABUW_3742	NZ_CP008706.1	3797868	3798474	-	WP_001102011	znuC	zinc ABC transporter ATP-binding protein ZnuC	1034.710048	-2.397489355	0.15419482	-10.55650167	1.44E-54	5.62E-53	52.2502368
ABUW_RS01555	ABUW_0316	NZ_CP008706.1	333832	339210	+	WP_000149374.1		hypothetical protein	436.9271852	-2.397971382	0.238444684	-10.05671864	8.58E-24	5.87E-23	22.230519
ABUW_RS1185	ABUW_2299	NZ_CP008706.1	2286699	2286259	-	WP_001500731.1		FxaA family protein	8654.927459	-2.401188762	0.33716162	-17.02644265	1.05E-12	3.35E-12	11.4749519
ABUW_RS02585	ABUW_0526	NZ_CP008706.1	534124	534975	-	WP_001161539.1		PHP domain-containing protein	683.8062704	-2.40390049	0.84518802	-10.05797944	5.72E-39	9.16E-38	37.04048162
ABUW_RS02030	ABUW_0410	NZ_CP008706.1	436322	436735	-	WP_000941215.1	rgpP	50S ribosomal protein L16	147895.373	-2.412346192	0.315036988	-17.600865525	2.00E-14	7.31E-14	10.860262
ABUW_RS04465	ABUW_0992	NZ_CP008706.1	1004219	1004782	-	WP_000836019.1	pal	peptidoglycan-associated lipoprotein Pal	5270.859591	-2.423129103	0.205819872	-11.76853353	5.67E-32	6.21E-31	30.2069084
ABUW_RS01795	ABUW_0366	NZ_CP008706.1	387343	389412	-	WP_000333906.1		glycine - tRNA ligase subunit beta	16029.34371	-2.427420963	0.24190378	-10.03465542	1.07E-23	7.32E-23	22.0548692
ABUW_RS16900	ABUW_3821	NZ_CP008706.1	3877000	3888175	-	WP_000393528.1		DegT/DmT/ErpC/DmS aminotransferase family protein	16058.69027	-2.434079422	0.52326427	-10.9739364	1.78E-57	8.43E-56	55.07417243
ABUW_RS17740	ABUW_3643	NZ_CP008706.1	3706334	3705181	-	WP_000128741.1		2,3-bisphosphoglycerate-independent phosphoglycerate mu	7635.6300303	-2.4346061	0.823675747	-10.32788609	1.59E-40	2.76E-39	38.55909902
ABUW_RS00048	ABUW_0097	NZ_CP008706.1	109890	110203	-	WP_001020799.1	serB	phosphoserine phosphatase SerB	3787.788393	-2.436546988	0.138228752	-17.82691862	1.53E-49	1.47E-47	66.83266667
ABUW_RS15005	ABUW_3235	NZ_CP008706.1	3327534	3328382	-	WP_000843362.1		panotase - beta-alanine ligase	2548.367278	-2.437801973	0.809095909	-14.46375256	4.08E-47	1.04E-45	44.98296066
ABUW_RS00710	ABUW_0143	NZ_CP008706.1	156596	158717	-	WP_001919818.1		TonB-dependent siderophore receptor	6489.028059	-2.4422177839	0.281638262	-6.405910368	1.49E-10	3.97E-10	9.401200493
ABUW_RS02625	ABUW_0711	NZ_CP008706.1	1769324	1769871	-	WP_001062813.1	phb	1-phosphotriphosphatase	739.5559454	-2.448347878	0.82020959	-11.44803695	3.18E-41	5.7E-40	29.24330389
ABUW_RS01910	ABUW_0267	NZ_CP008706.1	264668	266185	-	WP_001275655.1		efflux RND transporter periplasmic adaptor subunit	447.2181927	-2.449746284	0.17258802	-14.8843032	1.08E-45	2.61E-44	43.98335949
ABUW_RS11755	ABUW_3646	NZ_CP008706.1	3707621	3709069	-	WP_000734449.1		leucyl aminopeptidase	7421.1864813	-2.450346727	0.20981816	-10.85187803	2.86E-79	4.80E-77	763.18719876
ABUW_RS18170	ABUW_3733	NZ_CP008706.1	3790775	3791644	-	WP_001028497.1	atpG	FGF1ATP synthase subunit gamma	55467.57216	-2.452523389	0.269358707	-19.05045887	8.82E-20	4.44E-19	81.36261703
ABUW_RS01550	ABUW_0316	NZ_CP008706.1	337334	338395	-	WP_000079197.1		PWW family protein	353.5546306	-2.454862436	0.2652169	-10.20500085	2.14E-20	1.95E-20	19.93554201
ABUW_RS04210	ABUW_0491	NZ_CP008706.1	503901	504329	-	WP_000003709.1		CtpAp protease specificity-enhancing factor	1606.450897	-2.45875673	0.242073888	-10.6750056	3.08E-24	2.9E-23	22.66647831
ABUW_RS01345	ABUW_0894	NZ_CP008706.1	129297	1292358	-	WP_000164454.1	carA	l-lysine-hydroxylating carbamoyl-phosphate synthase small sub	8564.727879	-2.462064657	0.265235585	-10.24781461	2.29E-20	1.24E-19	90.0557431
ABUW_RS02010	ABUW_0163	NZ_CP008706.1	161909	162946	-	WP_000198070.1	gltM	phosphoglucoamase mutase	6879.826009	-2.464636069	0.29159625	-10.0800505	3.18E-81	6.40E-79	78.9382003
ABUW_RS16116	ABUW_3064	NZ_CP008706.1	3033233	3033305	+	WP_00136002.1		peptidylglyoxylase	3875.619133	-2.46545889	0.10633035	-21.32123723	7.21E-101	4.45E-98	97.318919
ABUW_RS18463	ABUW_2809	NZ_CP008706.1	2808896	2809255	-	WP_000416092.1		hypothetical protein	604.2196602	-2.466510603	0.184476881	-10.37030737	9.02E-41	1.07E-39	38.80410035
ABUW_RS02215	ABUW_0471	NZ_CP008706.1	482883	483740	-	WP_001101438.1		23S rRNA (adenine(2050)-N(6))-methyltransferase RsmJ	2941526604	-2.466751909	0.129468373	-10.05295510	6.21E-81	1.96E-78	77.62240804
ABUW_RS01750	ABUW_0236	NZ_CP008706.1	151239	152532	-	WP_000758190.1		hypothetical protein	9307.759059	-2.466843748	0.403137855	-6.119105674	9.41E-10	2.36E-09	14.443887997
ABUW_RS04275	ABUW_0871	NZ_CP008706.1	859033	851643	-	WP_000086385.1		succinate dehydrogenase iron-sulfur subunit	20701.68453	-2.467193197	0.215635547	-11.4545242	2.21E-30	2.15E-29	28.68761154
ABUW_RS01765	ABUW_0500	NZ_CP008706.1	1514944	153273	-	WP_000094544.1		cytochrome c ubiquinol oxidase subunit IV	3173.104239	-2.468322105	0.23633748	-10.65614201	1.63E-26	1.31E-25	24.8827287
ABUW_RS02065	ABUW_0420	NZ_CP008706.1	438853	439248	-	WP_000062616.1	tpsh	30S ribosomal protein S8	14162.86771	-2.477282302	0.253649088	-19.766572872	1.57E-22	9.77E-22	210.910544
ABUW_RS01880	ABUW_0433	NZ_CP008706.1	440163	440680	-	WP_001141825.1	tpse	30S ribosomal protein S5	12717.11771	-2.483118318	0.27858281	-18.904582367	5.36E-99	2.61E-18	71.58335949
ABUW_RS00995	ABUW_0400	NZ_CP008706.1	164228	164578	-	WP_000191815.1		aspartate reductase	1003.452954	-2.483673959	0.22075738	-11.25069905	2.30E-29	2.07E-28	27.68402965
ABUW_RS02070	ABUW_0121	NZ_CP008706.1	433962	439795	+	WP_000199332.1	rgpF	50S ribosomal protein L6	77599.17305	-2.495471051	0.26038077	-19.583931072	9.34E-22	5.49E-21	20.2642666
ABUW_RS02330	ABUW_0516	NZ_CP008706.1	529947	527282	-	WP_001293924.1		TGCRD244 family phosphatase	162.943448	-2.499487238	0.204678088	-10.2179688	2.69E-34	3.46E-33	32.4850218
ABUW_RS18975	no	NZ_CP008706.1	332174	3321825	-	WP_012973641.1	htC	translation initiation factor F-3	19125.63424	-2.50193734	0.81771484	-10.24984939	4.52E-40	3.50E-39	78.1897822
ABUW_RS1540	ABUW_3148	NZ_CP008706.1	3180079	3198828	-	WP_000195882.1	bacC	malonyl-ACP-O: methyltransferase BacC	1733.301845	-2.504964065	0.11915454	-10.54177299	1.65E-54	6.33E-53	52.9859620
ABUW_RS01760	ABUW_0519	NZ_CP008706.1	1514055	1534033	-	WP_000191639.1	cydE	prothionine C-formyltransferase	10407.49179	-2.508895091	0.21081975	-11.7883198	4.48E-32	4.99E-31	30.10918945
ABUW_RS08630	ABUW_1772	NZ_CP008706.1	1718988	1727744	-	WP_000880358.1	pspP	phosphoenolpyruvate--protein phosphotransferase	1936.868398	-2.509688447	0.18034845	-10.919775	5.08E-44	1.08E-42	41.96651924
ABUW_RS17990	ABUW_3696	NZ_CP008706.1	3757419	3755372	-	WP_001018868.1		TGCRD730 family Rossmann fold protein	2141.02196	-2.511744936	0.219386259	-11.44886195	2.38E-30	2.30E-29	28.3827216
ABUW_RS18716	no	NZ_CP008706.1	851927	852056	+			hypothetical protein	99.196285	-2.512532102	0.17850281	-14.07962824	5.07E-45	1.02E-43	42.95071188
ABUW_RS18930	ABUW_0888	NZ_CP008706.1	3950453	3956826	-	WP_000550111.1	mpl	stylmuramate-L-alanyl-gamma-D-glutamyl-meso-diaminop	8444.72133	-2.51900773	0.200822498	-12.5152594	6.06E-36	8.34E-35	34.07883395
ABUW_RS04410	ABUW_0399	NZ_CP008706.1	895188	897083	-	WP_001028662.1	ftsH	ATP-dependent cyclic metallopeptidase FtsH	66757.44407	-2.51868133	0.221866924	-11.35221837	7.63E-29	28.16E-63	69.162163
ABUW_RS17085	ABUW_3512	NZ_CP008706.1	3595865	3596426	-	WP_000008979.1		catenon-pore antipore	1015.45293	-2.522827167	0.14455028	-17.45904167	2.94E-68	2.69E-66	65.57024772
ABUW_RS00735	ABUW_0408	NZ_CP008706.1	163187	164093	+	WP_000003665.1		D-alanine - D-alanine ligase	6865.225733	-2.52507721	0.80913695	-10.9590964	2.77E-44	5.97E-43	42.22402667
ABUW_RS13255	ABUW_2731	NZ_CP008706.1	2719389	2719624	-	WP_000029359.1		aspartate carbamoyltransferase	3039.282274	-2.534788807	0.219595312	-11.54304409	8.00E-31	8.10E-30	29.0195188
ABUW_RS17680	ABUW_3631	NZ_CP008706.1	3690250	3690501	-	WP_000194501.1		hypothetical protein	4801.089486	-2.544069147	0.24868229	-10.2950303	1.62E-24	1.95E-23	22.93554201
ABUW_RS01825	ABUW_1393	NZ_CP008706.1	1234800	1236692	-	WP_000055191.1		DXR4-5 domain-containing protein	1703.905958	-2.548235055	0.2305548	-10.8418254	2.20E-27	1.81E-26	26.7421493
ABUW_RS16010	ABUW_0616	NZ_CP008706.1	3283836	3291395	-	WP_000062476.1	panB	3-methyl-2-oxoglutarate-hydroxymethyltransferase	3506.91197	-2.549588305	0.17720816	-14.38017472	6.16E-47	1.07E-45	44.38041033
ABUW_RS02040	ABUW_0416	NZ_CP008706.1	439929	437186	-	WP_001291845.1	tpsQ	30S ribosomal protein S17	35740.46642	-2.554718494	0.31018722	-18.23775885	1.76E-16	7.33E-16	51.048903
ABUW_RS02075															

ABLUW_RS03340	ABLUW_0679	NZ_CP008706.1	683804	684 966	+	WP_00019096.1		response regulator	1923.299273	-2.788689844	0.96989864	-1.16708935	1695-45	3.986-44	43.4001693
ABLUW_RS07780	ABLUW_0693	NZ_CP008706.1	658486	659 125	+	WP_000888596.1		bifunctional aconitate hydratase 22-methylsuccinate dehydratase	400.8.50632	-2.79056296	0.96925276	-1.17063693	1396-45	3.306-44	43.4818406
ABLUW_RS01935	ABLUW_0208	NZ_CP008706.1	286 975	289333	+	WP_000353983.1		CuA/CuA family heavy metal reductase RND transporter	1697.990466	-2.795454095	0.27466608	-0.85466429	8.936-38	1222-36	35.1064617
ABLUW_RS07945	ABLUW_0223	NZ_CP008706.1	926336	926 472	+	WP_000 87073.1	meiF	methyleneethanoldehydrogenase reductase [NAD(P)H]	4566.026744	-2.796783078	0.21926032	-1.25236098	4326-40	2786-39	38.1786862
ABLUW_RS1495	ABLUW_2363	NZ_CP008706.1	234370	235031	+	WP_001009738.1		hydrophobic protein	4816.07873	-2.79721994	0.9625006	-1.70067976	1046-71	1205-69	68.8208185
ABLUW_RS02765	ABLUW_0563	NZ_CP008706.1	562998	5638 9	+	WP_00164004.1		carbamoyl-phosphate synthase class D beta-lactamase OXA-23	33002.84624	-2.799453367	0.96963463	-16.50587509	3336-61	2065-58	66.86619278
ABLUW_RS1690	ABLUW_3633	NZ_CP008706.1	3692372	3692635	+	WP_00199102.1		ferritin iron transporter protein A	2492.346434	-2.80343892	0.249906765	-11.22 8021	3 956-29	2855-28	27.5451619
ABLUW_RS01440	ABLUW_0293	NZ_CP008706.1	3 92720	3 92797	+	WP_000695059.1		plus assembly protein PAP	402.453548	-2.819486707	0.225724546	-12.46873 926	116-35	119-34	33.82162305
ABLUW_RS19345	ABLUW_3696	NZ_CP008706.1	3744267	3744794	+	WP_000102443.1	ppa	inorganic diphosphatase	9635.383429	-2.82234479	0.173779903	-16.24091688	2595-59	1435-57	56.84466336
ABLUW_RS02025	ABLUW_0412	NZ_CP008706.1	435566	4363 8	+	WP_000529922.1	rpsC	30S ribosomal protein S3	12966.0493	-2.82666356	0.32194279	-8.79641946	14 9-18	6.735-18	17.17 88404
ABLUW_RS16470	ABLUW_3185	NZ_CP008706.1	3213253	3214536	+	WP_000025826.1		ribonucleotide-diphosphate reductase subunit beta	26891.0215	-2.828391901	0.80502345	-15.66955761	2445-55	1016-53	52.99567863
ABLUW_RS01065	ABLUW_0258	NZ_CP008706.1	272077	274425	+	WP_000131198.1		RNA-binding transcriptional accessory protein	14293.87794	-2.834710085	0.243404506	-11.64608714	2405-31	2556-30	29.59345982
ABLUW_RS01855	ABLUW_0331	NZ_CP008706.1	36792	39476	+	WP_000250576.1	ppc	phosphoenolpyruvate carboxylase	7098.511614	-2.841602573	0.244038446	-11.64325793	2485-31	6286-30	29.80444425
ABLUW_RS01935	ABLUW_0308	NZ_CP008706.1	331325	331378	-	WP_000909000.1		RfaA family protein	674.7818872	-2.841922563	0.257919211	-11.01899586	3096-28	2686-27	26.57186521
ABLUW_RS01235	ABLUW_0467	NZ_CP008706.1	480 921	481187	+	WP_000810006.1		malate dehydrogenase	47695.03791	-2.848541939	0.229209316	-0.42768439	1856-35	5256-34	33.59859946
ABLUW_RS02235	ABLUW_0469	NZ_CP008706.1	48 9565	482092	+	WP_000021434.1		hypothetical protein	1430.738018	-2.857994 05	0.393162042	-7.269437348	3 616-13	1206-12	119.0281875
ABLUW_RS04380	ABLUW_0893	NZ_CP008706.1	887984	89 424	-	WP_001026293.1	carB	carbamoyl-phosphate synthase large subunit	59623.98425	-2.863863807	0.25334048	-11.40340665	1256-29	1 95-28	27.93902402
sRNA48	no	no	no	no	no	no	no	no	90.425978	-2.87 84 873	0.386919 8	-7.36953422	17 9-13	5.635-13	52.2343145
ABLUW_RS01355	ABLUW_0710	NZ_CP008706.1	716939	720817	-	WP_000190568.1	galA	Asp- tRNA(Ala)/Glu- tRNA(Gln) amidotransferase subunit GalA	6046.194345	-2.872932919	0.209493021	-11.7974045	8405-43	1655-41	40.73258006
ABLUW_RS01985	ABLUW_3736	NZ_CP008706.1	3753862	3794332	+	WP_001031691.1		FGF1 ATP synthase subunit B	36085.43341	-2.881958795	0.293321923	-9.820376431	8 976-23	5655-22	21.24718357
ABLUW_RS01865	ABLUW_0034	NZ_CP008706.1	40420	41520	+	WP_001050643.1		eIF4R RND transporter periplasmic adaptor subunit	6267.8 8798	-2.883353562	0.23204523	-0.42660997	1875-35	2545-34	33.5956628
ABLUW_RS1610	ABLUW_3417	NZ_CP008706.1	3465750	3466586	+	WP_000959085.1		proton/peptide diacylglycerol transferase	9692.18671	-2.886349296	0.292565022	-9.865667726	5865-23	21426-12	64.2429196
ABLUW_RS01800	ABLUW_3655	NZ_CP008706.1	37 8718	37 8056	+	WP_000780326.1	gHk	P. flammily nitrogen regulator	3489.939907	-2.905623678	0.9896065	-14.63007794	18 16-48	5025-47	46.29928268
ABLUW_RS1115	ABLUW_0031	NZ_CP008706.1	2271936	2271826	+	WP_000189795.1	puP	sulfamoylpeptide symporter PuP	22222.76953	-2.923275962	0.302793987	-9.654339363	4 716-22	4786-20	29.50284197
ABLUW_RS10465	ABLUW_2896	NZ_CP008706.1	2904 933	2905091	+	WP_000104048.1	cysD	sulfate adenylyltransferase subunit CysD	7626.503791	-2.927184831	0.21881089	-11.75023422	5086-43	1016-41	40.99567683
ABLUW_RS1320	ABLUW_2519	NZ_CP008706.1	36 8267	36 8707	+	WP_000107528.1	rvxX	Holliday junction resolvase RvxX	2028.792214	-2.936924919	0.202654301	-14.49231231	1366-47	666-45	45.3851891
ABLUW_RS17280	ABLUW_3551	NZ_CP008706.1	3608835	3609696	+	WP_001162277.1		peptidyl peptidase	643.232198	-2.938199339	0.18 3165	-16.2 869197	3848-59	2045-57	56.60038983
ABLUW_RS04290	ABLUW_0874	NZ_CP008706.1	856313	857746	+	WP_000802619.1	lpdA	dihydrolypoyl dehydrogenase	63526.55658	-2.938687101	0.249605726	-11.7731907	5365-32	5906-31	30.22947901
ABLUW_RS19720	ABLUW_2823	NZ_CP008706.1	2826865	2831023	+	WP_001986427.1	argG	argininosuccinate synthase	8253.635988	-2.93899944	0.237900867	-0.35382886	4646-35	6 916-34	33.20839305
ABLUW_RS01825	ABLUW_0873	NZ_CP008706.1	850504	856250	+	WP_000197876.1	cdhB	1a dehydrogenase complex dithiolylpyruvate-residue succinyl	32270.21645	-2.940496706	0.24505811	-0.22830658	2195-34	776-33	32.5435568
ABLUW_RS14765	ABLUW_2065	NZ_CP008706.1	30979769	30979338	+	WP_000633710.1		beta-ketoadipyl-ACP synthase II	44223.66246	-2.9489066	0.95089193	-15.9325927	3765-57	1745-55	54.75045076
ABLUW_RS16220	ABLUW_3104	NZ_CP008706.1	2086645	2087963	+	WP_000890437.1		aspartate aminase-lyase	5497.219332	-2.953394699	0.331223942	-8.96577954	4 816-19	7 3255-19	67.6298324
ABLUW_RS04500	ABLUW_0917	NZ_CP008706.1	923186	923476	+	WP_000655579.1		coo- chaperone GroES	6337.100597	-2.95339665	0.255623626	-11.55369204	7075-31	7165-30	29.14327111
ABLUW_RS14930	ABLUW_3157	NZ_CP008706.1	3204292	3204843	+	WP_001074552.1	ndhC	NADH:quinone oxidoreductase subunit A	5871537667	-2.95416283	0.25724726	-11.48408821	1595-30	1565-29	28.8608764
ABLUW_RS17200	ABLUW_3535	NZ_CP008706.1	3595166	3595554	+	WP_000624229.1		Na ⁺ /H ⁺ antiporter subunit C	473.763635	-2.95586109	0.269206205	-10.97991943	4776-28	4076-27	26.30045559
ABLUW_RS01020	ABLUW_0624	NZ_CP008706.1	27363	26867	+	WP_000084730.1	rnfB	16S rRNA [cytosine16E7 C5]-methyltransferase RnfB	1775.496683	-2.960778433	0.15616067	-19.09082868	3 016-81	7386-79	76.1957932
ABLUW_RS04225	ABLUW_2899	NZ_CP008706.1	2864694	2865722	+	WP_001090021.1		alpha/beta hydrolase	1093.400649	-2.960794686	0.1829254	-26.40273487	1246-163	2506-150	64.86206
ABLUW_RS01275	ABLUW_0443	NZ_CP008706.1	451 976	457320	+	WP_000266455.1		M3 family metallopeptidase	6798.460322	-2.981105505	0.292699353	-10.84877221	2325-24	1645-23	22.7815616
ABLUW_RS08175	ABLUW_0782	NZ_CP008706.1	798686	1978285	+	WP_000859846.1		cysD operon YggE family protein	324.3220714	-2.985479 86	0.430731924	-6.931803755	4 165-12	1256-11	10.90309999
ABLUW_RS1195	ABLUW_2424	NZ_CP008706.1	2416721	2411880	+	WP_00104472.1		amino acid ABC transporter permease	1511379628	-2.98581071	0.359633705	-8.30267182	1025-16	4 335-16	56.353521
ABLUW_RS01390	ABLUW_0280	NZ_CP008706.1	281653	282166	+	WP_000721434.1		hypothetical protein	4441725076	-2.910689967	0.255894637	-11.78626977	4596-32	5 105-31	30.29242982
ABLUW_RS05045	ABLUW_1033	NZ_CP008706.1	154233	156851	+	WP_000192279.1		ATP-binding protein	5097.738301	-2.936287375	0.176670635	-17.9614627	3375-66	2725-64	63.656431
ABLUW_RS14540	ABLUW_2676	NZ_CP008706.1	2992 93	2993527	+	WP_001027133.1		amino acid permease	704.2848933	-2.937472023	0.233511667	-13.00779555	1195-38	1725-37	36.76447155
ABLUW_RS1565	ABLUW_2193	NZ_CP008706.1	2160 89	2160789	+	WP_000956973.1		acetyltransferase	9119.432033	-2.946323863	0.965779905	-5.38488465	7255-08	1565-07	6.800587102
ABLUW_RS01730	ABLUW_0788	NZ_CP008706.1	9717286	1978387	+	WP_000207076.1	cysX	cysteine hemolysin-like oxidase subunit CysX	394.1633744	-2.948504797	0.4817528 6	-6.59769619	4 866-11	1 971-10	9.9319108
ABLUW_RS19185	ABLUW_2719	NZ_CP008706.1	2706676	2710729	+	WP_000552796.1	atpC	peroxate deoxygenase	5516.14806	-2.961079079	0.247242907	-0.38340511	3 216-35	4325-34	33.3645825
ABLUW_RS1685	ABLUW_3632	NZ_CP008706.1	3695022	3692375	+	WP_001078226.1		ferritin iron transporter B	9168.961091	-2.966057399	0.29475774	-10.51608 14	7065-26	5476-25	24.2620207
ABLUW_RS05265	ABLUW_0672	NZ_CP008706.1	1064741	1066978	+	WP_000896677.1		NADP-dependent isocitrate dehydrogenase	48169.08892	-2.970298958	0.98109467	-16.2355693	2835-59	1525-57	56.8189641
ABLUW_RS04280	ABLUW_0872	NZ_CP008706.1	85224	850504	+	WP_001084866.1		2-oxoglutarate dehydrogenase E1 component	54226.3156	-2.990623145	0.2619884 8	-11.819 8986	3 146-32	3585-31	30.4461967
ABLUW_RS01430	ABLUW_0676	NZ_CP008706.1	95976	95995	+	WP_000114637.1	sucD	succinate-CoA ligase subunit alpha	49529.37226	-2.105301661	0.227339435	-11.65918193	1785-42	4141-40	46.47245652
ABLUW_RS02885	ABLUW_2897	NZ_CP008706.1	2905084	2905216	+	WP_000210285.1		hypothetical protein	1798.95203	-2.123242223	0.229834623	-11.68906665	4695-42	8726-41	40.00949352
ABLUW_RS17185	ABLUW_2422	NZ_CP008706.1	2409332	2410063	+	WP_001103039.1		amino acid ABC transporter ATP-binding protein	163.561962	-2.125021655	0.371622455	-8.4275691	4005-17	1765-16	57.5448733
ABLUW_RS17315	ABLUW_3555	NZ_CP008706.1	3189797	319 593	+	WP_001018555.1	nuoN	NADH:quinone oxidoreductase subunit NuoN	9637.7839	-2.133647364	0.225436008	-13.90038524	6305-44	1326-42	11.67942607
ABLUW_RS02019	ABLUW_0631	NZ_CP008706.1	530969	540970	+	WP_001070222.1	secD	protein translocase subunit SecD	25123.8518	-2.155319737	0.263517065	-11.97838333	4875-33	5846-32	312.353587 6
ABLUW_RS04295	ABLUW_0875	NZ_CP008706.1	857894	859090	+	WP_001048573.1	sucC	ADP-forming succinate-CoA ligase subunit beta	53007.1766	-2.168058962	0.245939999	-0.8400222	9486-38	1456-36	53.83632
ABLUW_RS01590	ABLUW_0285	NZ_CP008706.1	267476	269890	-	WP_000505344.1		acetyl-CoA hydrolase/transferase family protein	9966.206566	-2.169195056	0.319323857	-9.969932638	2065-23	1375-22	21.88327343
ABLUW_RS04745	ABLUW_1119	NZ_CP008706.1	1140333	114 295	+	WP_000897187.1	schB	protease SchB	9116.455887	-2.176666 95	0.251961925	-0.258703528	2486-36	3495-35	34.4571947
ABLUW_RS17275	ABLUW_3550	NZ_CP008706.1	3607699	3608835	+	WP_000									

ABUW_RS15395	ABUW_3170	NZ_CP008706.1	3195608	3195150	-	WP_000276693.1	nuoI	NADH:quinone oxidoreductase subunit NuoI	12274.49772	-4.165408954	0.276996875	-15.03774711	4.15E-51	136E-49	48.86646109
ABUW_RS05245	ABUW_0168	NZ_CP008706.1	1079141	1079623	-	WP_000123995.1		peptidylglycol isomerase	6945.332805	-4.190658829	0.20197785	-20.63891095	1.62E-96	7.74E-94	93.11029904
ABUW_RS15390	ABUW_3169	NZ_CP008706.1	3195090	3195608	-	WP_012578792.1	nuoJ	NADH:quinone oxidoreductase subunit J	11311.80451	-4.20912783	0.26191585	-16.07065773	4.10E-58	2.06E-56	55.88613278
ABUW_RS13140	ABUW_2708	NZ_CP008706.1	2691713	2691713	+	WP_00198515.1		heavy-metal-associated domain-containing protein	1418.186303	-4.311382746	0.372447492	-1157581361	5.47E-31	5.60E-30	29.25191197
ABUW_RS05010	ABUW_1021	NZ_CP008706.1	1031947	1032954	-	WP_001212600.1		sulfate ABC transporter substrate-binding protein	524.9851564	-4.412834237	0.585628448	-7.53521542	4.88E-14	1.73E-13	12.7619539
sRNA00	no	no	no	no	no	no	no	no	3156.530264	-4.504136675	0.274427797	-16.42390146	1.29E-60	7.53E-59	58.12320502
ABUW_RS15410	ABUW_3173	NZ_CP008706.1	3199885	3201216	-	WP_001091096.1	nuoF	NADH:quinone oxidoreductase subunit NuoF	22232.86764	-4.592555159	0.329808172	-13.92492635	4.47E-44	9.53E-43	42.0209071
sRNA2	no	no	no	no	no	no	no	no	138801.352	-4.784616704	0.242293602	-19.74718554	8.48E-87	2.01E-84	83.69680394
sRNA99	no	no	no	no	no	no	no	no	20022.18512	-5.727998903	0.339668034	-16.86352063	8.35E-64	6.01E-62	61.12212553

Table S13. RNA-seq data: Absolute and relative expression (Tet/MEP > 2-fold up)

locus_tag	'old_locus_tag'	chrom	start	stop	strand	refseq_id	symbol	name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	-log10
ABUW_RS20160	no	NZ_CP008706.1	1697527	1697621	+			hypothetical protein	15.9172919	6.835274162	1.254836581	5.44714289	5.12E-08	1.12E-07	6.950781977
ABUW_RS20425	ABUW_0650	NZ_CP008706.1	655407	655565	-	WP_000692859.1		hypothetical protein	6450.455749	6.57627588	0.31684415	20.82098743	2.79E-96	1.88E-93	92.72584215
ABUW_RS03205	ABUW_0651	NZ_CP008706.1	655569	656774	-	WP_000512708.1		RtcB family protein	16281.97678	6.437260319	0.343215338	18.75574778	1.74E-78	2.19E-76	75.65955589
ABUW_RS19345	ABUW_4069	NZ_CP008707.1	40921	41418	+	WP_000756889.1		molecular chaperone DnaJ	220.6958265	6.24370475	0.419939721	14.86809759	5.31E-50	150E-48	47.82390874
ABUW_RS09950	ABUW_2049	NZ_CP008706.1	2028487	2028705	-	WP_002035543.1		hypothetical protein	117.7089018	6.099142525	0.460901788	13.23306328	5.65E-40	8.86E-39	38.05256628
sRNA73	no	no	no	no	no	no	no	no	40.4282639	5.852871247	0.645065581	9.073296453	1.15E-19	5.50E-19	18.25963731
ABUW_RS12725	ABUW_2621	NZ_CP008706.1	2618549	2619007	-	WP_001127331.1		hypothetical protein	4941.499428	5.723634802	0.370232463	15.45957034	6.50E-54	2.22E-52	51.65364703
sRNAs	no	no	no	no	no	no	no	no	3.947129552	5.638599832	1.130922023	4.307036892	1.65E-05	2.92E-05	4.53461749
ABUW_RS12615	ABUW_2596	NZ_CP008706.1	2589981	2590541	-	WP_0011033098.1		TetR/Acr family transcriptional regulator	217.9133828	5.4471970268	0.873033966	6.240272979	4.37E-10	1.11E-09	8.954677021
ABUW_RS09900	ABUW_2039	NZ_CP008706.1	2021992	2022210	-	WP_002035543.1		hypothetical protein	17.7699016	5.391904352	0.432162983	12.47597559	1.01E-35	12.6E-34	33.89962945
ABUW_RS13120	ABUW_2703	NZ_CP008706.1	2687015	2687371	+	WP_001088962.1		four-helix bundle copper-binding protein	7279.866477	5.369852708	0.456723777	11.5713319	6.47E-32	6.44E-31	30.1911143
ABUW_RS09895	ABUW_2038	NZ_CP008706.1	2020835	2021992	-	WP_000505023.1		replication initiation factor domain-containing protein	908.1308232	5.273102395	0.212234382	24.84565577	2.88E-136	1.16E-132	13.935542
ABUW_RS09310	ABUW_1912	NZ_CP008706.1	1919491	1914069	+	WP_002035810.1		TetR/Acr family transcriptional regulator	59.5115441	5.251724927	0.610746185	8.598866529	8.05E-18	3.43E-17	16.64470588
ABUW_RS19340	ABUW_4068	NZ_CP008707.1	40571	40885	+	WP_000708714.1		hypothetical protein	53.1146116	5.038824621	0.562578807	8.95665559	3.35E-19	1.54E-18	17.8247928
ABUW_RS09945	ABUW_2048	NZ_CP008706.1	2027330	2028487	-	WP_000505023.1		replication initiation factor domain-containing protein	906.4096723	4.995888692	0.219639174	22.7458909	1.58E-114	3.17E-111	110.4989407
ABUW_RS00420	ABUW_0085	NZ_CP008706.1	93475	93759	+	WP_000766201.1		hypothetical protein	129.3886579	4.946689639	0.360127676	13.73593303	6.19E-43	1.18E-41	40.92811799
ABUW_RS06065	ABUW_241	NZ_CP008706.1	1282739	1283191	-	WP_000835608.1		DUF962 domain-containing protein	639.0061519	4.877872202	0.259904353	18.7671951	1.38E-78	1.79E-76	75.74714697
ABUW_RS13575	ABUW_2795	NZ_CP008706.1	2793499	2793837	-	WP_000671932.1		hypothetical protein	37.71235294	4.748225085	0.578593712	8.206492722	2.28E-16	8.82E-16	15.05453141
ABUW_RS16200	ABUW_3335	NZ_CP008706.1	3368532	3368792	-	WP_000790979.1		hypothetical protein	144.3185675	4.743441008	0.737485857	6.49130776	NA	NA	#VALUE!
ABUW_RS08700	ABUW_1787	NZ_CP008706.1	1783246	1783605	+	WP_000185571.1		hypothetical protein	4077.391826	4.720280276	0.355821432	13.26586836	3.65E-40	5.84E-39	38.23358715
ABUW_RS13070	ABUW_2693	NZ_CP008706.1	2680667	2681056	-	WP_000427182.1		hypothetical protein	175.1028066	4.685804193	0.275565235	17.00433728	7.63E-65	5.30E-63	62.27572143
ABUW_RS09460	ABUW_1682	NZ_CP008706.1	1687675	1688934	+	WP_001013990.1		outer membrane protein transport protein	832.0989181	4.659000497	0.213042098	12.6493409	1.05E-108	1.41E-105	104.8507809
ABUW_RS12980	ABUW_2674	NZ_CP008706.1	2667054	2667332	+	WP_000072985.1		hypothetical protein	324.4144914	4.621925311	0.457585209	10.10068774	5.49E-24	3.42E-23	22.46597389
ABUW_RS16290	ABUW_3353	NZ_CP008706.1	3389159	3389722	-	WP_000122215.1		TetR/Acr family transcriptional regulator	103.9165587	4.571332223	0.387259974	11.80429822	3.17E-32	3.74E-31	30.4271284
ABUW_RS19405	ABUW_4082	NZ_CP008707.1	51428	51880	-	WP_000776261.1		hypothetical protein	326.0126942	4.377892224	0.350750144	12.4815225	9.42E-36	1.18E-34	33.92811799
ABUW_RS01750	ABUW_2992	NZ_CP008706.1	380432	380740	+	WP_000457408.1		hypothetical protein	96.2306246	4.377083999	0.39200353	11.8593007	5.99E-29	4.95E-28	27.3053948
ABUW_RS10025	ABUW_2064	NZ_CP008706.1	2045977	2046213	-	WP_000044010.1		hypothetical protein	395.3538908	4.367331996	0.695433329	6.280014507	3.39E-10	8.65E-10	9.06293893
ABUW_RS07305	ABUW_1498	NZ_CP008706.1	1484921	1485475	+	WP_000792929.1		TetR/Acr family transcriptional regulator	69.5915107	4.362930581	0.334417483	13.04635913	6.67E-39	9.80E-38	37.00877392
ABUW_RS14530	ABUW_2992	NZ_CP008706.1	3012455	3012429	+	WP_000675270.1		hypothetical protein	42.19574725	4.353298326	0.539145336	8.074443072	6.78E-16	2.54E-15	14.59516698
ABUW_RS19225	ABUW_4040	NZ_CP008707.1	23711	23893	+	WP_000373385.1		hypothetical protein	192.3356475	4.328694756	0.38334582	11.29187396	1.44E-29	1.24E-28	27.90657831
ABUW_RS13380	ABUW_2756	NZ_CP008706.1	2746479	2746706	-	WP_000608974.1		hypothetical protein	837.5659352	4.326155557	0.275441565	15.70607382	1.37E-55	5.13E-54	53.28986263
ABUW_RS10425	ABUW_2145	NZ_CP008706.1	2150417	2130683	-	WP_000183702.1		hypothetical protein	1494.69286	4.319286179	0.286147604	15.09460893	1.76E-51	5.32E-50	49.27408837
ABUW_RS19075	ABUW_4011	NZ_CP008706.1	6469	6684	+	WP_001012847.1		hypothetical protein	523.0526961	4.251491087	0.272522994	10.6048575	7.22E-55	2.62E-53	52.58169871
ABUW_RS14020	ABUW_2886	NZ_CP008706.1	2893565	2893888	+	WP_000688341.1		hypothetical protein	132.3608326	4.215045478	0.355990768	11.84032244	4.25E-32	2.47E-31	30.60730305
ABUW_RS12210	no	NZ_CP008706.1	2504847	2505388	-			TetR/Acr family transcriptional regulator	134.5420987	4.211051059	0.492956604	8.542437665	1.31E-17	5.54E-17	16.25649024
ABUW_RS19100	no	NZ_CP008706.1	11184	11594	+	WP_001998891.1		SAM-dependent DNA methyltransferase	127.2963753	4.184416666	0.342517941	12.2163499	2.53E-34	2.93E-33	32.53312328
ABUW_RS08090	ABUW_1660	NZ_CP008706.1	1652839	1654422	-	WP_000193596.1	ABC-F family ATP-binding cassette domain-containing pro	749.2675832	4.182211577	0.286254099	15.70759508	1.34E-55	5.05E-54	53.29670862	
ABUW_RS16285	ABUW_3352	NZ_CP008706.1	3388369	3388941	+	WP_000043984.1		TetR/Acr family transcriptional regulator	492.5632601	4.175601795	0.327491725	12.75025192	3.11E-37	4.19E-36	35.3778598
ABUW_RS19360	ABUW_4072	NZ_CP008706.1	42340	42534	+	WP_000560244.1		hypothetical protein	267.469145	4.15925962	0.340880049	12.20153433	3.05E-34	3.15E-33	32.45469288
ABUW_RS11915	ABUW_2449	NZ_CP008706.1	2435735	2436406	-	WP_001029902.1		class I SAM-dependent methyltransferase	578.580408	4.094207912	0.291723262	14.03456097	9.58E-45	2.04E-43	42.69036983
ABUW_RS09765	ABUW_2010	NZ_CP008706.1	2004664	2004882	-	WP_002074156.1		hypothetical protein	117.7492727	4.087180171	0.319916107	12.77578742	2.24E-37	3.04E-36	35.51712642
ABUW_RS00270	ABUW_0552	NZ_CP008706.1	5541968	555162	-	WP_000696053.1		hypothetical protein	192.8780432	4.071951409	0.356473418	11.42287533	3.21E-30	2.88E-29	28.54060751
ABUW_RS13855	ABUW_2850	NZ_CP008706.1	2862934	2863536	+	WP_000950253.1		amino acid transporter	602.7580995	4.067118763	0.291542538	13.95034425	3.13E-44	6.47E-43	42.18909572
ABUW_RS02355	ABUW_0479	NZ_CP008706.1	491708	492058	+	WP_000455817.1		GFA family protein	103.9145629	4.058125659	0.374862615	10.82563449	2.60E-27	1.97E-26	25.7055377
ABUW_RS19235	ABUW_4042	NZ_CP008707.1	24797	25180	+	WP_000654348.1		hypothetical protein	367.3845986	4.055419793	0.32664272	12.41545493	2.15E-35	2.64E-34	33.57839607
ABUW_RS19220	ABUW_4039	NZ_CP008707.1	23096	23662	+	WP_000710385.1		hypothetical protein	497.882776	4.052473617	0.247134321	16.39785848	1.98E-60	9.98E-59	58.00086946
ABUW_RS09530	ABUW_1959	NZ_CP008706.1	1963555	1964103	+	WP_002019791.1		TetR/Acr family transcriptional regulator	65.66696081	4.038509351	0.453468857	8.90581413	5.30E-19	2.41E-18	17.6798296
ABUW_RS19175	ABUW_4030	NZ_CP008707.1	18647	18904	+	WP_000834290.1		hypothetical protein	22.29851508	4.035493407	0.567647728	7.109150989	1.17E-12	3.57E-12	11.44733178
ABUW_RS19355	ABUW_4071	NZ_CP008707.1	41992	42324	+	WP_000597531.1		hypothetical protein	160.1050162	4.028948406	0.344300637	11.703257	1.25E-31	1.23E-30	29.91004989
ABUW_RS07105	ABUW_1464	NZ_CP008706.1	1453227	1454795	+	WP_000181972.1		CoA-acylating methylmalonate-semialdehyde dehydrogen	524.0297573	4.000971805	0.273476946	16.60835962	2.48E-48	6.50E-47	46.8708664
ABUW_RS08590	ABUW_1763	NZ_CP008706.1	1760845	1761288	+	WP_001020251.1		universal stress protein	1077.486021	4.007101624	0.362995102	11.02412841	2.92E-28	2.33E-27	46.16204464
ABUW_RS11910	ABUW_2448	NZ_CP008706.1	2434209	2435492	-	WP_001991866.1		hypothetical protein	362.566937	3.99618005	0.297292747	14.4421029	3.44E-41	5.82E-40	39.25077072
ABUW_RS19370	ABUW_4074	NZ_CP008707.1	43471	43941	+	WP_000192272.1		hypothetical protein	96.73348833	3.992076073	0.399128082	9.48414804	7.27E-24	4.21E-22	21.3571797
ABUW_RS09715	ABUW_1999	NZ_CP008706.1	1998188	1998406	-	WP_002074156.1		hypothetical protein	120.2460439	3.91949555	0.312709028	12.53375886	4.88E-36	6.20E-35	34.20760831
ABUW_RS11860	ABUW_2437	NZ_CP008706.1	2426277	2427886	-	WP_001145690.1		iron-containing redox enzyme family protein	6730.665542	3.91988294	0.41470438	9.449693884	3.40E-21	1.80E-20	19.74472749
ABUW_RS07300	no	NZ_CP008706.1	1484186	1484282	-			ADP-ribose phosphorylase	29.4702157	3.908766343	0.51410889	7.60222419	2.91E-14	1.80E-14	10.0877392
sRNA75	no	no	no	no	no	no	no	no	4615842247	3.89074531	0.409074029	9.51103207	1.89E-21	1.01E-20	19.99567863
ABUW_RS12550	ABUW_2313	NZ_CP008706.1	2298188	2299207	+	WP_0001738477.1		ferrihal protein	1210.105986	3.890330433	0.374600811	11.9186986	4.47E-49	3.71E-48	27.43062098
ABUW_RS12230	ABUW_2514	NZ_CP008706.1	2507164	2507484	-	WP_0003385117.1		hypothetical protein	200.4946675	3.79333357	0.667494244	5.80369523	6.49E-29	5.15E-28	7.82102305

ABLUW_RS098.6	ABLUW_2021	NZ_CP008706.1	201141	201059	-	WP_002074.66.1	hypothetical protein	120.68455	3.85005091	0.3684097.0	10.45304983	1426.25	9.7 E-25	24.0.0.78077
ABLUW_RS0335	ABLUW_3168	NZ_CP008706.1	3185300	3185527	-	WP_000543705.1	hypothetical protein	252.194201	3.84802356	0.34322284	1.1205.684	3.62E-29	3.03E-28	27.5.95537
ABLUW_RS0665	ABLUW_2032	NZ_CP008706.1	201768	201736	-	WP_002074.66.1	hypothetical protein	117.003658	3.844035576	0.3520425.97	10.9623671	9.33E-28	7.28E-27	26.1378682
ABLUW_RS0655	ABLUW_2811	NZ_CP008706.1	280901	281241	-	WP_000773509.1	hypothetical protein	438.0049261	3.839582237	0.32365598	11.882806.12	1.85E-32	1.9E-31	30.7.896663
ABLUW_RS0965	no	NZ_CP008706.1	266492	266568	-		transposase	93.443802	3.823465345	0.383392309	9.9727.8009.1	2.0 E-23	12.0E-22	19.2808.975
ABLUW_RS0305	no	NZ_CP008706.1	943830	944864	+	WP_0059.90973.1	hypothetical protein	16.9345802	3.822044742	0.9.0564322	4.8329613	2.87E-05	4.97E-05	4.303643611
ABLUW_RS1920	ABLUW_2450	NZ_CP008706.1	2436477	2438.071	-	WP_00183733.1	AMP-binding protein	17617.8743	3.821992231	0.314243477	12.8325.9803	4.92E-34	5.59E-33	32.252588.9
ABLUW_RS02.80	ABLUW_19.18	NZ_CP008706.1	1917241	1917381	+	WP_000770264.1	hypothetical protein	87.0.032377	3.819710528	0.4434856.8	8.59489.006	8.33E-18	3.55E-17	16.44977.65
ABLUW_RS0460	ABLUW_2162	NZ_CP008706.1	216678	2167485	-	WP_0009.34.74.1	methyltransferase domain-containing protein	83.53.05449	3.806584393	0.338539383	11.244.14051	2.47E-29	2.11E-28	27.6757.054
ABLUW_RS0795	no	NZ_CP008706.1	965636	965633	+		GNA1 family N-acetyltransferase	28.12202.114	3.783609358	0.448.06342	8.443562354	3.08E-17	1.26E-16	15.8996249
ABLUW_RS19.025	ABLUW_4021	NZ_CP008707.1	00658	1165	+	WP_00.0067227.1	hypothetical protein	138.9.024617	3.765525694	0.361005293	10.39709565	2.56E-25	1.72E-24	23.76447.95
ABLUW_RS0065	ABLUW_2692	NZ_CP008706.1	2680084	2680629	-	WP_00.010.9681.1	N-acetylhydrolase	17.5177091	3.738004246	0.232530888	16.04433833	6.26E-58	2.74E-56	55.56224944
sRNA56								13.12046502	3.7228.86002	0.78058893	4.769240069	1.85E-06	3.54E-06	5.450996738
ABLUW_RS0755	ABLUW_2629	NZ_CP008706.1	2626050	2626064	-	WP_0032.11204.1	TetR/AcrR family transcriptional regulator	27.46681933	3.69904.982	0.46076.862	8.028093906	9.90E-16	3.68E-15	14.434.102
ABLUW_RS0445	ABLUW_4593	NZ_CP008707.1	57264	57695	-	WP_001190813.1	hypothetical protein	227.3754781	3.693746337	0.221990724	16.63874253	3.65E-62	2.07E-60	59.68402965
ABLUW_RS0005	ABLUW_2678	NZ_CP008706.1	2666997	2670326	-	WP_000247.66.1	hypothetical protein	772.2938274	3.69319734	0.393573251	9.38376.904.1	6.37E-21	3.28E-20	19.484.026
ABLUW_RS0040	ABLUW_2686	NZ_CP008706.1	2675924	2676382	-	WP_001217319.1	hypothetical protein	1393.96074	3.688485947	0.380617458	0.683868864	3.53E-22	1.97E-21	20.70553377
ABLUW_RS0335	ABLUW_4091	NZ_CP008707.1	56668	56327	+	WP_00058.089.1	RNA	594.2973545	3.65553.61	0.31.9.53368	1.6172.8003	1.77E-30	1.7E-30	29.76700398
ABLUW_RS19.065	ABLUW_4028	NZ_CP008707.1	9146	1249	+	WP_000933769.1	toxic amino resistance protein	223.366022	3.6322.197	0.298247084	2.17853.19	0.49E-34	6.60E-33	32.337242.17
ABLUW_RS19.065	ABLUW_2508	NZ_CP008706.1	3554170	3555054	-	WP_000643.74.1	hypothetical protein	105.9.93238	3.599359392	0.426.09832	8.272300736	13 E-16	5.8 E-16	15.28567024
ABLUW_RS03365	ABLUW_0684	NZ_CP008706.1	692272	693663	+	WP_000355862.1	radic acid SAM protein	650.6.030296	3.597293.6	0.431939961	8.3357684.6	7.70E-17	3.08E-16	15.5144928
ABLUW_RS20485	ABLUW_0420	NZ_CP008707.1	06270	64.0	+	WP_00069.9026.1	hypothetical protein	69.58426426	3.5924812	0.424455027	8.460482837	2.65E-17	1.09E-16	15.9625735
ABLUW_RS0130	ABLUW_1463	NZ_CP008706.1	145174	145316	+	WP_00.086638.1	aspartate aminotransferase family protein	367.7955966	3.5770068.0	0.361673522	9.728758269	2.27E-22	1.28E-21	20.89279003
sRNA44								4.738.078039	3.573244267	1.307558509	2.73276059	0.006280598	0.00624584	2.06429.984
ABLUW_RS0760	ABLUW_2831	NZ_CP008706.1	2837325	2842.04	-	WP_0020.07455.1	RNase repeat protein	6937.8793.8	3.57079384	0.19243.931	19.57339067	6.8 E-85	6.57E-83	82.8243463
ABLUW_RS0350	ABLUW_4070	NZ_CP008707.1	41963	41847	+	WP_001190813.1	hypothetical protein	90.6468.026	3.565.9524	0.308510525	15.55967.05	8.89E-31	6.4 E-30	29.903.1497
ABLUW_RS0460	ABLUW_024	NZ_CP008706.1	033820	033826	+	WP_000.08204.1	hypothetical protein	24.05395814	3.558354571	0.534.974.027	6.66.75.184	2.7 E-11	7.5 E-11	10.12436006
ABLUW_RS0875	no	NZ_CP008706.1	2650238	2651252	+		site-specific integrase	9.06.828623	3.5568105.9	0.376350766	9.450785911	3.36E-21	1.78E-20	9.74.958
ABLUW_RS0465	ABLUW_025	NZ_CP008706.1	033623	033841	+	WP_00108.3663.1	hypothetical protein	19.42723645	3.574.9759	0.560880594	6.30847904	2.82E-10	7.24E-10	9.4026.4434
ABLUW_RS0065	ABLUW_2673	NZ_CP008706.1	2663326	2666784	-	WP_001038417.1	hypothetical protein	4617.200979	3.5253324.1	0.386.02537	10.5018358	6.85E-20	3.32E-19	19.47886.92
ABLUW_RS01.980	ABLUW_3330	NZ_CP008706.1	3365795	3366206	-	WP_000732630.1	hypothetical protein	263.8775904	3.519.6469	0.392.079239	8.958.03825	3.30E-19	1.52E-19	17.8.95641
ABLUW_RS09940	ABLUW_2047	NZ_CP008706.1	2027031	2027327	-	WP_000983.97.1	hypothetical protein	434.13.0664	3.509710233	0.22528.751	15.57877.226	1.9 E-54	3.59E-53	52.444.00555
sRNA4								23.9.0.6.8784	3.494425249	0.5.0266244	6.812273051	9.8 E-12	2.76E-11	10.55909092
ABLUW_RS19.060	ABLUW_3122	NZ_CP008706.1	3142445	3143296	+	WP_001064773.1	osfB	639.033208	3.48428569	0.579732508	0.010.9093	1.85E-09	4.49E-09	8.34773569
ABLUW_RS01.980	ABLUW_0646	NZ_CP008706.1	05.974	65.917	+	WP_001076585.1	VOC family protein	1234.266871	3.4655083.9	0.350706059	9.879860068	5.08E-23	2.97E-22	21.52724355
ABLUW_RS00180	ABLUW_2037	NZ_CP008706.1	2020336	2020832	-	WP_000983.97.1	hypothetical protein	436.7770889	3.4593483.6	0.22847.021	16.25947.693	1.42E-52	4.52E-51	50.34486.97
ABLUW_RS01.980	ABLUW_1474	NZ_CP008706.1	1462122	1462727	-	WP_000429477.1	LyxR family translocator	32.978245	3.44486104	0.457025602	7.53756704	4.79E-14	1.60E-13	12.79588002
ABLUW_RS0450	ABLUW_4094	NZ_CP008707.1	57721	58056	-	WP_00.074611.1	hypothetical protein	59.7691074	3.4402736.02	0.267343235	12.86837726	6.78E-38	9.39E-37	36.027.33441
ABLUW_RS01.945	ABLUW_0210	NZ_CP008706.1	237.620	237.85	-		rRNA-17r	1300.9.9795	3.434945925	0.336996407	10.950248	2.08E-24	133E-23	22.876.14836
ABLUW_RS00180	ABLUW_0810	NZ_CP008706.1	790240	790644	-	WP_000854583.1	hypothetical protein	116.837329	3.43393.85	0.288240677	11.934.0794	1.0 E-32	1.06E-31	30.974694.01
ABLUW_RS0380	ABLUW_4019	NZ_CP008706.1	6689	7.85	+	WP_00086.0205.1	thymonucleoside family protein	1103.227772	3.425443282	0.205615659	16.643.923	2.38E-62	139E-60	59.8589852
ABLUW_RS19.063	ABLUW_2438	NZ_CP008706.1	2420572	2420898	-	WP_000795915.1	hypothetical protein	217.5339568	3.405816781	0.29493.026	1.54037826	8.26E-31	7.59E-30	19.7815822
ABLUW_RS01.990	ABLUW_2652	NZ_CP008706.1	2644223	2654996	+	WP_002039934.1	DUF4882 family protein	375.148.58	3.38475998	0.218.91169	15.51705841	2.66E-54	9.23E-53	52.0347.983
ABLUW_RS19.060	ABLUW_2818	NZ_CP008706.1	2823260	2823384	-	WP_002034621.1	TetR/AcrR family transcriptional regulator	91.05.9007	3.380320325	0.3206239	10.84.0398	2.96E-27	1.67E-26	27.7712833
sRNA32								48.58663453	3.373536831	0.457034376	7.385340021	1.52E-13	4.06E-13	12.30980392
ABLUW_RS0330	no	NZ_CP008706.1	3870899	3871033	+		hypothetical protein	5.5.4448.729	3.362.032.11	0.9.6300763	3.67325.838	0.000239483	0.000378978	3.42.886
ABLUW_RS19005	ABLUW_2325	NZ_CP008706.1	2306990	2306950	+	WP_000037.85.1	TetR/AcrR family transcriptional regulator	0.47.020834	3.35035.084	0.445333236	7.5248.19724	5.28E-14	1.75E-13	12.75696.95
ABLUW_RS02020	ABLUW_2143	NZ_CP008706.1	212970	2129874	+	WP_000086293.1	hypothetical protein	28.82.697.964	3.345633689	0.337295673	9.91928767	3.43E-23	2.03E-22	21.69250396
ABLUW_RS01.980	ABLUW_1419	NZ_CP008706.1	1410867	1410927	+	WP_000333834.1	hypothetical protein	0.72746027	3.345447444	1.746886362	1.915.02907	0.005476053	0.063358411	1.6520084.1
ABLUW_RS01.935	no	NZ_CP008707.1	1081	1958	+	WP_00.0998892.1	hypothetical protein	295.7223.014	3.345.64689	0.222480084	15.03074894	4.28E-51	1.27E-49	48.896.9628
ABLUW_RS01.970	ABLUW_2009	NZ_CP008706.1	2003252	2004664	-	WP_005.42463.1	replication initiation factor domain-containing protein	378.674.963	3.344545709	0.230542794	14.5072723	1.09E-47	2.74E-46	45.56224944
ABLUW_RS0330	ABLUW_2600	NZ_CP008706.1	2592795	2593145	-	WP_0004.14788.1	hypothetical protein	1115733008	3.342747769	0.376864667	8.6889904	7.32E-19	3.30E-18	17.48184806
ABLUW_RS0335	ABLUW_0881	NZ_CP008706.1	988888	9897577	+	WP_000372262.1	hypothetical protein	1024.288302	3.3377440.8	0.201708429	16.11777.078	1.9 E-58	8.47E-57	56.0721859
ABLUW_RS01.970	ABLUW_2628	NZ_CP008706.1	2624476	2625970	-	WP_00069397.1	MFS transporter	91.1803458	3.337.02944	0.28680.663	11.63566.82	2.7 E-31	2.57E-30	29.59006688
ABLUW_RS0335	ABLUW_0068	NZ_CP008706.1	72582	73130	+	WP_00014.845.1	VOC family protein	24.90.96693	3.334055481	0.353585.96	9.429285438	4.18E-21	2.97E-20	19.65354027
ABLUW_RS0500	ABLUW_3182	NZ_CP008706.1	3222203	3222487	-	WP_000650927.1	hypothetical protein	120.117804	3.32255093	0.368964.98	9.050077031	2.96E-19	1.0 E-18	19.9567.6863
ABLUW_RS1475	ABLUW_4099	NZ_CP008707.1	59990	60468	+	WP_000376692.1	conjugial transfer protein: TraE	87.7609307	3.320066937	0.268672066	12.38732092	4.45E-35	5.38E-34	33.28621772
ABLUW_RS07750	ABLUW_2008	NZ_CP008706.1	2003224	2003499	-	WP_000897348.1	hypothetical protein	303.3044455	3.3196.8942	0.238655324	10.90067061	5.53E-44	1.1E-42	14.1954677.07
ABLUW_RS0330	ABLUW_4091	NZ_CP008706.1	1	1176	+	WP_002031424.1	replication initiation protein	16.4.286.586	3.303.97946	0.330420029	9.94733.82	1.6 E-23	9.69E-23	22.00767622
ABLUW_RS0370	ABLUW_2672	NZ_CP008706.1	2665673	26660.97	-	WP_00100.4672.1	hypothetical protein	70.7652231	3.28287.1887	0.548728.989	5.98269082	2.91E-09	5.30E-09	8.275724.3
ABLUW_RS02.0	ABLUW_2102	NZ_CP008706.1	2085633	2085854	-	WP_000668585.1	hypothetical protein	30.020574.14	3.2828049					

ABUW_RS1045	ABUW_2312	NZ_CP008706.1	2295654	2298191	+	WP_00516797.1		fmbrl/biogenesis outer membrane usher protein	359.9428773	3.079965443	0.294122259	0.4717183	1.076-25	8.14E-25	24.0893756
ABUW_RS2050	ABUW_2297	NZ_CP008706.1	2284943	2285191	-	WP_000966850.1		hypothetical protein	351733127	3.077143504	0.9296185	0.94691741	2.996-57	1.20E-55	54.89962945
ABUW_RS0330	ABUW_2579	NZ_CP008706.1	2517975	25173456	-	WP_001666523.1	tsuC	type V secretion system contactile sheath large subunit	4496.179915	0.373417406	0.264325445	1.62739895	2.996-31	2.80E-30	29.5528497
ABUW_RS1616	ABUW_3217	NZ_CP008706.1	3249351	3250346	+	WP_006290304.1	add	adenosine deaminase	9.95267694	3.070626687	0.4371671	7.42243603	1.9E-10	3.74E-13	0.4271284
ABUW_RS0440	ABUW_4092	NZ_CP008707.1	50584	57222	+	WP_001955382.1		recombinase family protein	1737.259632	0.252958109	0.209287409	54.587395	3.38E-48	8.67E-47	46.0619809
ABUW_RS1626	ABUW_2163	NZ_CP008706.1	2085946	2086101	-	WP_000922092.1		hypothetical protein	7.57918899	3.048355978	0.953382911	3.9740992	0.001026645	2.693264107	
ABUW_RS0285	ABUW_0058	NZ_CP008706.1	63239	63432	-	WP_000418560.1		hypothetical protein	025.3951735	3.044564037	0.370875328	8.209100847	2.23E-16	8.69E-16	16.0529839
ABUW_RS0070	ABUW_698	NZ_CP008706.1	697048	698988	-	WP_005162463.1		replication initiation factor domain-containing protein	454.409042	3.043167428	0.205936999	9.77722042	2.05E-49	5.71E-48	47.24336389
ABUW_RS0805	ABUW_2016	NZ_CP008706.1	2009700	2009996	-	WP_000983197.1		hypothetical protein	402.58253	3.036485909	0.20921294	9.51096742	9.88E-48	2.50E-46	45.60205999
ABUW_RS0300	ABUW_610	NZ_CP008706.1	91194	912576	-	WP_000304497.1		amidohydrolase	280.5165212	3.034788921	0.37199643	6.57696034	2.94E-16	1.0E-15	14.9469256
ABUW_RS0845	ABUW_0775	NZ_CP008706.1	0774456	1774701	-	WP_000949688.1		hypothetical protein	2649.474744	3.034131464	0.262854816	11.54299362	8.07E-31	7.40E-30	29.10376828
ABUW_RS1505	ABUW_1393	NZ_CP008706.1	3222614	3223078	-	WP_000876111.1		hypothetical protein	287.562945	3.032841956	0.287471488	0.55006176	5.08E-26	3.62E-25	24.4412943
ABUW_RS0370	ABUW_0685	NZ_CP008706.1	693671	694552	+	WP_000870306.1		alpha/beta fold hydrolase	287.6001099	3.032828871	0.420308321	7.216724083	5.36E-10	1.67E-12	11.7772853
ABUW_RS19240	no	NZ_CP008707.1	25247	25726	+			hypothetical protein	363.2718329	3.026570892	0.249582464	0.2063661	7.64E-34	8.50E-33	32.07058107
ABUW_RS09620	ABUW_6178	NZ_CP008706.1	6182596	6184108	-	WP_001097729.1		NAD(P)FAD-dependent oxidoreductase	524.2164710	3.022285596	0.984840501	6.35077579	4.29E-60	2.08E-58	57.6893667
ABUW_RS0285	ABUW_0667	NZ_CP008706.1	673231	673680	+	WP_00090594.1		SRPBCC family protein	567.8995335	3.0209482	0.271728404	111975283	1.03E-28	8.36E-28	27.07779372
ABUW_RS1805	ABUW_2447	NZ_CP008706.1	2432924	2434182	+	WP_000781142.1		SGNHGDSL hydrolase family protein	905.7350975	3.020521017	0.299938382	0.09688225	5.70E-24	3.55E-23	22.44071243
ABUW_RS0250	ABUW_889	NZ_CP008706.1	899600	900409	+	WP_000992595.1		metal-dependent hydrolase	95.142623	0.30194195	0.25193666	1.98669055	4.07E-33	4.32E-32	31.3641925
ABUW_RS0240	no	NZ_CP008706.1	2573969	2574600	-			hypothetical protein	941.438783	3.016743335	0.266593451	11.25338819	1.41E-29	1.23E-28	27.1909049
ABUW_RS0900	ABUW_3891	NZ_CP008706.1	3949650	3950555	+	WP_001041561.1		matrin family metalloprotease	287.4623919	3.098620526	0.283694602	0.5345623	5.99E-26	4.25E-25	24.3716107
ABUW_RS0375	ABUW_4075	NZ_CP008707.1	43948	46165	+	WP_000644960.1		type IV secretion system DNA-binding domain-containing protein	454.0738957	2.997877296	0.249178906	11.99087375	3.97E-33	4.22E-32	31.37468755
ABUW_RS0335	ABUW_2580	NZ_CP008706.1	2517449	2573952	-	WP_001180421.1	tsbB	type V secretion system contactile sheath small subunit	9055.932878	2.987419564	0.285634108	0.548990438	133E-25	9.17E-25	24.03763066
ABUW_RS1045	ABUW_2333	NZ_CP008706.1	231878	231695	-	WP_000803363.1		amino acid ABC transporter substrate-binding protein	5036.265782	2.985766966	0.95041962	0.90098617	3.75E-73	3.36E-71	70.4736072
ABUW_RS0430	ABUW_0904	NZ_CP008706.1	899218	900081	+	WP_001030035.1		alkaline phosphatase D family protein	1077.06141	2.981030872	0.229103065	0.00955224	1.08E-38	1.98E-37	38.80142491
ABUW_RS0200	ABUW_4035	NZ_CP008707.1	20560	2118	+	WP_000790084.1		hypothetical protein	935.5361077	2.978950671	0.291931145	0.22069417	1.60E-24	1.02E-23	22.9919993
ABUW_RS0100	ABUW_0325	NZ_CP008706.1	347427	348458	-	WP_001189459.1		lipase secretion chaperone	975.0243109	2.977465553	0.292885163	0.18685184	2.27E-24	1.44E-23	22.8416371
ABUW_RS0480	ABUW_0633	NZ_CP008706.1	943756	944061	-	WP_000371001.1		hypothetical protein	47.747576	2.974257487	0.319338001	0.453485577	2.83E-17	1.8E-16	9.93554201
ABUW_RS0785	ABUW_2016	NZ_CP008706.1	2007127	2007411	-	WP_000505492.1		DUF2523 domain-containing protein	91.52870962	2.973441944	0.550348409	5.402835545	5.66E-08	1.42E-07	6.84717656
ABUW_RS2015	ABUW_0382	NZ_CP008706.1	406290	406475	+	WP_000471951.1		hypothetical protein	12.011632	2.971974906	0.472808705	9.64643733	3.75E-12	1.0E-11	9.95860731
ABUW_RS0580	ABUW_2796	NZ_CP008706.1	2794448	2794458	-	WP_001059568.1		DUF4265 domain-containing protein	129.2800501	2.970077553	0.364381852	8.16100246	3.61E-16	1.37E-15	14.86237943
ABUW_RS0695	ABUW_0786	NZ_CP008706.1	792379	792530	-	WP_000616034.1		hypothetical protein	2409.360416	2.966130006	0.296064191	0.10194451	1.26E-23	7.69E-23	22.1603766
ABUW_RS1910	ABUW_4018	NZ_CP008707.1	8988	9677	+	WP_000389916.1		DUF2785 domain-containing protein	616.0278291	2.965595958	0.245990296	0.05575867	1.81E-33	1.07E-32	3.17053337
ABUW_RS0445	ABUW_0914	NZ_CP008706.1	910874	911812	+	WP_001047651.1		NAD(P)+NADHase	725.0938052	2.965016191	0.20810467	9.38387432	6.53E-47	1.55E-45	44.8096683
ABUW_RS0005	ABUW_2080	NZ_CP008706.1	2041677	2041842	-	WP_001273381.1		hypothetical protein	3287.67935	2.9638456	0.271738337	6.210409703	5.28E-10	1.34E-09	8.17289502
ABUW_RS1860	ABUW_3326	NZ_CP008706.1	3362788	3363198	-	WP_000688220.1		copper resistance protein CopC	713.1058368	2.963269324	0.288260087	0.27984608	8.69E-25	5.64E-24	23.2487209
ABUW_RS0230	ABUW_2512	NZ_CP008706.1	2503638	2506504	-	WP_000076368.1		hypothetical protein	144.293627	2.961413397	0.61864045	4.808734069	1.52E-06	2.92E-06	5.53461749
ABUW_RS0230	ABUW_2516	NZ_CP008706.1	2507870	2508022	+	WP_001079164.1		hypothetical protein	61.86091751	2.960576795	0.751866237	3.937532902	6.23E-05	0.00016551	3.86470516
ABUW_RS0705	ABUW_6987	NZ_CP008706.1	696747	697043	-	WP_000983197.1		hypothetical protein	398.3938284	2.959292397	0.40248446	0.286951731	1.06E-34	1.20E-33	32.89962945
ABUW_RS1870	ABUW_3875	NZ_CP008706.1	3942924	3943164	-	WP_000733015.1		hypothetical protein	2956.819631	2.94630216	0.346181764	0.518083169	1.73E-17	7.9E-17	9.1432711
ABUW_RS0610	ABUW_0580	NZ_CP008706.1	0585236	0595703	-	WP_001021977.1		hypothetical protein	34.91638041	2.944194357	0.40205716	7.328282498	2.43E-10	1.21E-99	
ABUW_RS0580	ABUW_4121	NZ_CP008707.1	82570	82821	-	WP_000572025.1		hypothetical protein	276.1431293	2.940165273	0.257432729	114208624	3.29E-30	2.95E-29	28.53017798
ABUW_RS0455	ABUW_2771	NZ_CP008706.1	2703198	2704898	-	WP_000735566.1		OpC family outer membrane protein	966.7648798	2.939640399	0.322442299	9.14634395	7.87E-20	3.81E-19	14.16075052
ABUW_RS0400	ABUW_2040	NZ_CP008706.1	2022324	2022518	+	WP_000301761.1		hypothetical protein	1385.166488	2.93405601	0.249335477	11.67503197	5.74E-32	5.74E-31	30.2419881
ABUW_RS0995	ABUW_2050	NZ_CP008706.1	2028189	2029070	-	WP_000301761.1		hypothetical protein	1390.801872	2.929433997	0.249719726	11.73088744	8.85E-32	8.76E-31	30.0574969
ABUW_RS0880	ABUW_2611	NZ_CP008706.1	2604316	2604852	+	WP_001995449.1		hypothetical protein	948.164647	2.925740197	0.321944797	0.087603945	1.01E-19	8.48E-19	9.13036373
ABUW_RS1930	ABUW_2452	NZ_CP008706.1	2439044	2440216	+	WP_001053639.1		isovaleryl-CoA dehydrogenase	2343.051086	2.925714065	0.398297569	8.143778716	3.83E-16	1.48E-15	14.83364714
ABUW_RS0395	ABUW_4079	NZ_CP008707.1	50326	50892	-	WP_001093170.1		hypothetical protein	166.332507	2.920775961	0.264051033	11.06140707	1.93E-28	1.55E-27	28.8096683
ABUW_RS0260	ABUW_0480	NZ_CP008706.1	492078	492641	+	WP_000888414.1		DUF4256 domain-containing protein	222.2239159	2.920404207	0.307248875	9.50501877	2.00E-21	1.07E-20	9.97061622
ABUW_RS0320	ABUW_0800	NZ_CP008706.1	776544	776714	+	WP_000538616.1		Act family DNA-binding protein	614.9158932	2.918754305	0.305662639	1.984279565	1.41E-15	5.22E-15	9.14822326
ABUW_RS0495	ABUW_0916	NZ_CP008706.1	910857	922945	+	WP_000250932.1		lg-like domain repeat protein	22636.85735	2.916515443	0.185377008	6.722637123	1.06E-55	4.06E-54	53.31947397
ABUW_RS0360	ABUW_680	NZ_CP008706.1	686528	686901	-	WP_001059828.1		FAD-binding oxidoreductase	1020.119116	2.915707234	0.21633454	0.74508283	5.45E-43	1.04E-41	40.0826666
ABUW_RS0440	ABUW_3383	NZ_CP008706.1	3421462	3421203	+	WP_000686565.1		phosphatase PAP2 family protein	303.080245	2.910133119	0.287124514	0.86061962	1.78E-27	1.37E-26	28.86327943
ABUW_RS0905	ABUW_4008	NZ_CP008707.1	5454	6050	+	WP_000958225.1		hypothetical protein	0202.963952	2.910014859	0.266542425	0.8806268	1.43E-27	1.0E-26	25.95860731
ABUW_RS0435	ABUW_2475	NZ_CP008706.1	2468645	2469454	+	WP_000618658.1		enoyl-CoA hydratase	48.7829173	2.899028704	0.348182824	8.301538261	1.03E-16	4.09E-16	15.38827669
ABUW_RS0105	ABUW_640	NZ_CP008706.1	640006	6409430	-	WP_000551711.1		hypothetical protein	774.3626627	2.887848673	0.257612239	121.959347	3.49E-29	2.93E-28	27.53153238
ABUW_RS0715	ABUW_640	NZ_CP008706.1	629269	6294740	+	WP_001050009.1		circularly permuted type 2 ATP-grasp protein	880.506564	2.887825661	0.247018812	11.6911829	1.42E-31	1.38E-30	29.86012091
ABUW_RS0405	ABUW_0939	NZ_CP008706.1	946349	946924	+	WP_001046786.1		helicum-helic transcriptional regulator	38.2051044	2.881610293	0.373496983	7.716229445	1.21E-14	4.81E-14	13.8786272
ABUW_RS0780	ABUW_3507	NZ_CP008706.1	3554228	3554596	+	WP_000434938.1		RNA-binding protein	119.179793	2.877162215	0.206484938	0.3393288	3.83E-44	7.84E-43	42.0568363
ABUW_RS0275	ABUW_0589	NZ_CP008706.1	568907	569512	-	WP_001058005.1		phage tail protein I	95.3208014	2.874504621	0.296897141	9.747109017	2.61E-22	1.46E-21	21.80364741
ABUW															

ABLW_RS089.9	ABLW_9332	NZ_CP008706.1	827946	182899	+	WP_000121760.1	CoA transferase subunit B	94.29694725	2.70442605	0.33816226	7.99765793	1.27E-15	4.70E-16	14.3279024
ABLW_RS174.9	ABLW_3577	NZ_CP008706.1	3635.928	363586	-	WP_000525251.1	hypothetical protein	2513820288	2.702073231	0.224884.9	0.01840204	2.95E-33	3.56E-32	31.50108945
ABLW_RS1960	ABLW_2456	NZ_CP008706.1	244465	244455	+	WP_0002889.0	hydroxymethylglutaryl-CoA lyase	900.7197706	2.692461424	0.286738538	0.38995414	6.00E-21	3.18E-20	16.50723961
ABLW_RS0955	ABLW_2669	NZ_CP008706.1	2662975	2664465	-	WP_0008349.1	phage terminase large subunit	615922403	2.689678084	0.31107304	8.644666604	5.40E-18	2.32E-17	16.63451202
ABLW_RS0505	ABLW_37.0	NZ_CP008706.1	3768222	3768770	-	WP_001059732.1	GNAT family N-acetyltransferase	563.9009353	2.682354351	0.21852709	0.61824927	7.5E-37	9.99E-36	35.00043451
ABLW_RS0740	ABLW_1465	NZ_CP008706.1	145499	1456296	-	WP_000508165.1	amino acid permease	8159319751	2.681005057	0.267533218	0.02.97347	1.22E-23	7.45E-23	22.12784373
ABLW_RS0995	ABLW_2676	NZ_CP008706.1	2666657	2668648	-	WP_00045792.1	hypothetical protein	817.8895879	2.67984194	0.28877589	9.28003599	1.69E-20	8.83E-20	19.08905907
ABLW_RS0765	ABLW_2832	NZ_CP008706.1	2842332	2842655	+	WP_000725059.1	hypothetical protein	261.0895851	2.668.69529	0.306300811	8.7.0960725	3.0E-18	1.31E-17	16.8827287
ABLW_RS0325	ABLW_0066	NZ_CP008706.1	70383	71438	+	WP_000353.63.1	4-hydroxyphenylpyruvate dioxygenase	934.5332.15	2.667733296	0.325429071	8.97587543	2.45E-16	9.47E-16	15.02365002
ABLW_RS0380	ABLW_0077	NZ_CP008706.1	82160	83827	+	WP_000208428.1	uracinate hydratase	7983.6429	2.663.02365	0.4477956.16	5.947.80269	2.73E-09	6.53E-09	8.950868.9
ABLW_RS1870	no	NZ_CP008706.1	3273353	3274.95	-		C39 family peptidase	308.9784756	2.662899795	0.288373896	9.23491954	2.60E-20	1.30E-19	16.88605665
ABLW_RS1060	ABLW_28.0	NZ_CP008706.1	2809373	28.12609	-	WP_00036993.1	ATP-binding protein	4.139.430525	2.658886442	0.93954602	16.2.17214	3.81E-59	1.7E-57	56.76700389
ABLW_RS185.6	ABLW_4187	NZ_CP008707.1	67345	67845	+	WP_001058570.1	signal peptidase I	84.35772592	2.658.166845	0.264302964	9.0527272.9	8.53E-24	5.21E-23	22.28316228
ABLW_RS0260	ABLW_0053	NZ_CP008706.1	58924	58782	-	WP_000490287.1	DUF1281 domain-containing protein	5808.425003	2.650548026	0.353919506	7.489295993	6.92E-14	2.28E-13	12.6420055
ABLW_RS1925	ABLW_2451	NZ_CP008706.1	2438282	2438899	-	WP_000020693.1	TetR/AC-R family transcriptional regulator	3957.96207	2.649032179	0.253336954	9.45655652	1.37E-25	9.37E-25	24.02826041
ABLW_RS0455	ABLW_0928	NZ_CP008706.1	936148	937260	-	WP_0009846.03.1	transglycosylase SLT domain-containing protein	764.9672.02	2.647858053	0.2.8617378	12.118.9711	9.14E-34	1.0E-32	31.99567863
ABLW_RS0490	ABLW_951	NZ_CP008706.1	956228	953076	+	WP_075847472.1	hypothetical protein	92.77509314	2.644044409	0.277549229	9.526397963	1.63E-21	8.78E-21	20.05605058
ABLW_RS0400	ABLW_957	NZ_CP008706.1	953046	955055	+	WP_00021699.1	amidase	4.19.3931482	2.637435268	0.52640072	5.57.933462	2.5E-07	5.5E-07	6.29036881
ABLW_RS0495	ABLW_2667	NZ_CP008706.1	2667687	266.9687	-	WP_00073094.1	minor capsid protein	76.9448541	2.637.92746	0.36843954	7.97782367	8.20E-13	2.53E-12	11.99687948
ABLW_RS1025	ABLW_23.0	NZ_CP008706.1	2294255	2294701	+	WP_0007.94.30.1	type I fibrinogen protein	14.9.462962	2.636737571	0.394.17842	6.682602274	2.35E-11	6.59E-11	10.8237857
ABLW_RS0845	ABLW_1754	NZ_CP008706.1	1745678	175014	-	WP_000573225.1	GNAT family N-acetyltransferase	304.760239	2.6267002.18	0.242080563	0.85052094	1.98E-27	152E-26	25.8.96641
ABLW_RS0670	ABLW_2185	NZ_CP008706.1	218189	218242	-	WP_00099341.11	alkane 5-monooxygenase	236.9.8285	2.62628198	0.25596065	0.26048748	1.06E-24	6.83E-24	23.9357973
ABLW_RS1875	ABLW_2920	NZ_CP008706.1	2929.948	2930824	+	WP_0008736.11	arylsulfatase	234.5821059	2.624992497	0.280689491	9.35.944673	8.61E-21	4.42E-20	19.35447737
ABLW_RS1745	ABLW_3243	NZ_CP008706.1	3272.802	3273307	-	WP_000370427.1	hypothetical protein	503.1004285	2.622203058	0.96346.85	15.76352986	5.54E-56	2.7E-54	53.63354027
ABLW_RS1385	ABLW_2757	NZ_CP008706.1	2747075	2748265	-	WP_000256739.1	NAD(P)FAD-dependent oxidoreductase	177.489627	2.619218519	0.267467755	9.788886596	1.26E-22	7.56E-22	21.45699396
ABLW_RS0975	ABLW_2004	NZ_CP008706.1	2000651	2000935	-	WP_000050492.1	DUF2523 domain-containing protein	18.5148264	2.61636999	0.483794623	5.408017768	6.37E-08	1.38E-07	16.66020914
ABLW_RS1935	ABLW_2453	NZ_CP008706.1	2440241	24.8442	+	WP_00072777.1	methylcrotonyl-CoA carboxylase	29.0.262352	2.614672375	0.33808.974	7.73347383	1.04E-14	3.63E-14	30.44009337
ABLW_RS05475	ABLW_169	NZ_CP008706.1	168850	187.407	+	WP_002017886.1	TetR/AC-R family transcriptional regulator	97.4533435	2.614497509	0.358374256	7.295438954	2.99E-13	9.43E-13	12.02548831
ABLW_RS1480	ABLW_2187	NZ_CP008706.1	219265	219690	-	WP_000065213.1	GFA family protein	72.482608	2.610648855	0.387549779	7.644028762	1.54E-11	4.36E-11	10.3605193
ABLW_RS1270	ABLW_2620	NZ_CP008706.1	2618026	26.9454	+	WP_000406271.1	GNAT family N-acetyltransferase	95.6377002	2.6104.9506	0.283801937	9.548844.12	3.73E-20	1.04E-19	16.732982.8
ABLW_RS0550	ABLW_975	NZ_CP008706.1	984442	938925	-	WP_00048355.11	hypothetical protein	39.9840.675	2.605255102	0.438242445	9.540524382	2.76E-09	6.65E-09	8.97979541
ABLW_RS02705	ABLW_0551	NZ_CP008706.1	554945	554960	-	WP_000109486.1	Rfa family transcriptional regulator	334.39327.15	2.60448729	0.209595996	0.429.95591	1.82E-35	2.24E-34	33.6497958
ABLW_RS0690	ABLW_164	NZ_CP008706.1	182271	183443	+	WP_000049455.1	hypothetical protein	95.400381	2.60459297	0.248078999	10.48873772	8.75E-26	6.14E-25	24.2183.83
ABLW_RS04425	ABLW_0902	NZ_CP008706.1	8945.6	898860	-	WP_032068.06.1	hypothetical protein	453.7988756	2.60249.105	0.248993296	9.46466.85	1.26E-25	8.70E-25	24.06048075
ABLW_RS1090	ABLW_2697	NZ_CP008706.1	2682890	268296	-		RNA-Met	1582.9752.18	2.602493737	0.40166893	6.84208403	8.92E-11	2.37E-10	9.62525954
sRNA22								4.05750211	2.596458343	0.94.802.805	2.756904.99	0.008383944	0.008056819	2.093836393
ABLW_RS16235	ABLW_3158	NZ_CP008706.1	316.629	3163940	-	WP_001038901.1	hypothetical protein	954.91233	2.596380533	0.195816.9	9.973.8494	2.27E-44	4.74E-43	42.32422466
ABLW_RS08135	ABLW_2026	NZ_CP008706.1	2010604	201888	-	WP_000050492.1	DUF2523 domain-containing protein	19.73908256	2.5847940.2	0.490628151	5.268244403	1.38E-07	2.89E-07	6.539.62792
ABLW_RS0860.5	ABLW_642	NZ_CP008706.1	638393	638575	-	WP_000666584.1	hypothetical protein	32.0.143045	2.583830986	0.48507097	9.32670718	1.00E-07	2.02E-07	6.673664169
ABLW_RS1250	ABLW_2730	NZ_CP008706.1	2716760	27.9175	-	WP_000024646.1	OmpA family protein	759.248.95	2.57857703	0.204203448	6.6274906	1.49E-36	1.94E-35	34.7.0.9827
ABLW_RS0945	ABLW_2042	NZ_CP008706.1	2023029	2024246	-	WP_0000840.16	DNA replication protein	87.5451907	2.576314425	0.97.90853	13.76303585	4.25E-43	8.8E-42	11.08883094
ABLW_RS1775	ABLW_2834	NZ_CP008706.1	2843.498	2843508	+	WP_000744506.1	hypothetical protein	388.7433293	2.57624203	0.239724901	8.667943706	4.40E-18	1.69E-17	16.7235832
ABLW_RS1000	ABLW_2324	NZ_CP008706.1	2307851	23087.4	-	WP_001047439.1	hypothetical protein	279.4984583	2.571001293	0.2757.871	9.325810584	1.95E-20	5.61E-20	25.92937.4
ABLW_RS08565	ABLW_9758	NZ_CP008706.1	9754361	1754207	+	WP_000525475.1	alpha/beta hydrolase	5687.93943	2.5688763.18	0.26329497	9.769949575	1.52E-23	8.59E-22	21.06606084
ABLW_RS093.5	ABLW_9703	NZ_CP008706.1	974149	974664	+	WP_000719604.1	hypothetical protein	137.8568493	2.564082373	0.37807021	9.618939579	4.72E-12	2.18E-11	18.800.0091
ABLW_RS1055	ABLW_23.14	NZ_CP008706.1	2298784	2299963	+	WP_000805609.1	hypothetical protein	14.5470.878	2.56107839	0.5853929.8	4.375033865	1.21E-05	2.78E-05	4.693540266
ABLW_RS04285	ABLW_0289	NZ_CP008706.1	1304.95	130899	+	WP_000378508.1	hypothetical protein	817.0007.01	2.554240995	0.379059506	6.738364.76	1.60E-11	4.82E-11	10.34486.67
ABLW_RS07125	ABLW_1462	NZ_CP008706.1	14507.9	145365	-	WP_000802869.1	LysR family transcriptional regulator	356.45.0262	2.55344221	0.27829095	9.175465948	4.50E-20	2.21E-19	16.65560773
ABLW_RS08130	ABLW_0254	NZ_CP008706.1	1282468	1292731	-	WP_000717852.1	hypothetical protein	23.44660944	2.550599983	0.414246511	6.193400058	7.30E-10	1.84E-09	8.735.92717
ABLW_RS1920	ABLW_4108	NZ_CP008707.1	638362	638470	-	WP_000672680.1	type-F conjugative transfer system protein TraW	73.26655471	2.549204486	0.238052502	7.00858004	9.28E-27	6.80E-26	25.96749.69
ABLW_RS07965	ABLW_9332	NZ_CP008706.1	829.95	829869	+	WP_000739311.1	molecular chaperone	944.5360.95	2.537048175	0.43656269	5.81902354	6.19E-09	1.45E-08	7.83863.996
ABLW_RS1480	ABLW_2921	NZ_CP008706.1	2930821	293.828	+	WP_000769047.1	fomylglyoxal-generating enzyme family protein	815041004	2.534667927	0.264.60038	9.59556145	8.35E-22	4.57E-21	20.3400838
ABLW_RS02365	ABLW_0481	NZ_CP008706.1	492778	493947	+	WP_001976667.1	acyl-CoA dehydrogenase family protein	478.7224629	2.534558474	0.235273048	10.77240207	4.65E-27	3.45E-26	25.462809
ABLW_RS0895	ABLW_3474	NZ_CP008706.1	352872	352851	+	WP_00009415.1	YnfJ family transcriptional regulator	481.491475	2.532964748	0.94699399	9.00968.18	1.08E-38	1.58E-37	38.9034291
ABLW_RS07260	ABLW_949	NZ_CP008706.1	9470627	1476045	+	WP_000876475.1	Cou family histone protein CouB	12.4.073787	2.52767001	1.30748449	19.32922935	0.003245692	0.063705021	1.8240.9441
ABLW_RS0335	ABLW_819	NZ_CP008706.1	819567	977085	+	WP_000336693.1	SMK/MK family protein	260.87887.9	2.525972339	0.207528925	12.97208.13	3.25E-34	5.93E-33	32.22864531
ABLW_RS1920	ABLW_2784	NZ_CP008706.1	2779.943	2779932	+	WP_000372413.1	Psat1 family thioesterase	33.9.932834	2.519000275	0.56094665	4.88848049	7.16E-06	1.35E-05	4.88728704
sRNA71								229.3661001	2.519281102	0.373114693	6.74668403	1.5E-11	4.28E-11	10.38855623
ABLW_RS19455	ABLW_4103	NZ_CP008707.1	63264	63524	+	WP_000876.84.1	hypothetical protein	26.90446355	2.51924038	0.46408449	5.424475872	5.83E-08	1.27E-07	6.896.96279
ABLW_RS1915	ABLW_0083	NZ_CP008706.1	2063558	2064592	+	WP_0009656.03.1	anion channel 1.2-dioxygenase electron transfer component	9149394566	2.516954656	0.255392324	9.854538588	6.55E-23	3.80E-22	21.4202.84
ABLW_RS18755	ABLW_2830	NZ_CP008706.1	2832624	28373.0	-	WP_00086594.1	RHS repeat-associated core domain							

ABUW_RS08530	ABUW_1751	NZ_CP080706.1	1748425	1748784	+	WP_000798370.1		hypothetical protein	139.7445939	2.40913259	0.369773661	6.520743231	6.776-11	1.82E-10	9.739928612
ABUW_RS08550	ABUW_414	NZ_CP080707.1	73493	74920	+	WP_000692620.1		conjugal transfer protein TraH	3.8.9045266	2.40368971	0.200803239	1155167512	7.25E-31	6.73E-30	29.1794844
ABUW_RS08360	ABUW_2806	NZ_CP080706.1	2804292	2805543	+	WP_000428942.1		APC family permease	250.3002645	2.399726439	0.27268872	8.8002412	1.37E-16	6.02E-16	17.2240351
ABUW_RS04725	ABUW_0963	NZ_CP080706.1	973225	974205	+	WP_001022403.1		glycosyltransferase family 2 protein	90.86496627	2.396090198	0.2553071	9.387479617	6.8E-21	3.8E-20	16.9757288
ABUW_RS02690	ABUW_0548	NZ_CP080706.1	553035	553226	+	WP_001043411.1		hypothetical protein	83.58032267	2.39167993	0.3041254	7.863056204	3.75E-15	1.34E-14	13.8728952
srpNA4	no	no	no	no	no	no	no	no	3728.887349	2.389373815	0.441587766	5.41715192	6.24E-08	1.36E-07	6.866461932
ABUW_RS0520	no	NZ_CP080706.1	386518	386534	-	WP_000350168.1		hypothetical protein	69.2611911	2.382272341	0.395888863	6.017520599	1.77E-09	4.30E-09	8.365531644
ABUW_RS16510	ABUW_1984	NZ_CP080706.1	3232358	3223809	+	WP_001162572.1		YerUAcR family transcriptional regulator	40.66063937	2.378790322	0.345617243	6.88273044	5.87E-12	1.71E-11	10.76703089
ABUW_RS06290	ABUW_0290	NZ_CP080706.1	938558	130919	+	WP_000435252.1		hypothetical protein	100.4257185	2.378140510	0.325933544	7.308505331	2.70E-10	8.50E-10	12.0600684
ABUW_RS1915	ABUW_2702	NZ_CP080706.1	2686206	2686535	+	WP_000898495.1		hypothetical protein	190.1027261	2.374534436	0.431048547	5.504908856	3.69E-08	8.81E-08	7.08724696
ABUW_RS02730	ABUW_0555	NZ_CP080706.1	556947	557147	+	WP_001030085.1		TraR/DnaK C4-type zinc finger protein	34.0185448	2.372385381	0.426290032	5.565190838	2.62E-08	5.86E-08	7.23212384
ABUW_RS16755	ABUW_3245	NZ_CP080706.1	3274482	3275369	+	WP_000781588.1		hypothetical protein	2351178804	2.370593231	0.203496974	1164928002	2.31E-31	2.21E-30	29.65560773
ABUW_RS20465	ABUW_1663	NZ_CP080706.1	655820	655993	+	WP_001159332.1		hypothetical protein	37.25054944	2.369458988	0.449433255	5.273162269	1.34E-07	2.82E-07	6.549750892
ABUW_RS12580	ABUW_2589	NZ_CP080706.1	2581722	2582075	+	WP_001118143.1		helic-tum-helic transcriptional regulator	40.38190387	2.362679766	0.304729127	7.753376864	8.95E-15	3.13E-14	19.0445566
ABUW_RS10350	ABUW_0620	NZ_CP080706.1	621975	622190	-	WP_000919228.1		metal-dependent hydrolase	304.3910207	2.36202045	0.23398311	9.10564368	4.04E-24	2.53E-23	22.59687948
ABUW_RS14425	ABUW_2349	NZ_CP080706.1	2335033	2335022	+	WP_000804509.1		tautomerase family protein	1324.073997	2.355867767	0.243383806	9.679640581	3.68E-22	2.05E-21	20.6882464
ABUW_RS02675	ABUW_0545	NZ_CP080706.1	545925	546808	-	WP_001178668.1		hypothetical protein	1810290682	2.353517466	0.181262271	14.5976053	2.91E-48	7.51E-47	46.12436006
ABUW_RS06395	ABUW_0752	NZ_CP080706.1	745641	751165	+	WP_000933101.1		AAA family ATPase	87.47110033	2.35316637	0.260816572	9.222033894	1.84E-19	8.68E-19	10.0618027
ABUW_RS02335	ABUW_2537	NZ_CP080706.1	2530673	2530052	-	WP_000470954.1		L-serine ammonia-lyase	193.078033	2.350926257	0.155816235	9.58791159	1.95E-51	5.91E-50	49.23562397
ABUW_RS06555	ABUW_1756	NZ_CP080706.1	1760576	1762006	+	WP_000632782.1	lytU	lytU	291.3009204	2.350975401	0.17195146	9.65998474	1.54E-42	2.83E-41	40.54821503
ABUW_RS06890	ABUW_3473	NZ_CP080706.1	3521217	3521822	+	WP_000053846.1		glutathione S-transferase family protein	1229.767908	2.348824508	0.171987064	9.10822657	2.95E-39	4.44E-38	37.35261703
ABUW_RS05055	ABUW_0239	NZ_CP080706.1	921663	923279	+	WP_001091558.1		AacA family ABC transporter permease	64.45730412	2.348269264	0.360835233	5.507871513	7.62E-11	2.04E-10	9.69036833
ABUW_RS08985	ABUW_2056	NZ_CP080706.1	2035097	2036884	+	WP_000718470.1		DUF4882 family protein	429.0684263	2.34305803	0.29978109	7.80014903	5.45E-15	1.92E-14	13.71669877
ABUW_RS19890	no	NZ_CP080706.1	281990	2816437	-			hypothetical protein	78.5932906	2.340781559	0.398387608	6.575588269	4.21E-09	9.93E-09	8.003050752
ABUW_RS07265	ABUW_1490	NZ_CP080706.1	1416039	1416872	+	WP_001886519.1	cusC	Cus fibrillar biogenesis chaperone CusC	304.6606152	2.337159464	1.02483682	2.080270293	0.037500748	0.047245314	13.0264156
ABUW_RS14505	ABUW_2395	NZ_CP080706.1	2383496	2383897	+	WP_000587903.1	madL	metal-dependent hydrolase	158.182647	2.336891789	0.265012333	8.818305685	1.16E-16	5.17E-16	17.28605946
ABUW_RS18445	ABUW_2479	NZ_CP080706.1	2410317	2410453	+	WP_000912951.1		hypothetical protein	249.4369006	2.335958212	0.336017789	6.951888158	3.60E-12	1.07E-11	10.9701622
ABUW_RS18101	ABUW_2649	NZ_CP080706.1	2670707	2671000	+	WP_000644336.1		DUF4142 domain-containing protein	1525.376016	2.335599210	0.603910673	3.86743182	0.000109562	0.000195466	37.458246266
srNA7.4	no	no	no	no	no	no	no	no	67.06418988	2.334052651	0.31437296	7.446633432	9.58E-14	3.10E-13	12.50445506
ABUW_RS06860	ABUW_1607	NZ_CP080706.1	1608598	1607317	+	WP_001223091.1		hypothetical protein	59.68875101	2.330843352	0.274109625	5.503475031	1.84E-17	7.65E-17	16.18633586
ABUW_RS04716	ABUW_0961	NZ_CP080706.1	971189	972355	+	WP_001188068.1		glycosyltransferase family 39 protein	100.145824	2.329796684	0.228746291	8.9506967	2.31E-24	1.47E-23	22.83268207
ABUW_RS11415	ABUW_2353	NZ_CP080706.1	2336186	2336918	+	WP_000451873.1		LygE family transcription factor	85.50730511	2.328575254	0.302312191	7.702324611	1.34E-14	4.61E-14	13.33829907
ABUW_RS19165	ABUW_1323	NZ_CP080706.1	1343284	1344714	+	WP_001040106.1		trehalase-6-phosphate synthase	9244.358405	2.3284615	0.149569404	5.616572556	1.95E-08	4.40E-08	7.356847324
ABUW_RS11400	ABUW_2344	NZ_CP080706.1	2327461	2328198	+	WP_000342693.1		Csp/Flr family transcriptional regulator	212.8547762	2.326078985	0.216425394	9.74771745	6.07E-27	4.50E-26	25.34478749
ABUW_RS19305	ABUW_2700	NZ_CP080706.1	2684897	2685621	+	WP_000825869.1		hypothetical protein	704.1874478	2.32309071	0.222746184	6.42931768	1.82E-25	1.24E-24	23.90657631
ABUW_RS01370	ABUW_0279	NZ_CP080706.1	296818	297117	+	WP_000690905.1		hypothetical protein	3203.81973	2.322668567	0.191519985	11.90257784	1.15E-32	1.20E-31	30.92081875
ABUW_RS04425	ABUW_0117	NZ_CP080706.1	9310265	9311996	+	WP_000439615.1		hypothetical protein	3185.732323	2.321093336	0.276701817	3.381763961	4.96E-17	2.01E-16	16.69803394
ABUW_RS10335	ABUW_2685	NZ_CP080706.1	2675827	2675631	+	WP_001004676.1		hypothetical protein	718.121852	2.32104527	0.490815556	4.728978253	2.26E-06	4.30E-06	5.366531544
ABUW_RS06160	ABUW_0757	NZ_CP080706.1	752047	175453	+	WP_000937775.1		amino acid permease	17.8273526	2.318901235	0.217748452	10.64944994	1.75E-26	1.27E-25	24.89819628
ABUW_RS06200	ABUW_0270	NZ_CP080706.1	929195	929912	+	WP_000200304.1		replication protein	49.912657	2.31620996	0.325680156	7.10367174	1.21E-12	3.70E-12	14.1179828
ABUW_RS04825	ABUW_0694	NZ_CP080706.1	959126	959179	+	WP_000920020.1	rdaA	rhambo-target A	190.691683	2.310280079	0.19731625	11.2077754	9.98E-32	9.83E-31	30.0074468
ABUW_RS12360	ABUW_3149	NZ_CP080706.1	3167284	3167472	+	WP_000735804.1		NF0382 family lipoprotein	102.945047	2.310231919	0.388004194	6.458167943	1.08E-10	2.85E-10	9.54515514
ABUW_RS12455	ABUW_3149	NZ_CP080706.1	3164714	3166807	+	WP_000200956.1		hypothetical protein	139.458006	2.305518875	0.221891473	9.39029597	2.74E-25	1.84E-24	23.7331812
ABUW_RS08705	ABUW_0188	NZ_CP080706.1	1783706	1784032	+	WP_000955082.1		hypothetical protein	185.633958	2.30433962	0.187662581	12.79271061	1.17E-34	1.37E-33	32.86327943
ABUW_RS04340	ABUW_0118	NZ_CP080706.1	931896	932630	+	WP_000959543.1		hypothetical protein	984.206219	2.301944562	0.255017734	9.02662458	1.77E-19	8.38E-19	16.0781032
ABUW_RS09520	ABUW_1657	NZ_CP080706.1	1658926	1659366	+	WP_000931019.1		HD domain-containing protein	145.069345	2.300218658	0.219389547	6.72916488	7.43E-27	5.48E-26	25.26121844
ABUW_RS19100	ABUW_4016	NZ_CP080707.1	8119	8451	+	WP_000665581.1		hypothetical protein	867.9854412	2.299173172	0.101216162	9.94219049	7.25E-28	5.67E-27	26.24416104
ABUW_RS08780	ABUW_2014	NZ_CP080706.1	2005890	2007104	+	WP_000609268.1		hypothetical protein	428.283719	2.293852348	0.172636628	13.28719072	2.75E-40	4.43E-39	38.35596627
ABUW_RS08620	ABUW_0988	NZ_CP080706.1	1042569	1042760	+	WP_001072331.1		hypothetical protein	34.2834844	2.284167983	0.618318609	5.486566612	4.10E-08	9.03E-08	7.04431225
ABUW_RS13835	ABUW_3372	NZ_CP080706.1	341010	341170	+	WP_001085070.1		4'-phosphopentetheinyl transferase superfamily protein	7613.908076	2.280959852	0.169989934	6.14820242	4.73E-41	7.94E-40	39.1001795
ABUW_RS08880	ABUW_2654	NZ_CP080706.1	2651066	2652004	+	WP_000471735.1		hypothetical protein	24.6180945	2.280860149	0.355983457	6.406741255	1.49E-10	3.89E-10	9.410050399
ABUW_RS07285	ABUW_1494	NZ_CP080706.1	1481995	1481592	+	WP_000997611.1		hypothetical protein	24.5088255	2.280453758	0.336709176	6.727169868	1.26E-11	3.60E-11	10.4436975
ABUW_RS09375	ABUW_0812	NZ_CP080706.1	786993	790199	+	WP_000107290.1		hypothetical protein	1456.005810	2.27894289	0.275168084	8.282944556	1.20E-16	4.75E-16	32.5330639
srNA2.1	no	no	no	no	no	no	no	no	55.78686547	2.278197233	0.466593607	4.882615619	1.05E-06	2.06E-06	5.68619278
ABUW_RS10195	ABUW_2469	NZ_CP080706.1	2416560	2462421	+	WP_000101937.1		SDR family oxidoreductase	2137.113262	2.277884289	0.39508831	5.765502123	8.16E-09	1.89E-08	7.72330838
ABUW_RS05995	ABUW_0227	NZ_CP080706.1	926730	9269675	+	WP_000576648.1		acryl-CoA dehydrogenase	2404.047217	2.276263441	0.334673364	8.80143802	1.04E-11	2.97E-11	52.1742315
ABUW_RS07110	ABUW_1659	NZ_CP080706.1	1650338	1650411	+		srNA_Ttp	6075.738996	2.274746891	0.312645465	7.278803572	3.44E-10	1.08E-12	11.96657624	
ABUW_RS19165	ABUW_4034	NZ_CP080707.1	20322	20540	+	WP_001043201.1		hypothetical protein	20.99719377	2.272157163	0.465805502	4.877909854	1.07E-06	2.10E-06	5.771807705
ABUW_RS06440	ABUW_0220	NZ_CP080706.1	933301	933389	+	WP_000277446.1		hypothetical protein	45.1023011	2.269107157	0.324912295	6.9837			

ABLUW_RS187.0	ABLUW_3843	NZ_CP008706.1	3912.159	3913184	-	WP_000994544.1	ferredoxin reductase	677.296432	2.179940972	0.21603218	0.17774299	3.76E-24	2.35E-23	22.628932
ABLUW_RS0660	ABLUW_986	NZ_CP008706.1	990238	991886	+	WP_038405894.1	replication initiation factor domain-containing protein	454.6804761	2.172488611	0.28123072	7.72492378	1.0E-14	3.88E-14	10.4118827
ABLUW_RS0237.5	ABLUW_0484	NZ_CP008706.1	494759	496564	+	WP_00002862.1	DUF1446 domain-containing protein	270.2043139	2.17810447	0.363900279	5.96745061	2.4E-09	5.79E-09	8.23721436
ABLUW_RS02430	ABLUW_0790	NZ_CP008706.1	748784	748951	+	WP_000047869.1	hydrolytical protein	67.1250866	2.170619743	0.232799191	7.41339272	1.23E-13	3.99E-13	22.3990271
ABLUW_RS1915	ABLUW_4019	NZ_CP008707.1	9682	9918	+	WP_001057663.1	hydrolytical protein	762.2242829	2.19503375	0.216677849	0.101057573	1.34E-23	8.14E-23	22.0893756
ABLUW_RS0340	ABLUW_2128	NZ_CP008706.1	210872	214275	+	WP_001087542.1	lysA	665.6628746	2.183043874	0.457354997	4.72980804	2.25E-06	4.28E-06	5.36556231
ABLUW_RS0720	ABLUW_2000	NZ_CP008706.1	898587	8988723	+	WP_000747909.1	hydrolytical protein	335.06538	2.180055968	0.201654943	0.71695855	8.47E-27	8.24E-26	25.20481541
ABLUW_RS04125	ABLUW_1253	NZ_CP008706.1	125215	1232456	-	WP_000100805.1	hydrolytical protein	40.20597404	2.153695655	0.336776808	6.400688805	1.54E-10	4.03E-10	9.394694954
ABLUW_RS09555	ABLUW_965	NZ_CP008706.1	967276	968189	-	WP_00068018.1	alpha-beta hydrolase	1217760811	2.154725847	0.233646363	9.222167284	2.9E-20	1.45E-19	18.836632
ABLUW_RS180.6	ABLUW_3702	NZ_CP008706.1	3759685	3760185	-	WP_00029528.1	DUF2726 domain-containing protein	465.4388762	2.15542245	0.21035864	0.08452558	6.47E-24	4.00E-23	22.39794001
ABLUW_RS1895	ABLUW_2445	NZ_CP008706.1	2431915	2431905	+	WP_001985862.1	hydrolytical protein	39.76594994	2.149004358	0.390761673	5.499526971	3.8E-08	8.42E-08	7.074687909
ABLUW_RS6330	ABLUW_3157	NZ_CP008706.1	319336	3185072	-	WP_001001666.1	mechanosensitive ion channel	4149.22778	2.147534506	0.310633387	7.10684342	1.08E-12	3.13E-12	11.48017201
ABLUW_RS0265	ABLUW_2523	NZ_CP008706.1	2514893	2515276	-	WP_001017104.1	Paal family thioesterase	68.1266517	2.148070719	0.403635678	5.31850908	1.06E-07	2.24E-07	6.649751982
ABLUW_RS1070	ABLUW_2094	NZ_CP008706.1	2078185	2077297	-	WP_001121559.1	hydrolytical protein	5110162548	2.145433866	0.351742936	5.997222174	2.0E-09	4.85E-09	8.34258261
ABLUW_RS05690	ABLUW_183	NZ_CP008706.1	190332	189085	+	WP_001133225.1	TetR/AcrR family transcriptional regulator	26.7121692	2.109883127	0.385077937	5.55701062	2.74E-08	6.10E-08	7.212539525
ABLUW_RS10290	ABLUW_2322	NZ_CP008706.1	2306188	2307420	-	WP_000108033.1	integrase family protein	464.4134373	2.10454225	0.20929621	7.935730005	2.09E-15	7.61E-15	14.1861534
ABLUW_RS125.9	ABLUW_2575	NZ_CP008706.1	2568076	2569074	-	WP_001180395.1	tsxG type VI secretion system baseplate subunit TssG	369.6562697	2.13502689	0.261676973	8.16216252	3.29E-16	1.25E-16	14.90308999
ABLUW_RS07320	ABLUW_8601	NZ_CP008706.1	897650	897868	+	WP_00035055.1	hydrolytical protein	132.817892	2.132447731	0.446364317	4.777370526	1.78E-06	3.40E-06	5.48521883
ABLUW_RS1575	ABLUW_3125	NZ_CP008706.1	316270	3166734	-	WP_001214863.1	bfr	9289.31849	2.12877471	0.402810841	5.28479958	1.26E-07	2.65E-07	6.57619633
ABLUW_RS1010	ABLUW_2701	NZ_CP008706.1	2685172	2685705	-	WP_000253373.1	LysE family transporter	259.475051	2.127738976	0.286881993	7.41779962	1.02E-13	3.89E-13	12.4105054
ABLUW_RS08485	ABLUW_1403	NZ_CP008706.1	1404285	1405897	+	WP_000090168.1	hydrolytical protein	104.2236248	2.12149016	0.280758519	7.557202613	4.10E-14	1.38E-13	12.88012091
ABLUW_RS02655	ABLUW_903	NZ_CP008706.1	9013508	9003931	-	WP_000170633.1	hydrolytical protein	18.6996649	2.119305271	0.473266172	4.478049447	7.53E-06	1.37E-05	4.863279433
ABLUW_RS1890	ABLUW_2108	NZ_CP008706.1	2080195	2081254	+	WP_000414929.1	short-chain fatty acid transporter	1402.91259	2.117610459	0.356943786	5.93262452	2.98E-09	7.12E-09	16.5720006
ABLUW_RS9630	ABLUW_4190	NZ_CP008706.1	69525	70232	+	WP_000173353.1	e-F conjugative transfer system pilin assembly protein T	103.8727321	2.117218123	0.243910173	8.49614419	1.95E-17	8.10E-17	16.0191468
ABLUW_RS0616	ABLUW_1251	NZ_CP008706.1	1201897	121912	-	WP_001091999.1	hydrolytical protein	106.657513	2.110737182	0.231326492	9.151713379	5.60E-20	2.75E-19	18.5606671
ABLUW_RS0355	ABLUW_2101	NZ_CP008706.1	218856	2117818	-	WP_0010177517.1	thiamine pyrophosphate-dependent dehydrogenase E1 component	638.3666658	2.10779055	0.593198246	5.68437651	0.000359198	0.000560185	3.251691783
ABLUW_RS105	ABLUW_0338	NZ_CP008706.1	380776	382121	+	WP_001019048.1	S8 family serine peptidase	272.4199303	2.10877477	0.20588384	10.26734046	9.89E-25	6.40E-24	23.9382003
sRNA154	no	no	no	no	no	no	no	427.5802554	2.108931033	0.395058574	5.399405057	6.69E-08	1.45E-07	6.838631998
ABLUW_RS08285	ABLUW_1702	NZ_CP008706.1	1699654	1699244	-	WP_001025253.1	ANTAR domain-containing protein	32.76561499	2.107643346	0.322971955	6.25726371	1.677E-11	1.92E-10	9.73992861
ABLUW_RS08555	ABLUW_1406	NZ_CP008706.1	1406561	1406591	+	WP_000175487.1	hydrolytical protein	54.76596759	2.105993302	0.243000724	6.66597186	4.45E-18	1.51E-17	12.7836663
ABLUW_RS146.1	ABLUW_3781	NZ_CP008706.1	3841027	3842856	-	WP_000696976.1	AMP-binding protein	693.513358	2.10454818	0.387866103	5.42623239	5.76E-08	1.25E-07	6.90306997
ABLUW_RS1295	ABLUW_4055	NZ_CP008707.1	32905	32741	-	WP_000480966.1	APH(6)-family aminoglycoside O-phosphotransferase	480.2397999	2.1028994	0.434808936	4.83652844	1.32E-06	2.95E-06	5.19160035
ABLUW_RS08935	ABLUW_936	NZ_CP008706.1	933206	933361	+	WP_000186123.1	MFS transporter	91199398	2.102380277	0.31044966	6.70742036	1.98E-11	5.56E-11	10.25492521
ABLUW_RS1465	ABLUW_3388	NZ_CP008706.1	342811	3429424	-	WP_001084480.1	alpha-beta hydrolase	1650.71289	2.101059191	0.19623437	6.70191596	9.23E-27	6.77E-26	25.9941053
sRNA8	no	no	no	no	no	no	no	975.1777727	2.095368137	0.293202245	7.105080089	8.64E-13	2.66E-12	11.57518136
ABLUW_RS0430	ABLUW_1205	NZ_CP008706.1	1019736	1020053	+	WP_000916029.1	NF3.1	843.184283	2.09554354	0.193345203	12.8304823	1.04E-37	1.43E-36	35.84466336
ABLUW_RS0560	ABLUW_962	NZ_CP008706.1	958484	958699	+	WP_001050637.1	aromatic-mg-hydrolyzing dioxygenase subunit beta	714.8232455	2.093664323	0.430385197	4.864629033	1.05E-06	2.24E-06	5.649751982
ABLUW_RS0430	ABLUW_1310	NZ_CP008706.1	1322244	1322759	+	WP_001185605.1	hydrolytical protein	38.81504465	2.088614161	0.424403057	4.9858894	8.81E-07	1.74E-06	5.759450752
ABLUW_RS025	ABLUW_2578	NZ_CP008706.1	2571422	2571825	+	WP_000653195.1	type VI secretion system tube protein Hcp	7035.970453	2.079499907	0.243460432	8.54142868	1.13E-17	5.58E-17	16.2313658
ABLUW_RS1585	ABLUW_2787	NZ_CP008706.1	2794454	2794878	-	WP_002017624.1	hydrolytical protein	114.791816	2.078706529	0.281272069	7.390376653	1.46E-13	4.73E-13	12.3251886
ABLUW_RS04730	ABLUW_0964	NZ_CP008706.1	974202	974996	-	WP_001140939.1	OrnG/Hsp45 family deacetylase	17.6187345	2.07884516	0.228720084	9.08169106	10.9E-19	4.84E-19	16.31516454
ABLUW_RS0835	ABLUW_0749	NZ_CP008706.1	748422	748688	+	WP_000051086.1	hydrolytical protein	213.703718	2.078430491	0.263051741	7.901460871	2.76E-15	9.93E-15	14.0030575
ABLUW_RS1250	ABLUW_3749	NZ_CP008706.1	3805847	3805855	-	WP_000625445.1	glutathione-S-transferase	939.019193	2.076372106	0.169940518	12.98215211	1.54E-38	2.22E-37	36.5534703
ABLUW_RS1635	ABLUW_2329	NZ_CP008706.1	239907	2319623	-	WP_000525882.1	energy transducer TonB	67.8827313	2.07394173	0.254909946	8.13214917	4.23E-16	1.60E-16	14.79888002
ABLUW_RS0590	ABLUW_267239	NZ_CP008706.1	2672329	2678463	-	WP_000366300.1	hydrolytical protein	226.7999471	2.072143758	0.425483129	4.87010547	1.05E-06	2.86E-06	5.66143506
ABLUW_RS16290	ABLUW_3757	NZ_CP008706.1	3813340	3813777	-	WP_000483007.1	DoxB family protein	910.6206783	2.065188982	0.204802769	10.08382378	6.5E-24	4.03E-23	22.39408495
ABLUW_RS16085	ABLUW_3311	NZ_CP008706.1	3345204	3346025	+	WP_000697823.1	SCR family NAD(P)-dependent oxidoreductase	276.0305649	2.064716107	0.216302923	9.535670396	1.49E-21	8.05E-21	20.0942041
ABLUW_RS06760	ABLUW_1386	NZ_CP008706.1	1397810	1398100	-	WP_00051210.1	hydrolytical protein	9149219891	2.063259561	0.274852329	7.06042424	6.05E-14	2.01E-13	12.69680394
ABLUW_RS06730	ABLUW_1379	NZ_CP008706.1	1392461	1392841	-	WP_000720499.1	hydrolytical protein	132.909218	2.061086729	0.382128571	5.393214471	6.92E-08	1.49E-07	6.826815732
ABLUW_RS0470	ABLUW_2155	NZ_CP008706.1	2158211	2158435	-	WP_00026811.1	hydrolytical protein	910.573221	2.061027616	0.262929228	7.839648076	4.52E-15	1.60E-14	13.79588002
ABLUW_RS1000	ABLUW_2677	NZ_CP008706.1	2668857	2669210	-	WP_000105451.1	hydrolytical protein	3114473985	2.059540073	0.247901635	8.307892251	9.74E-17	3.88E-16	11.618827
ABLUW_RS04730	ABLUW_1561	NZ_CP008706.1	1545854	1545047	-	WP_000020771.1	hydrolytical protein	3114948929	2.058258383	0.215149385	6.65412494	4.62E-22	2.57E-21	20.9006688
ABLUW_RS06270	ABLUW_1286	NZ_CP008706.1	1306188	1306541	+	WP_000193006.1	hydrolytical protein	504.7512917	2.05653845	0.377449996	3.56157891	0.000388801	0.000575039	3.2403207
ABLUW_RS0145	ABLUW_0257	NZ_CP008706.1	1293889	1294740	+	WP_0001993522.1	PD-(D)EJK nuclease-like domain-containing protein	49.3803484	2.055059518	0.29407668	6.988298628	2.78E-12	8.29E-12	10.19845447
ABLUW_RS1675	ABLUW_2166	NZ_CP008706.1	216934	2169134	-	WP_000564581.1	hydrolytical protein	2939.355429	2.054163432	0.358705437	5.72602436	1.02E-08	2.36E-08	7.627076799
ABLUW_RS0160	ABLUW_867	NZ_CP008706.1	854338	154276	+	WP_000513011.1	pgsA	95.4392074	2.05263948	0.27129591	7.567903898	3.79E-14	1.27E-13	12.6961928
ABLUW_RS1490	ABLUW_3180	NZ_CP008706.1	3220777	3221236	+	WP_001063741.1	hydrolytical protein	209.8196384	2.051666472	0.312080262	6.57483305	4.88E-11	1.33E-10	9.87614839
ABLUW_RS10220	ABLUW_2724	NZ_CP008706.1	2716587	2719901	+	WP_001037898.1	hydrolytical protein	7937.004811	2.045472405	0.384787238	5.31853026	1.06E-07	2.25E-07	6.647817482
ABLUW_RS10710	ABLUW_3039	NZ_CP008706.1	306535	3066097	-	WP_000890283.1	GNA1 family N-acetyltransferase	103.818814	2.0436719813	0.2583723	7.909825927	2.58E-15	9.29E-15	10.93198429
ABLUW_RS1660	ABLUW_4116	NZ_CP008707.1	77886	78528	-	WP_001070851.1	transglycoylase SL1 domain-containing protein	232.0896999	2.03976886	0.20919168	9.73238743	2.19E-22	1.24E-21	20.90657831
ABLUW_RS0585	ABLUW_25													

ABUW_RS0880	ABUW_1761	NZ_CP080706.1	1758355	1758993	-	WP_00032547.1	SOS response-associated peptidase family protein	561.7360635	1.975092986	0.361694595	5.460664922	4.74E-08	1.04E-07	6.08266661
ABUW_RS1035	ABUW_2087	NZ_CP080706.1	2007717	2008955	-	WP_00_125281.1	hypothetical protein	53.9691006	1.969690256	0.31990073	6.3133067	7.23E-10	7.03E-10	9.63044675
irNA22	no	no	no	no	no	no	no	240.0879651	1.969321094	0.267459368	7.363066421	1.80E-10	5.77E-10	12.2388491
ABUW_RS105	ABUW_0226	NZ_CP080706.1	24784	247372	-	WP_00_125535.1	hypothetical protein	294.4005845	1.967699347	0.28841018	6.82250947	8.95E-12	2.58E-11	9.08838029
ABUW_RS2865	ABUW_0583	NZ_CP080706.1	57742	578220	+	WP_000289874.1	terminase family protein	18.3857239	1.964073468	0.230670249	8.94889946	2.59E-10	9.67E-10	5.01645753
ABUW_RS2970	ABUW_2011	NZ_CP080706.1	2004993	2005199	+	WP_000747908.1	hypothetical protein	329.3991918	1.957408510	0.197346698	9.92366697	3.28E-23	1.95E-22	2.170996539
ABUW_RS0550	ABUW_1771	NZ_CP080706.1	2162260	2163003	-	WP_000787501.1	adenosylcobalamin-GDP ribazoletransferase	273.7706471	1.957164236	0.169339584	2.28297901	1.07E-34	1.32E-33	32.87942607
ABUW_RS20420	ABUW_0544	NZ_CP080706.1	549097	549287	-	WP_00_161076.1	hypothetical protein	69.88054721	1.952819454	0.226897625	8.64203401	7.04E-10	3.01E-17	8.5214355
ABUW_RS03235	ABUW_0257	NZ_CP080706.1	14694	141885	+	WP_00_1039861.1	hypothetical protein	5.954970032	1.952473943	0.677919485	2.6797911	0.003979387	0.005600053	2.251807863
ABUW_RS1810	ABUW_2427	NZ_CP080706.1	241050	241651	+	WP_00116398.1	response regulator	174.494041	1.95228938	0.232926267	8.379551351	5.33E-17	2.16E-16	15.6675654
ABUW_RS06480	ABUW_0328	NZ_CP080706.1	1340370	1340558	+	WP_00_187968.1	hypothetical protein	108.7459871	1.949051242	0.288335571	6.75107723	1.47E-11	4.18E-11	10.38090667
ABUW_RS19390	ABUW_4078	NZ_CP080707.1	41962	50288	-	WP_00_152522.1	hypothetical protein	250.9757814	1.944561971	0.198024404	8.918809735	9.25E-23	5.51E-22	2.127490548
ABUW_RS03525	ABUW_915	NZ_CP080706.1	91454	915933	+	WP_00_125710.1	hypothetical protein	130.8599751	1.943901823	0.232644695	8.356633304	6.55E-17	2.61E-16	15.83335949
ABUW_RS12375	ABUW_2546	NZ_CP080706.1	253869	2533799	-	WP_00_00615330.1	(2Fe-2S)-binding protein	36.8866973	1.943494326	0.352912849	5.507006701	3.65E-08	8.09E-08	7.092051478
ABUW_RS03970	ABUW_0811	NZ_CP080706.1	789307	789573	+	WP_000091211.1	hypothetical protein	1370.389869	1.930787737	0.232412594	8.307586546	9.77E-17	3.89E-16	5.4100504
ABUW_RS20760	ABUW_0543	NZ_CP080706.1	548787	549104	-	WP_000469558.1	hypothetical protein	17.362769	1.92703677	0.225517756	8.542678139	1.33E-17	5.54E-17	16.25649024
ABUW_RS08855	ABUW_1820	NZ_CP080706.1	181469	1816876	+	WP_000171433.1	nuclear transport factor 2 family protein	135.264739	1.92699177	0.236086356	8.22255591	3.29E-16	1.25E-15	14.90308999
ABUW_RS0685	ABUW_1753	NZ_CP080706.1	175416	175188	-	WP_00056920.1	CBS domain-containing protein	1330.431949	1.92602542	0.230057867	8.37191653	5.67E-17	2.28E-16	5.64260515
ABUW_RS1620	ABUW_2429	NZ_CP080706.1	2418383	2418836	-	WP_000376210.1	LysX/Csr family transcriptional regulator	148.5125537	1.925545547	0.24418076	7.88516049	3.12E-15	1.9E-15	1.95078798
ABUW_RS1790	ABUW_2505	NZ_CP080706.1	2500223	2501039	-	WP_000606070.1	MF5 transporter	77.9750462	1.92350522	0.276891625	5.94702395	3.73E-12	1.10E-11	8.95060731
ABUW_RS07990	ABUW_1637	NZ_CP080706.1	1635040	1635723	+	WP_000920711.1	SDR family NAD(P)-dependent oxidoreductase	232.589153	1.923143046	0.37449682	6.110124261	9.96E-10	2.47E-09	8.607303047
ABUW_RS12715	ABUW_2619	NZ_CP080706.1	2618733	2619780	+	WP_002117666.1	serine hydrolase	411.048039	1.921993827	0.162716681	12.58535622	2.54E-36	3.28E-35	34.48412616
ABUW_RS00995	ABUW_1668	NZ_CP080706.1	1665485	1666702	+	WP_085920624.1	hypothetical protein	9.08203253	1.920626755	0.49544214	9.321925794	8.73E-05	0.000144228	3.84094594
ABUW_RS19635	ABUW_6001	NZ_CP080709.1	1	1182	+	WP_002171233.1	protein exp	865.122095	1.920288079	0.108203628	17.74700064	1.62E-10	1.47E-08	67.8326207
ABUW_RS1910	ABUW_2090	NZ_CP080706.1	201670	2016120	-	WP_000664114.1	LyxR family transcriptional regulator	30.40782222	1.919108088	0.388828333	4.93319191	8.09E-07	1.60E-06	5.79580071
ABUW_RS01920	ABUW_0212	NZ_CP080706.1	121061	121504	-	WP_000464149.1	DUF7275 domain-containing protein	300.722539	1.918249196	0.289031754	6.629167591	3.36E-11	9.22E-11	10.0326908
ABUW_RS02995	ABUW_1609	NZ_CP080706.1	1610252	1610932	-	WP_000276394.1	hypothetical protein	96.21282281	1.918286428	0.221759221	6.636783176	5.78E-16	2.48E-17	6.60548132
ABUW_RS00975	ABUW_2054	NZ_CP080706.1	2032229	2034787	+	WP_00_1104963.1	fmbral/biogenesis outer membrane usher protein	1242.003872	1.918208001	0.416438991	4.60281867	4.19E-06	7.78E-06	5.190920403
ABUW_RS12115	ABUW_0720	NZ_CP080706.1	725967	726196	+	WP_001103936.1	hypothetical protein	906.004108	1.918242036	0.203091046	8.270519475	1.33E-16	5.25E-16	12.978407
ABUW_RS05665	ABUW_1167	NZ_CP080706.1	1165247	1166161	+	WP_000773316.1	DMT family transporter	615.9776709	1.908883389	0.276792901	8.696431889	5.33E-12	1.56E-11	10.8087574
ABUW_RS05625	ABUW_1169	NZ_CP080706.1	1167559	1167749	+	WP_000887451	aromatic acid-hydroxylating dihydrogenase subunit alpha	433.5593402	1.906450648	0.239192712	7.91747203	1.57E-15	5.77E-15	14.23828194
ABUW_RS0490	ABUW_0330	NZ_CP080706.1	1340816	1341151	+	WP_00_183861.1	hypothetical protein	854.097805	1.905351161	0.250939565	7.592889033	3.10E-14	1.08E-13	12.9788107
ABUW_RS08290	ABUW_1793	NZ_CP080706.1	1799629	1799970	+	WP_000114559.1	hypothetical protein	5.131636546	1.904851610	0.769039037	2.476930362	0.012310775	0.017499641	1.756970861
ABUW_RS09860	ABUW_2055	NZ_CP080706.1	2034794	2035794	+	WP_000821735.1	type II fibrinogen	424.176817	1.904099976	0.32576536	5.846307209	5.03E-09	1.18E-08	7.92811799
ABUW_RS19160	ABUW_4033	NZ_CP080707.1	19633	20282	+	WP_000719033.1	hypothetical protein	662.36331	1.904635569	0.26895684	7.08166537	1.43E-12	4.32E-12	11.36451625
ABUW_RS00870	ABUW_1759	NZ_CP080706.1	1755337	1756815	+	WP_00_1264004.1	S8 family peptidase	892.6927832	1.903553254	0.191242832	9.953592071	2.43E-23	1.45E-22	2.1386832
ABUW_RS02025	ABUW_0233	NZ_CP080706.1	1275970	1277508	-	WP_000976525.1	OmpW family protein	353.0831077	1.90246341	0.26209338	2.258723626	3.99E-13	1.22E-12	1.91064017
ABUW_RS03640	ABUW_0900	NZ_CP080706.1	118168	1181481	-	WP_000692540.1	stress-responsive nuclear envelope protein	20.43787207	1.909886914	0.4032315953	4.71133513	2.46E-06	4.68E-06	5.32974547
ABUW_RS19875	ABUW_2237	NZ_CP080706.1	2226621	2228168	+	WP_085920587.1	NAD(P)FAD-dependent oxidoreductase	276.9686729	1.897576365	0.239352765	6.927948389	2.23E-16	8.08E-16	14.09258864
ABUW_RS08525	ABUW_0564	NZ_CP080706.1	174526	191776	+	WP_000032556.1	glycosyltransferase family 2 protein	1291489325	1.89610379	0.259289983	7.310576586	2.62E-10	8.34E-13	12.07883393
ABUW_RS0820	ABUW_2022	NZ_CP080706.1	2011470	2011676	+	WP_000747909.1	glucanase	352.707229	1.895098965	0.192039816	8.68620731	5.78E-23	3.33E-22	2.147755577
ABUW_RS0320	ABUW_3341	NZ_CP080706.1	3373439	3375497	+	WP_000534868.1	lysine-type recombinase/Integrase	1988.99801	1.893346331	0.19303674	7.9640371	1.52E-22	8.62E-22	2.10649271
ABUW_RS07620	ABUW_1641	NZ_CP080706.1	1627863	1628459	+	WP_000243522.1	alpha-E domain-containing protein	258.0434316	1.891878345	0.278788011	6.785006058	1.6E-11	3.32E-11	10.4786862
ABUW_RS17330	ABUW_2309	NZ_CP080706.1	2393458	2393808	-	WP_00_1061911.1	hypothetical protein	184.197011	1.88970132	0.388183738	6.5581912	5.45E-11	1.48E-10	9.829738285
ABUW_RS03930	ABUW_0306	NZ_CP080706.1	820050	8200810	-	WP_000175448.1	enoyl-CoA hydratase/isomerase family protein	714.2614983	1.887386302	0.227355512	6.289494317	1.09E-16	4.31E-16	16.3652273
ABUW_RS19105	ABUW_4017	NZ_CP080707.1	84665	88869	+	WP_00_170890.1	hypothetical protein	276.4095979	1.886889244	0.260617232	7.240278587	4.48E-10	1.40E-10	11.6538796
ABUW_RS19535	ABUW_4111	NZ_CP080707.1	70277	72239	+	WP_002072594.1	tsaN conjugate transfer protein TraN	647.519621	1.885023449	0.14567384	12.9493501	3.37E-37	3.34E-37	36.4782353
ABUW_RS03935	ABUW_0111	NZ_CP080706.1	12333	124020	+	WP_00_1258718.1	DUF3800 domain-containing protein	569.8471089	1.884189613	0.216669297	6.89061634	3.35E-16	1.45E-17	9.838632
ABUW_RS1635	ABUW_2371	NZ_CP080706.1	2337960	2338388	+	WP_000380131.1	arsC	8.27682319	1.882634311	0.410509142	4.558238915	6.29E-06	9.76E-06	5.01550592
ABUW_RS19210	ABUW_2237	NZ_CP080706.1	22327	22356	+	WP_00_106429.1	helicium-helic transcriptional regulator	498.8043035	1.882365051	0.337955626	5.96858598	2.55E-08	5.72E-08	7.242603971
ABUW_RS00260	ABUW_1602	NZ_CP080706.1	1602188	1603495	+	WP_000849751.1	sorbitone dehydrogenase family protein	998.888758	1.879663458	0.26260573	7.51610467	8.30E-10	2.56E-12	11.69176003
ABUW_RS06465	ABUW_1683	NZ_CP080706.1	1689175	169432	-	WP_03845895.1	hypothetical protein	4918.01842	1.878950072	0.253677318	7.398918663	1.37E-10	4.44E-13	12.3526793
ABUW_RS0895	ABUW_3880	NZ_CP080706.1	3848556	3849473	+	WP_000714235.1	matrin family metalloproteinase	5144406483	1.868252611	0.367913292	5.07769886	3.8E-07	7.7E-07	6.11205462
ABUW_RS0925	ABUW_0801	NZ_CP080706.1	776711	777712	+	WP_000835376.1	KiA-N domain-containing protein	9502.655765	1.867921665	0.220082532	4.87264906	2.12E-17	7.7E-17	10.0570041
ABUW_RS1805	ABUW_2426	NZ_CP080706.1	2410094	2411003	+	WP_000062627.1	response regulator transcription factor	88.03424971	1.865232589	0.199941256	9.329003045	1.07E-20	5.45E-20	19.2636035
ABUW_RS14025	ABUW_2887	NZ_CP080706.1	2894571	2894721	+	WP_000749178.1	copper resistance protein NprE	1285.46824	1.864750726	0.329310336	6.862564754	1.49E-08	3.40E-08	7.46852103
ABUW_RS19140	ABUW_4023	NZ_CP080707.1	1251	12924	+	WP_000724905.1	Park family protein	3454.018665	1.861983642	0.199299992	9.343991035	9.28E-21	4.76E-20	19.32393905
ABUW_RS19900	no	NZ_CP080706.1	284329	2844051	+		glutathione S-transferase	11.3323059	1.85817918	0.23569148	7.886547798	3.18E-15	1.11E-14	13.95467702
ABUW_RS12870	ABUW_2609	NZ_CP080706.1	2602371	2603812	-	WP_00_1048897.1	LyxR family transcriptional regulator/MunR	627.6972322	1.858443816	0.252925287	7.347691414	2.02E-10	6.46E-10	12.89276748
ABUW_RS14890	ABUW_3008	NZ_CP080706.1	3095531	3096091	+	WP_00_1884886.1	hypothetical protein	242.7292224	1.85					

ABLUW_RS0965	ABLUW_567	NZ_CP008706.1	969305	197047	-	WP_000049720.1	SDR family NAD(P)-dependent oxidoreductase	62.35559783	1.77788810	0.252761545	7.033066731	2.02E-12	6.07E-12	11.268181
newcardRNA1	no	no	no	no	no	no	no	238.6279859	1.77702596	0.675606702	2.630232339	0.008532653	0.01510381	193860844
ABLUW_RS0360	ABLUW_2102	NZ_CP008706.1	219893	219169	+	WP_000364558.1	lipA	500.7776	1.7482971	0.33905671	5.23404343	1.65E-07	3.45E-07	6.462490905
ABLUW_RS0470	ABLUW_0083	NZ_CP008706.1	91299	91937	+	WP_000414387.1		278.3767724	1.77321058	0.227756395	7.785566719	6.94E-15	2.44E-14	9.61061017
ABLUW_RS1675	ABLUW_2400	NZ_CP008706.1	2387183	2387462	+	WP_000448952.1	malonate decarboxylase subunit delta	185.82535069	1.71725705	0.488855335	3.625718484	0.000288161	0.000452456	3.344423648
ABLUW_RS0495	ABLUW_2860	NZ_CP008706.1	2140911	2142017	+	WP_000734917.1	porin	319.0609185	1.771965734	0.177896874	9.957261908	2.34E-23	1.46E-22	21.8537196
ABLUW_RS1055	ABLUW_2091	NZ_CP008706.1	2061843	2063508	+	WP_000204398.1	antA	63.5334186	1.789919710	0.31410629	5.634760499	1.75E-08	3.97E-08	7.401020943
ABLUW_RS0910	ABLUW_1210	NZ_CP008706.1	1250283	1251074	+	WP_000830596.1	hypothetical protein	1727.004105	1.768835563	0.17177412	10.33334682	4.98E-25	3.38E-24	23.84410616
ABLUW_RS0720	ABLUW_0962	NZ_CP008706.1	972845	973225	+	WP_000407363.1	GtaK family protein	24.46107772	1.768741957	0.407564387	4.339782758	1.43E-05	2.53E-05	4.596979479
ABLUW_RS0850	ABLUW_1755	NZ_CP008706.1	1750160	1750609	+	WP_001046785.1	Lrp/KonC family transcriptional regulator	10.2319464	1.766696267	0.290447703	6.082228393	1.19E-09	2.93E-09	8.53315238
ABLUW_RS0292	ABLUW_2052	NZ_CP008706.1	2074100	2074885	-	WP_000163854.1	3-hydroxybutyrate dehydrogenase	900.3414066	1.7634305	0.288725048	6.07646402	1.01E-09	2.51E-09	8.600326279
ABLUW_RS0970	ABLUW_1864	NZ_CP008706.1	1859752	1860705	+	WP_000218290.1	oxidoreductase	306.7263758	1.760271916	0.387684268	4.540476521	5.61E-06	1.03E-05	4.987162775
ABLUW_RS1805	ABLUW_2056	NZ_CP008706.1	2078651	2079355	+	WP_001045567.1	CoA transferase subunit A	2383.518961	1.760127045	0.327510669	5.374286854	7.69E-08	1.65E-07	6.782516056
ABLUW_RS0425	ABLUW_1271	NZ_CP008706.1	1299912	1301237	+	WP_000106166.1	AAA family ATPase	10.23406825	1.75901275	0.277462418	6.339643256	2.30E-10	5.94E-10	9.226215555
ABLUW_RS0530	ABLUW_1650	NZ_CP008706.1	1717551	1717881	+	WP_001185055.1	aldehyde dehydrogenase family protein	173.6355929	1.7570137	0.214318093	8.198235032	2.44E-16	9.43E-16	16.02548831
ABLUW_RS1265	ABLUW_2396	NZ_CP008706.1	23831951	2384883	-	WP_000146930.1	malonate decarboxylase subunit epsilon	255.9385441	1.75518845	0.252026586	6.064029053	3.38E-12	9.83E-12	11.00788851
ABLUW_RS1665	ABLUW_0542	NZ_CP008706.1	548446	548799	+	WP_002014678.1	sab	123.2808848	1.754838496	0.222610204	7.88294535	3.20E-15	1.14E-14	13.94300516
ABLUW_RS1070	ABLUW_237	NZ_CP008706.1	2301991	2302455	+	WP_001046928.1	hypothetical protein	713.2993559	1.754573148	0.362465528	4.8353314	1.33E-06	2.98E-06	5.588390294
ABLUW_RS0740	ABLUW_1517	NZ_CP008706.1	1503167	1503739	+	WP_000692365.1	nucleoside transferase 2 family protein	82.9493349	1.748090298	0.366442504	4.904270051	9.38E-07	1.85E-06	5.732828272
ABLUW_RS1655	ABLUW_3101	NZ_CP008706.1	314581	3125141	-	WP_000711615.1	GOYXLY domain-containing protein	474.4626595	1.746265597	0.165308059	11.26349075	1.99E-29	1.70E-28	27.769518
ABLUW_RS1635	ABLUW_3201	NZ_CP008706.1	3229151	3229739	+	WP_000807295.1	LysE family translocator	33.53337078	1.7424197505	0.337380227	5.16455105	2.41E-07	4.95E-07	6.305394801
ABLUW_RS1335	ABLUW_1621	NZ_CP008706.1	1619820	1620260	+	WP_000786781.1	MFS transporter	224.5867641	1.74218427	0.210706492	8.267991236	1.36E-16	5.36E-16	15.27083521
ABLUW_RS07745	ABLUW_1586	NZ_CP008706.1	1575915	1577337	+	WP_000105561.1	glutamine synthetase	142.2008056	1.741002499	0.198851508	8.845773717	1.09E-19	4.06E-18	17.39147397
ABLUW_RS0405	ABLUW_1237	NZ_CP008706.1	1280161	1280646	+	WP_000182520.1	DUF3465 domain-containing protein	331.3993169	1.738510602	0.193394673	8.989467141	1.48E-19	1.16E-18	17.93542401
ABLUW_RS1025	ABLUW_0230	NZ_CP008706.1	219413	214955	+	WP_000064186.1	type N acetyltransferase	73.1483526	1.738367509	0.226420591	7.677604158	1.62E-14	5.55E-14	13.25570702
ABLUW_RS1405	ABLUW_4164	NZ_CP008707.1	64284	64169	+	WP_000382192.1	taiv	245.69337	1.736488566	0.188261956	9.223789046	2.87E-20	1.43E-19	18.84466396
ABLUW_RS1940	ABLUW_3322	NZ_CP008706.1	3357157	3357882	-	WP_000053613.1	hypothetical protein	526.5190002	1.736322832	0.4032459	4.305866054	1.66E-05	2.93E-05	4.53315238
ABLUW_RS1790	ABLUW_2219	NZ_CP008706.1	2204612	2204980	+	WP_000197740.1	hypothetical protein	67.64746433	1.735256561	0.311460393	5.571055461	2.53E-08	5.67E-08	7.246416941
ABLUW_RS1005	ABLUW_1438	NZ_CP008706.1	1430917	1431906	-	WP_001053912.1	acyltransferase	49.82046937	1.734715084	0.469091243	3.693219967	0.0002244	0.00035091	3.542409366
ABLUW_RS10230	ABLUW_0655	NZ_CP008706.1	6107563	6107659	-	WP_000067479.1	hypothetical protein	495.6730488	1.731873654	0.266871879	4.68955481	8.61E-11	2.30E-10	3.74627184
ABLUW_RS10040	ABLUW_3707	NZ_CP008706.1	3766487	3766053	+	WP_000859337.1	basophilic family protein	60.71448759	1.732007255	0.36366255	4.509711885	6.49E-06	1.19E-05	9.024453009
ABLUW_RS1790	ABLUW_0355	NZ_CP008706.1	386667	387299	+	WP_000339167.1	hypothetical protein	187.089028	1.726858195	0.289903956	6.669879525	2.56E-11	7.15E-11	10.14752001
ABLUW_RS2105	ABLUW_1857	NZ_CP008706.1	1851777	1851608	+	WP_000161254.1	hypothetical protein	513.5381863	1.726067062	0.608534649	2.836431853	0.004062071	0.006377719	2.19533462
ABLUW_RS1612	ABLUW_3338	NZ_CP008706.1	3371851	3373072	+	WP_000388837.1	novirus-type Gp2 protein	271.2729493	1.721092977	0.21073001	8.003336307	12.1E-15	4.49E-15	14.3477366
ABLUW_RS0230	ABLUW_1678	NZ_CP008706.1	1609692	1610195	+	WP_001992587.1	YnfB/Ynf family MFS transporter	62.63640706	1.717143119	0.305732929	5.61480776	1.95E-08	4.40E-08	7.366547234
ABLUW_RS04905	ABLUW_1661	NZ_CP008706.1	1654882	1655125	+	WP_001108442.1	universal stress protein	8120.689663	1.713891967	0.219416279	6.133857625	8.58E-10	2.14E-09	6.86996227
ABLUW_RS13045	ABLUW_0619	NZ_CP008706.1	620271	621266	+	WP_000364272.1	DUF2804 domain-containing protein	304.1770249	1.713154124	0.225191853	7.608898952	2.70E-14	9.33E-14	10.0318136
ABLUW_RS1074	ABLUW_0260	NZ_CP008706.1	270884	271874	+	WP_001035486.1	SDR family NAD(P)-dependent oxidoreductase	1749.56875	1.70282814	0.461165163	3.714380734	0.000203702	0.000324265	3.489092995
ABLUW_RS04420	ABLUW_0901	NZ_CP008706.1	898201	898515	+	WP_000146267.1	hypothetical protein	657.935525	1.702036501	0.26182196	6.54496144	5.95E-11	1.61E-10	17.9371424
ABLUW_RS1010	ABLUW_0022	NZ_CP008706.1	25685	27183	+	WP_000132725.1	sodium-dependent transporter	0.88619454	1.707282254	0.188104516	0.1548679	3.16E-24	1.98E-23	22.70334841
sRNA B1	no	no	no	no	no	no	no	781.6671024	1.705642799	0.256027886	6.638944425	2.67E-11	7.41E-11	10.1018197
ABLUW_RS1085	ABLUW_1261	NZ_CP008706.1	1295066	129611	+	WP_000560785.1	hypothetical protein	1504.379185	1.70493446	0.193467426	10.4298185	1.81E-25	1.23E-24	23.91009489
ABLUW_RS1040	ABLUW_0779	NZ_CP008706.1	764737	764889	+	WP_001091449.1	hypothetical protein	3.937277268	1.703579194	1.009810555	1.687025108	0.091588518	0.16930884	0.9630884
ABLUW_RS0395	ABLUW_0794	NZ_CP008706.1	771810	774268	+	WP_000274931.1	helic-hum-helic domain-containing protein	2209.486695	1.703405923	0.205909844	8.267769197	1.36E-16	5.36E-16	15.27083521
ABLUW_RS0690	no	NZ_CP008706.1	1405799	1405649	+			59.72291029	1.702065444	0.27664467	6.162537874	7.83E-10	1.90E-09	8.786589771
ABLUW_RS1845	ABLUW_3059	NZ_CP008706.1	3085195	3086076	+	WP_000992299.1	metal-dependent hydrolase	394.9164091	1.70181085	0.203214833	8.37445703	5.55E-17	2.24E-16	15.64975168
ABLUW_RS0280	ABLUW_0570	NZ_CP008706.1	561012	570414	+	WP_000197381.1	baseplate Jig-47 family protein	108.0771966	1.699307932	0.261990264	6.48614919	8.81E-11	2.34E-10	9.63073416
ABLUW_RS1620	ABLUW_3141	NZ_CP008706.1	3167036	3168385	-	WP_001048745.1	hypothetical protein	1021.666093	1.697510217	0.15861493	10.70218236	9.95E-27	7.26E-26	25.13906338
ABLUW_RS1090	ABLUW_4014	NZ_CP008707.1	74570	7758	+	WP_000427815.1	hypothetical protein	828.0757456	1.694556689	0.305277411	5.5508748	2.84E-08	6.34E-08	17.9197472
ABLUW_RS03650	ABLUW_0743	NZ_CP008706.1	744596	744323	+	WP_000380102.1	hypothetical protein	44.24528267	1.694282176	0.29414109	5.76004171	8.41E-09	1.95E-08	7.709956389
ABLUW_RS1720	ABLUW_2409	NZ_CP008706.1	2396759	2396664	+	WP_000491917.1	LysR family pseudouridine regulator	86.9524798	1.686686875	0.104219998	9.90627434	3.91E-23	2.30E-22	21.63827216
ABLUW_RS0480	ABLUW_0116	NZ_CP008706.1	102616	1027356	+	WP_000866525.1	carO	40059.38539	1.68801210	0.265733532	6.352273716	2.10E-10	5.50E-10	9.296637311
ABLUW_RS1015	ABLUW_2123	NZ_CP008706.1	2107784	2108479	+	WP_000445449.1	MBL fold metallo-hydrolase	12.57353432	1.687646673	0.330176515	4.81947004	1.44E-06	2.78E-06	5.555955024
ABLUW_RS1700	ABLUW_2819	NZ_CP008706.1	2824478	2824744	+	WP_000730423.1	hypothetical protein	28.5727878	1.687301245	0.417731613	4.039199315	5.36E-05	9.06E-05	4.042871802
ABLUW_RS1945	ABLUW_4024	NZ_CP008707.1	15028	15184	+	WP_000106600.1	ParB/RepB/SpdJ family partition protein	4128.770335	1.685134184	0.205751705	8.911407019	2.59E-16	9.97E-16	15.0010048
ABLUW_RS1905	ABLUW_0867	NZ_CP008706.1	898636	898802	+	WP_000051688.1	hypothetical protein	59.10458879	1.684363675	0.320326572	5.252338781	1.50E-07	3.14E-07	6.503070352
ABLUW_RS1670	ABLUW_4118	NZ_CP008707.1	79719	81011	+	WP_000662932.1	Y-family DNA polymerase	355.4776989	1.678897091	0.233210041	7.18615134	6.66E-13	2.07E-12	11.68402965
ABLUW_RS0950	ABLUW_1884	NZ_CP008706.1	1885909	1886844	+	WP_000217937.1	helic-hum-helic transcriptional regulator	328.7198436	1.6750473	0.250358835	6.092583063	2.18E-11	6.18E-11	10.2153953
ABLUW_RS1765	ABLUW_1610	NZ_CP008706.1	1604758	1605016	+	WP_000242111.1	DMT family transporter	2.151941509	1.674509275	0.191070973	9.84010674	7.53E-23	4.35E-22	21.31651074
ABLUW_RS05330	ABLUW_1886	NZ_CP008706.1	101350	101513	+	WP_000367401.1	DUF9162 domain-containing protein	252.0199256	1.671020802	0.201456955	8.295671			

ABUW_RS0160	ABUW_0237	NZ_CP08706.1	259242	255931	-	WP_00145986.1	aaqZ	aquapoin Z	1071216277	1602103324	0.287924927	5.564309209	2.636E-08	5.896E-08	7.229884705
ABUW_RS0230	ABUW_3241	NZ_CP08706.1	3290664	3270431	-	WP_002692485.1	IEE	putative poly assembly protein FIE	638.8774502	1600244269	0.106857259	1.65279791	1.39E-31	1.36E-30	29.8664649
ABUW_RS0380	ABUW_0485	NZ_CP08706.1	496565	497496	-	WP_000121938.1		SDR family oxidoreductase	134.9988263	159847189	0.370347936	4.31956802	1.59E-05	2.82E-05	4.540750892
ABUW_RS0460	ABUW_3008	NZ_CP08706.1	304343	3036986	-	WP_001222398.1		DUF927 domain-containing protein	247.9891618	1590486432	0.17389992	9.1460029	5.91E-20	2.88E-19	9.46070751
ABUW_RS1605	ABUW_2385	NZ_CP08706.1	2373057	2374448	-	WP_001866580.1		LLM class7 iron-dependent oxidoreductase	906.91487	1589470441	0.302021242	7.938124524	2.05E-15	7.47E-15	14.506784
ABUW_RS0785	ABUW_0391	NZ_CP08706.1	0399322	1399930	-	WP_001823979.1		VtaA viral recombination family protein	79.95090587	1582906004	0.285395892	5.54631188	8.25E-08	6.49E-08	7.187570303
ABUW_RS0215	no	NZ_CP08706.1	171821	1719137	+	WP_002012156.1		hypothetical protein	612150569	1582604932	0.372009778	4.254202516	2.10E-05	3.87E-05	4.43533936
ABUW_RS0390	ABUW_3777	NZ_CP08706.1	3836763	3838116	-	WP_001193286.1		MFS family MFS transporter	209.0296393	1579157355	0.272808939	5.790649487	7.01E-09	1.63E-08	7.87812136
ABUW_RS0865	ABUW_042	NZ_CP08706.1	837597	933916	+	WP_00104256.1		carboxylate pump	249.4563322	157938293	0.18885801	6.357488926	6.41E-17	2.58E-16	15.6838029
sRNA7.1	no	no	no	no	no	no	no	no	155.292547	1572565252	0.204470265	7.690923924	1.46E-14	5.01E-14	13.3006227
ABUW_RS1010	ABUW_2082	NZ_CP08706.1	2063061	2063552	+	WP_00076817.1	anB	anthranilate 1,2-dioxygenase small subunit	8.70594606	1571734903	0.454593964	3.457447807	0.000545318	0.000837304	3.07718634
ABUW_RS0915	no	NZ_CP08706.1	8162167	1883471	+		abaQ	multidrug efflux MFS transporter AbaQ	30.58980082	1570071026	0.354067524	4.436924938	9.13E-06	1.60E-05	4.78259056
ABUW_RS1845	ABUW_3800	NZ_CP08706.1	380709	3861917	+	WP_000343018.1		8256-like element (Saba26) family transposase	458.391884	1569784251	0.2883219751	5.444557158	5.19E-08	1.19E-07	6.946921557
ABUW_RS0950	ABUW_0555	NZ_CP08706.1	957263	1958234	+	WP_012300601.1		acid phosphatase	57.64016102	1568434903	0.280407185	5.591624795	2.25E-08	5.06E-08	7.295849483
ABUW_RS0705	ABUW_1440	NZ_CP08706.1	1432445	1432987	+	WP_001019740.1		hypothetical protein	32.24159513	156825219	0.354475552	4.42414768	9.68E-06	1.74E-05	4.759450752
ABUW_RS1435	ABUW_2693	NZ_CP08706.1	3015642	3015259	-	WP_000624780.1		hypothetical protein	95.37571749	156718607	0.28263085	5.547379907	2.90E-08	6.46E-08	7.89767482
ABUW_RS1010	ABUW_2084	NZ_CP08706.1	2065042	2066100	+	WP_001070630.1		AraC family transcriptional regulator	87.0903886	1565555558	0.20894257	7.492038189	6.78E-14	2.24E-13	12.64975198
ABUW_RS0965	ABUW_0233	NZ_CP08706.1	921930	9221379	-	WP_00026040.1		SLC13 family permease	42.5961292	1565344069	0.356713856	4.386246701	1.14E-05	2.04E-05	4.69036933
ABUW_RS1285	ABUW_2320	NZ_CP08706.1	2304706	2306055	-	WP_001019553.1		LysR family transcriptional regulator	220.1234792	1565044892	0.24804383	3.69594911	8.20E-10	7.19E-10	9.1432711
ABUW_RS0495	ABUW_0936	NZ_CP08706.1	945094	945356	-	WP_000302057.1		hypothetical protein	38.06632097	1562635328	0.453223629	3.547274512	0.000550805	0.000945444	3.07294607
ABUW_RS0335	ABUW_2107	NZ_CP08706.1	210609	2110245	-	WP_000238448.1		acetylase	222.5593893	1562455263	0.38050815	4.106225742	4.02E-05	6.87E-05	4.163943263
ABUW_RS0615	ABUW_0397	NZ_CP08706.1	1402372	1402569	-	WP_001084883.1		hypothetical protein	15.34859244	156161017	0.473858892	2.954970774	0.000918274	0.001585507	2.836919482
ABUW_RS0760	ABUW_0663	NZ_CP08706.1	6515704	6522027	-	WP_000783724.1		hypothetical protein	307.0754027	1561401211	0.32280141	6.837066881	1.32E-06	2.56E-06	5.59176005
ABUW_RS1845	ABUW_3782	NZ_CP08706.1	3842938	3843828	-	WP_001017291.1	mmB	3-hydroxyisovalerate dehydrogenase	4.14.5369476	1560348483	0.473231466	2.97220484	0.000976468	0.001405025	2.83859460
ABUW_RS1395	ABUW_2759	NZ_CP08706.1	2749545	2750507	-	WP_00026456.1		metal-dependent hydrolase	39.9604067	1559888213	0.303170836	5.15228458	2.67E-07	5.47E-07	6.262012674
ABUW_RS0960	ABUW_0861	NZ_CP08706.1	897196	168473	+	WP_001084464.1		aromatic ring-hydroxylating dioxygenase subunit alpha	947.429429	1557765419	0.440659579	5.53076717	0.000407657	0.000632928	3.98845691
ABUW_RS0975	ABUW_2010	NZ_CP08706.1	2005481	2005723	-	WP_000166400.1		hypothetical protein	25.8181075	155504466	0.200262374	7.7601091	7.97E-15	2.80E-14	15.5528497
ABUW_RS0925	ABUW_2024	NZ_CP08706.1	201958	2012200	-	WP_000166400.1		hypothetical protein	260.289598	1552863339	0.20173948	6.709736912	1.39E-14	4.78E-14	9.3205721
ABUW_RS1845	ABUW_4501	NZ_CP08707.1	6181	62403	+	WP_000063840.1		conjugal transfer protein TraB	507.5342784	1552742488	0.148339564	0.46748858	1.22E-25	8.48E-25	24.07160415
ABUW_RS0215	no	NZ_CP08706.1	940976	941423	+			sulfite exporter/TauS/Est family protein	35.62483175	1551676041	0.382913786	0.52285544	5.07E-05	8.60E-05	0.05505949
ABUW_RS0260	ABUW_0582	NZ_CP08706.1	576447	577274	-	WP_000748563.1		GPO family D-xylose acyltransferase	57.3673469	1546109635	0.345292164	4.187076568	7.53E-06	1.37E-05	4.63376933
ABUW_RS0820	ABUW_3805	NZ_CP08706.1	3933639	3934191	+	WP_000964180.1		NAD(P)H-dependent oxidoreductase	781.5208805	1544349506	0.25616139	9.028345063	1.66E-09	4.04E-09	8.393679635
ABUW_RS0175	ABUW_0300	NZ_CP08706.1	324211	325098	+	WP_001017320.1		metal-dependent hydrolase	188.250566	1543728174	0.23860124	6.471023536	9.73E-11	2.58E-10	9.988380294
ABUW_RS0690	ABUW_2189	NZ_CP08706.1	2186027	2186462	-	WP_000368000.1		phasin family protein	1042.165345	1542854203	0.195636219	7.886342417	1.16E-11	1.12E-11	15.95078198
ABUW_RS0260	ABUW_0284	NZ_CP08706.1	1006243	1006541	+	WP_001017304.1		hypothetical protein	482.3277775	1542349923	0.30460898	5.062379244	4.14E-07	8.35E-07	6.078135525
ABUW_RS0250	no	NZ_CP08706.1	2060643	2060896	-			hypothetical protein	32.85499857	1540682166	0.466779329	3.30066411	0.00096456	0.001434557	2.843282161
ABUW_RS1795	ABUW_3679	NZ_CP08706.1	3737151	3737834	+	WP_001031947.1		ATP-binding protein	10.664619	1539292234	0.28000083	5.497455965	3.85E-08	8.52E-08	7.069560405
ABUW_RS1845	ABUW_2394	NZ_CP08706.1	2382600	2383451	-	WP_000387773.1	madM	malonate transporter subunit MadM	177.8893506	1538728695	0.237868917	6.498368719	8.12E-11	2.17E-10	9.663540266
ABUW_RS0045	ABUW_0009	NZ_CP08706.1	11026	12103	+	WP_000724999.1		hypothetical protein	6087.483227	1537928568	0.234078397	5.570143117	1.36E-10	9.66646102	
ABUW_RS0925	ABUW_0588	NZ_CP08706.1	959771	962767	+	WP_000192636.1		DEAD/DEAH box-like helicase family protein	1472.424893	1537252163	0.192755559	7.97513799	1.52E-15	5.61E-14	14.25307314
ABUW_RS0360	ABUW_0737	NZ_CP08706.1	740524	741102	-	WP_000150785.1		hypothetical protein	195.3434767	1535301474	0.19873187	7.725195361	1.11E-14	3.87E-14	9.14228903
ABUW_RS1815	ABUW_3492	NZ_CP08706.1	341355	3412089	-	WP_000716100.1		alpha/beta fold hydrolase	342.6516175	1534400667	0.25454396	6.325745621	2.52E-10	6.49E-10	9.57783503
ABUW_RS1010	ABUW_2028	NZ_CP08706.1	2487329	2488786	-	WP_001176564.1		NAD-dependent succinate-semialdehyde dehydrogenase	56.5209044	1533966412	0.290374834	5.822711091	1.27E-07	2.68E-07	6.57985206
ABUW_RS0295	ABUW_2922	NZ_CP08706.1	291938	2933102	+	WP_000854552.1		hypothetical protein	844.8374549	1530358879	0.375729093	4.075640953	4.59E-05	7.80E-05	4.97093057
ABUW_RS0490	ABUW_0916	NZ_CP08706.1	91919	91951	+	WP_000943493.1		metallophosphatase	640.584949	1530844943	0.11615274	8.43860417	3.27E-17	1.34E-16	16.8728952
ABUW_RS0950	ABUW_0563	NZ_CP08706.1	955456	955984	+	WP_000677758.1		TuG family protein	44.09188663	1529300039	0.31879934	4.91083483	9.04E-07	1.78E-06	5.749579998
ABUW_RS0390	ABUW_0773	NZ_CP08706.1	759531	760172	+	WP_000721922.1		hypothetical protein	57.0614102	1528332682	0.24061611	6.349662345	2.16E-10	5.59E-10	9.25258907
ABUW_RS0725	ABUW_1932	NZ_CP08706.1	1719364	1480383	+	WP_002019500.1	cusE	Cus family pilin adhesin CusE	294.4310251	1527421591	1.16230181	137.0770274	NA	NA	VALUE1
ABUW_RS0895	ABUW_1414	NZ_CP08706.1	1409521	1409844	+	WP_000356496.1		hypothetical protein	72.09046687	1524056439	0.253652373	6.00845416	1.87E-09	4.54E-09	8.342944741
ABUW_RS0970	ABUW_0663	NZ_CP08706.1	658980	1659719	+	WP_000815005.1		SDR family oxidoreductase	395.5863172	1522974751	0.429526513	5.545770904	0.000391958	0.000609108	3.21630506
ABUW_RS0960	ABUW_3102	NZ_CP08706.1	3102141	3109922	-	WP_001886868.1		DUF2187 domain-containing protein	1210.049465	1522267454	0.173720094	8.763335448	1.90E-18	8.28E-18	17.08166966
ABUW_RS1225	ABUW_3340	NZ_CP08706.1	3374093	3374385	+	WP_000538009.1		pyocyanin activator PrtN family protein	286.2591919	1521967147	0.19772169	7.697542743	1.39E-14	4.78E-14	9.3205721
ABUW_RS0100	ABUW_0020	NZ_CP08706.1	23706	24305	+	WP_000587889.1		glutathione S-transferase family protein	260.8215732	1520026602	0.193025764	7.878787817	3.30E-15	1.16E-14	19.92811799
ABUW_RS1420	ABUW_3010	NZ_CP08706.1	3037887	3038541	+	WP_001888245.1		hypothetical protein	37.25795372	1520671184	0.344330374	4.163149392	1.00E-05	1.80E-05	4.744727495
ABUW_RS0380	ABUW_0793	NZ_CP08706.1	773502	773801	+	WP_000335668.1		DUF4258 domain-containing protein	2287.631594	1519781231	0.19187806	8.09158695	5.88E-16	2.21E-15	16.6506773
ABUW_RS0385	ABUW_0708	NZ_CP08706.1	81815	81453	+	WP_000421800.1	huH	histidine aminon-lyase	478.618973	1519320417	0.360829753	4.21629537	2.55E-05	4.43E-05	4.353196274
ABUW_RS0240	no	NZ_CP08706.1	2508189	2509305	+	WP_000513921.1		hypothetical protein	98.0471892	151933006	0.46297667	3.278638219	0.001430093	0.001942248	2.18146317
ABUW_RS0350	ABUW_2100	NZ_CP08706.1	216823	216842	-	WP_001133050.1		alpha-ketolacid dehydrogenase subunit beta	788.1459166	15190716937	0.15717089	2.64431018	0.008185761	0.01187412	1.955522448
ABUW_RS1735	ABUW_3562	NZ_CP08706.1	3618004	3620103	+	WP_000925020.1		FLS family protein	755.7448087	1519059271	0.223499788	7.87519953	1.14E-11	3.20E-11	10.4867824
ABUW_RS0340	ABUW_0697	NZ_CP08706.1	699303												

ABLW_RS0330	ABLW_2106	NZ_CP008706.1	210972	210300	-	WP_000642315.1	2,3-butanediol dehydrogenase	837.240566	147.92696	0.239257675	6.152057453	7.65E-10	1925-09	8.76688771
ABLW_RS2455	ABLW_0273	NZ_CP008706.1	130182	130158	+	WP_001001967.1	hypothetical protein	14.1436135	1470957482	0.522644757	2.814449897	0.0004886079	0.000785941	2.88389921
ABLW_RS1015	ABLW_2782	NZ_CP008706.1	2777259	2778509	+	WP_000041032.1	Opt family porin	132.4764582	1469476767	0.348340767	4.2850536	2.46E-05	4.28E-05	4.38556231
ABLW_RS0505	ABLW_0194	NZ_CP008706.1	16610	16809	+	WP_000619878.1	alpha/beta fold hydrolase	92.8888829	146670191	0.174016575	8.428619282	3.50E-17	1.433E-16	15.84463636
ABLW_RS1000	ABLW_2462	NZ_CP008706.1	245034	245937	+	WP_000208930.1	MF5 transporter	63.1933137	1464714097	0.285709729	5.15681108	2.95E-07	6.02E-07	6.220403509
ABLW_RS0475	ABLW_2918	NZ_CP008706.1	907091	906860.53	-	WP_000868053.1	glycyl-S-phenylphosphate dehydrogenase	906.051878	1463723642	0.208854336	7.008346915	2.4E-12	7.21E-12	11.9240474
ABLW_RS1540	ABLW_2995	NZ_CP008706.1	301378	3015180	-	WP_001151982.1	DUF252 domain-containing protein	1321.232499	1462851898	0.162823885	8.981004354	2.68E-19	1.25E-18	17.90309999
ABLW_RS0735	ABLW_0385	NZ_CP008706.1	1396476	1397684	-	WP_000343019.1	B256-like element (SAbz6 family transposase	504.3074309	1462201058	0.241910549	6.044274885	1.90E-09	3.67E-09	8.433333936
ABLW_RS0680	ABLW_0369	NZ_CP008706.1	1384959	1385915	-	WP_000902236.1	MBL fold metallo-hydrolase	409.3807034	1462187109	0.192196143	9.738541913	2.06E-22	1.17E-21	20.9318144
ABLW_RS0340	ABLW_0288	NZ_CP008706.1	102598	105972	+	WP_000637362.1	cas3f type I-F CRISPR-associated holoecase Cas3	2369.632311	1451404018	0.100372105	14.46022854	2.16E-47	5.31E-46	45.27490548
ABLW_RS1885	ABLW_2622	NZ_CP008706.1	261620	261454	-	WP_001588631.1	hypothetical protein	93.8750509	1449517553	0.26056298	5.563021848	2.65E-08	5.92E-08	7.227678293
ABLW_RS2140	ABLW_0277	NZ_CP008706.1	1090570	1090695	+	WP_000854366.1	hypothetical protein	18.3883017	1449197275	0.432788846	3.348300883	0.000810087	0.001224449	2.913104662
ABLW_RS2330	ABLW_0487	NZ_CP008706.1	491963	500320	+	WP_000673016.1	acyl-CoA dehydrogenase family protein	363.2200255	1448710852	0.287499349	5.038966282	4.68E-07	9.41E-07	6.026410377
ABLW_RS0705	ABLW_0558	NZ_CP008706.1	1546276	1548105	+	WP_001061302.1	pgalB y-beta-16-N-acetyl-D-glucosamine N-deacetylase P	133.0239142	1447753999	0.243330065	5.949753882	2.69E-09	6.44E-09	8.19111133
rRNA D	no	no	no	no	no	no	no	7.59646914	1446866455	0.643871322	2.24715043	0.024031334	0.031825128	1499967736
ABLW_RS00140	ABLW_0256	NZ_CP008706.1	1292990	1293886	-	WP_001056663.1	hypothetical protein	72.32947648	14468669591	0.241900761	5.980255386	2.23E-09	5.37E-09	10.702025714
ABLW_RS01345	ABLW_0356	NZ_CP008706.1	379077	379338	-	WP_000783289.1	hypothetical protein	417.1672577	1445818642	0.238146933	6.07120154	1.27E-09	3.12E-09	8.508544506
ABLW_RS00105	ABLW_0261	NZ_CP008706.1	2795902	2799904	+	WP_000358172.1	Lsp/KazC family transcriptional regulator	2118438157	1445718334	0.336783992	4.292718664	1.77E-05	3.11E-05	4.02739611
ABLW_RS00520	ABLW_0603	NZ_CP008706.1	972081	9714325	+	WP_000750598.1	hypothetical protein	1709.858461	1444144575	0.242415064	5.957321928	2.95E-09	6.15E-09	8.21104884
ABLW_RS11645	ABLW_2373	NZ_CP008706.1	2356676	2360550	-	WP_000106119.1	amylomylase	403.6806019	1443904876	0.271026129	6.523879567	6.85E-11	1.84E-10	9.735182177
ABLW_RS01745	ABLW_0565	NZ_CP008706.1	1553602	1553964	-	WP_000108880.1	LysR family transcriptional regulator	318.1431143	1443631145	0.211822825	6.818851973	9.83E-12	2.71E-11	10.55909002
ABLW_RS01345	ABLW_0434	NZ_CP008706.1	447140	448612	-	WP_001050461.1	acyl-CoA dehydrogenase family protein	306.5600506	1443394319	0.224476247	6.430053679	1.28E-10	3.35E-10	9.474955193
ABLW_RS10060	ABLW_2478	NZ_CP008706.1	2472182	2473253	+	WP_000617420.1	acyl-CoA dehydrogenase family protein	48.183736	1441197376	0.351900529	4.10714514	4.91E-05	6.84E-05	4.16494388
ABLW_RS01880	ABLW_0845	NZ_CP008706.1	842061	843074	+	WP_0001009345.1	YaeJ/YaeJ family protein	68.8206438	1439940088	0.329632196	4.368323561	1.25E-05	2.23E-05	4.65190517
ABLW_RS01645	ABLW_2603	NZ_CP008706.1	2550521	2557939	-	WP_001189100.1	ATP-grasp domain-containing protein	228.223466	1438501074	0.316421911	1.56045055	5.10E-06	9.42E-06	5.025949097
ABLW_RS11865	ABLW_2053	NZ_CP008706.1	2074199	2076340	-	WP_000263726.1	GntP family permease	788.2064039	1436482753	0.267001995	5.380045021	7.45E-08	1.60E-07	6.79580107
ABLW_RS01820	ABLW_0709	NZ_CP008706.1	710241	711281	+	WP_00102300579.1	GTP 3'-cylase MoaA	491.5445099	1434119738	0.264210403	5.427339863	5.70E-08	1.24E-07	6.90657813
ABLW_RS01338	ABLW_0738	NZ_CP008706.1	711029	714788	-	WP_0001765548.1	hypothetical protein	270.5724897	1431757691	0.166618803	8.593103925	8.47E-18	3.60E-17	16.4436975
ABLW_RS01865	ABLW_0854	NZ_CP008706.1	850184	851450	+	WP_000421436.1	Opt family outer membrane porin	88.14095702	1430391668	0.312750093	4.573593097	4.79E-06	8.88E-06	5.01687034
ABLW_RS01595	ABLW_1612	NZ_CP008706.1	183482	185910	-	WP_000161843.1	hypothetical protein	418.5995034	1428052636	0.230047017	6.207555528	5.38E-10	1.36E-09	8.86641902
ABLW_RS11985	ABLW_2402	NZ_CP008706.1	2386349	2390028	-	WP_000399235.1	mdcA malonate decarboxylase subunit alpha	169.5201832	1427229961	0.359606994	3.969590051	7.19E-05	0.000102018	3.9201876
ABLW_RS0145	ABLW_2058	NZ_CP008706.1	2677144	2677599	-	WP_0003932376.1	NAD(P)+ binding domain-containing protein	1219.487287	1426475663	0.162822147	3.23422083	1.02E-20	5.20E-20	9.33966268
ABLW_RS08865	ABLW_0608	NZ_CP008706.1	1407335	1407739	+	WP_001081846.1	hypothetical protein	40.57540877	1425102931	0.34409632	4.14161498	3.45E-05	5.92E-05	4.227678293
ABLW_RS10110	ABLW_2681	NZ_CP008706.1	2671900	2672229	-	WP_001021983.1	hypothetical protein	212.3053802	1424663348	0.160566838	8.87261211	7.14E-19	3.22E-18	17.4921414
ABLW_RS10005	ABLW_2487	NZ_CP008706.1	2459376	2460530	-	WP_000617392.1	acyl-CoA dehydrogenase family protein	69.06641786	1423380588	0.348071307	4.938195031	4.33E-05	7.38E-05	4.19146318
ABLW_RS11590	ABLW_2718	NZ_CP008706.1	27195178	27196641	+	WP_000402089.1	amino acid permease	688.0580092	1422188879	0.358287838	3.969624759	7.20E-05	0.0001020295	3.917592454
ABLW_RS01270	ABLW_2940	NZ_CP008706.1	2954190	2955376	-	WP_0001753778.1	hypothetical protein	61.84667862	1420792105	0.265986828	5.341953896	9.19E-08	1.96E-07	6.707743929
ABLW_RS01635	ABLW_2601	NZ_CP008706.1	2559729	2594187	+	WP_000465123.1	self repeat family protein	292.13688	1420175238	0.279149152	5.087514608	3.63E-07	7.36E-07	6.13321862
ABLW_RS01285	ABLW_0486	NZ_CP008706.1	4971507	499120	+	WP_000164085.1	acetyl-CoA carboxylase carboxyltransferase subunit	92.7145279	1418073001	0.388780854	3.647486722	0.000264618	0.00041743	3.379416342
ABLW_RS21095	no	NZ_CP008706.1	269026	269154	-	WP_085918955.1	hypothetical protein	8.340724232	1416009196	0.557181887	2.537760173	0.01156441	0.04854362	1828145997
rRNA E	no	no	no	no	no	no	no	25.43713823	1410185536	0.505879567	2.793462377	0.005214709	0.007224919	2.14167018
ABLW_RS210275	no	NZ_CP008706.1	2872293	2873003	-	no	outer membrane assembly protein BamE	101843135	1412258802	0.351020333	4.023296288	5.74E-05	9.66E-05	4.015022784
ABLW_RS01740	ABLW_0605	NZ_CP008706.1	1909628	1909636	-	WP_000097958.1	pseudocytidine synthase	250.9588707	1411071571	0.210954814	6.91962718	2.20E-11	6.15E-11	9.2110248
ABLW_RS18865	ABLW_2871	NZ_CP008706.1	2942344	2942750	+	WP_001477478.1	hypothetical protein	401.8107049	1411619248	0.301931286	4.682872781	2.83E-06	5.36E-06	5.27035351
ABLW_RS11595	ABLW_2784	NZ_CP008706.1	2770638	2771777	+	WP_001054391.1	acyl-CoA dehydrogenase family protein	98.586632	1409843372	0.342216082	4.118979713	3.94E-05	6.74E-05	4.11940183
ABLW_RS019210	ABLW_0991	NZ_CP008706.1	8921075	8922667	+	WP_000044208.1	type 1 glutamine amidotransferase domain-containing protein	1710.050375	14052195756	0.411216817	3.41407778	0.000632205	0.0006164831	3.915548781
ABLW_RS10300	ABLW_2530	NZ_CP008706.1	252184	2522621	-	WP_001165642.1	enoyl-CoA hydratase/isomerase family protein	794.6383576	1405102637	0.524992064	2.676496989	0.007440232	0.010192841	1.994654684
ABLW_RS01210	ABLW_0141	NZ_CP008706.1	941949	9419886	-	WP_0001795395.1	Psal family phosphatase	535.981338	1403424821	0.260581927	5.385748005	7.2E-08	1.56E-07	6.068875402
ABLW_RS210220	ABLW_2498	NZ_CP008706.1	2494352	2495284	-	WP_001193252.1	flavin reductase family protein	106.2671809	14030093073	0.278319436	5.04159902	4.62E-07	9.30E-07	6.031517051
ABLW_RS11425	ABLW_3580	NZ_CP008706.1	3633838	3639290	+	WP_002014580.1	hypothetical protein	200.9587442	1402535642	0.193371699	9.144667379	5.98E-20	2.91E-19	18.53610701
ABLW_RS01780	ABLW_0735	NZ_CP008706.1	633575	634261	+	WP_001279985.1	glutathione S-transferase family protein	468.2070354	140153636	0.270133731	5.189109964	2.11E-07	4.37E-07	6.35918563
ABLW_RS08650	ABLW_0776	NZ_CP008706.1	1774661	1775380	-	WP_000838063.1	heme-binding protein	546.9363457	1398903695	0.24808506	5.8092761	6.27E-09	1475E-08	7.832628665
ABLW_RS01630	ABLW_0168	NZ_CP008706.1	118203	1184049	-	WP_001071690.1	type Itoxin-antitoxin system Phd/YefM family antitoxin	53.5624511	1398534071	0.264791809	5.28193646	1.28E-07	2.70E-07	6.588636262
ABLW_RS01505	ABLW_0306	NZ_CP008706.1	330212	330676	+	WP_000678123.1	bacterioferritin	5792.399281	1395971616	0.429191619	3.252798109	0.00127468	0.00088575	2.73774629
ABLW_RS01910	ABLW_0386	NZ_CP008706.1	1402052	1402372	+	WP_000518771.1	hypothetical protein	22.40298108	1395098036	0.38253196	3.64910733	0.000263129	0.000418093	3.38195459
ABLW_RS18405	ABLW_3780	NZ_CP008706.1	3841195	3841195	-	WP_001180756.1	acyl-CoA dehydrogenase family protein	643.9599498	1395400995	0.33119498	4.2132111	5.25E-05	4.38E-05	6.350525889
ABLW_RS10880	ABLW_2816	NZ_CP008706.1	2819465	2819737	-	WP_001040886.1	RVS repeat protein	7419.751947	13940557623	0.196589695	7.096530322	1.28E-12	3.89E-12	114105094
ABLW_RS01985	ABLW_0404	NZ_CP008706.1	431180	431950	+	WP_000835293.1	type 1 glutamine amidotransferase	60.6714966	1394622405	0.255242249	5.463899359	4.68E-08	1.02E-07	6.191098828
ABLW_RS01780	no	NZ_CP008706.1	449980	4499950	+	WP_000488738.1	DUF295 domain-containing protein	97.19004477	1391487173	0.319395385	4.40037322	8.89E-06	1.63E-05	4.787812396
ABLW_RS11635	ABLW_3622	NZ_CP008706.1	3680364	3680945	-	WP_000988520.1	TetR/AcrR family transcriptional regulator	73.45291651	1390					

ABUW_RS05605	ABUW_1445	NZ_CP008706.1	1770003	170929	+	WP_000695009.1	LyxR family transcriptional regulator	589.909449	134926982	0.174207648	7.745181001	9.54E-15	3.33E-14	13.47755577
ABUW_RS02040	ABUW_1692	NZ_CP008706.1	6189551	169103	-	WP_000043926.1	TerR/AcrR family transcriptional regulator	225.619557	134453777	0.29291994	5.900100005	4.43E-06	8.24E-06	5.084072788
ABUW_RS1175	ABUW_2408	NZ_CP008706.1	230627	2395648	-	WP_00102768.1	CodA/LyA family protein	40.84236402	1344474.03	0.276880307	8.857628339	1.20E-06	2.34E-06	5.637047843
ABUW_RS0095	ABUW_2009	NZ_CP008706.1	2000794	2006879	-	WP_000253153.1	modA methyl- and ABC transporter substrate-binding protein	243.5295999	1344216329	0.189988911	7.07522519	1.49E-12	4.51E-12	13.14582346
ABUW_RS167.6	ABUW_3438	NZ_CP008706.1	3442272	3442844	-	WP_000859455.1	HsdD family acid-resistance protein	116.74002	1342243795	0.302951474	4.430553125	9.40E-06	1.69E-05	4.772113295
ABUW_RS0540	ABUW_1941	NZ_CP008706.1	1941.95	19348.48	-	WP_000569883.1	ABC transporter permease	65.1026542	1341995703	0.269437233	4.978291032	3.38E-07	1.27E-06	5.896196279
ABUW_RS0260	ABUW_1541	NZ_CP008706.1	1547899	1548436	-	WP_00105747.1	3'-5' exonuclease	323.731652	1341020658	0.193299542	8.210254472	2.16E-16	8.38E-16	16.07779372
ABUW_RS01340	ABUW_1274	NZ_CP008706.1	292407	293291	-	WP_0010166587.1	hypothetical protein	147.1762873	13404535379	0.256289295	6.230236326	1.69E-07	3.53E-07	6.452225295
ABUW_RS04920	ABUW_1603	NZ_CP008706.1	161016	161941	+	WP_0010836951.1	multidrug efflux MFS transporter	768.1616367	1339588095	0.100593692	8.895462427	5.82E-19	2.63E-18	17.68044425
ABUW_RS10450	ABUW_2770	NZ_CP008706.1	2761888	2763558	+	WP_001064593.1	GMC family oxidoreductase	568.2770896	1337486693	0.210719344	6.450941616	1.07E-10	2.83E-10	9.548213564
ABUW_RS04430	ABUW_1903	NZ_CP008706.1	189936	189921	-		RNA-Leu	26.65423437	1337383962	0.523066649	2.556819675	0.010563578	0.014102272	1.850716919
ABUW_RS17465	ABUW_3588	NZ_CP008706.1	3646463	3646828	-	WP_000738603.1	hypothetical protein	843.7289397	1335629084	0.300728924	4.441970754	8.91E-06	1.61E-05	4.79314724
ABUW_RS06235	ABUW_1278	NZ_CP008706.1	1302718	1303167	+	WP_000356498.1	hypothetical protein	54.7418927	1334082043	0.272773349	4.811436111	1.50E-06	2.89E-06	5.53919267
ABUW_RS10285	ABUW_2483	NZ_CP008706.1	2478103	2478812	-	WP_000930941.1	putative 2-aminooxyphosphonate ABC transporter permease	49.55050229	1322380927	0.305395239	3.4362481	1.29E-05	2.29E-05	4.640164518
ABUW_RS02645	ABUW_1538	NZ_CP008706.1	1546080	1547167	+	WP_001078155.1	site-specific integrase	814.1673932	1330785568	0.193247761	7.262220056	3.81E-13	1.19E-12	1192445304
ABUW_RS02625	ABUW_1274	NZ_CP008706.1	1301655	1301666	+	WP_000801877.1	hypothetical protein	29.03694474	1328708029	0.368403054	3.606669422	0.000310152	0.000484572	3.19335810
ABUW_RS07525	ABUW_1642	NZ_CP008706.1	1628462	1629241	+	WP_000727583.1	transglutaminase family protein	115316633	1327164053	0.230626801	5.754595934	6.68E-09	2.01E-08	7.696803943
ABUW_RS01090	ABUW_1223	NZ_CP008706.1	245520	245936	-	WP_000455807.1	carboxymucronolactone decarboxylase family protein	74.763754	132648904	0.229042522	5.79475096	5.98E-09	1.62E-08	7.790446085
ABUW_RS01970	ABUW_1677	NZ_CP008706.1	1670232	1671491	+	WP_000588779.1	serine hydrolase	857.9571591	1323378	0.163636454	7.957162161	1.76E-16	6.45E-15	1.161400429
ABUW_RS01695	ABUW_1324	NZ_CP008706.1	1346371	1347310	-	WP_000916068.1	flax/glycerol lipase	406.5285106	132259996	0.262710688	6.035805823	4.70E-07	9.56E-07	6.019542108
ABUW_RS14225	ABUW_2930	NZ_CP008706.1	2944487	2945596	-	WP_000926505.1	SDR family oxidoreductase	130.2931657	1322647166	0.189754653	6.973016025	3.16E-12	9.40E-12	11.02876219
ABUW_RS01880	ABUW_2298	NZ_CP008706.1	2285450	2286365	+		hypothetical protein	225.7603063	1321892826	0.287812086	4.552916186	4.37E-06	8.16E-06	5.089049054
ABUW_RS16580	ABUW_3411	NZ_CP008706.1	3436639	3438857	+	WP_001080811.1	Sec-independent protein translocase subunit TaxA	35.10996885	1320657588	0.188272552	3.49147314	0.000479872	0.000740201	3.10060335
ABUW_RS19335	ABUW_3683	NZ_CP008706.1	3741107	3741919	+	WP_000975212.1	hypothetical protein	95.2322222	131956303	0.1618970272	3.69E-11	1.01E-10	9.956078626	
ABUW_RS01380	ABUW_1563	NZ_CP008706.1	1595550	1597059	-	WP_000323284.1	hypothetical protein	59.4270853	1318234515	0.116625083	11.0331919	1.27E-29	1.16E-28	27.95860731
ABUW_RS17895	ABUW_3675	NZ_CP008706.1	3732335	3733450	-	WP_00204550.1	TrnD family protein	795.107402	1318289511	0.185669192	8.294735534	1.09E-16	4.32E-16	36.36451625
ABUW_RS02640	ABUW_1852	NZ_CP008706.1	1810831	1811659	+	WP_000561082.1	FAD-binding oxidoreductase	108.7837719	1315040782	0.208536841	3.360035886	2.86E-10	7.34E-10	9.14310394
ABUW_RS01350	ABUW_1502	NZ_CP008706.1	1517877	1518245	+	WP_000524213.1	hypothetical protein	2.155605797	1314167578	0.405623637	3.235376073	0.001018426	0.001786326	2.748039811
ABUW_RS01485	ABUW_1521	NZ_CP008706.1	1514807	1514448	-	WP_000570321.1	DUF2238 domain-containing protein	178.3902381	1311866368	0.269179326	4.891077195	1.06E-06	2.07E-06	2.674029655
ABUW_RS19420	ABUW_3783	NZ_CP008706.1	3843430	3845357	-	WP_001082394.1	CoA-acylating methylmalonate-semialdehyde dehydrogenase	4524.02384	131433244	0.393632564	3.334164003	0.000855559	0.001081	2.89240087
ABUW_RS01975	ABUW_1678	NZ_CP008706.1	167539	167217	-	WP_000323807.1	TerR family transcriptional regulator	909.424638	1311603027	0.20338195	5.692742317	1.25E-08	2.87E-08	7.542116103
ABUW_RS02545	no	NZ_CP008706.1	154858	155634	+		ATP-binding cassette domain-containing protein	78.1662224	1310254885	0.239553563	5.473744028	4.41E-08	8.96E-08	7.014164643
ABUW_RS13320	ABUW_2744	NZ_CP008706.1	2732752	2733069	-	WP_000776215.1	hypothetical protein	132.066594	1310717969	0.271764978	4.822983376	1.41E-06	2.73E-06	5.563837353
ABUW_RS17730	ABUW_2623	NZ_CP008706.1	2619162	2620592	-	WP_000398495.1	3-hydroxyacyl-CoA dehydrogenase	448.3122468	1310096398	0.200000569	6.550463685	5.74E-11	1.55E-10	9.096868302
ABUW_RS02025	ABUW_2495	NZ_CP008706.1	2491665	2491908	-	WP_000943473.1	hypothetical protein	12.92819991	1308305766	0.463315609	2.823789533	0.004749594	0.006604991	2.18017277
ABUW_RS00610	ABUW_1446	NZ_CP008706.1	1470995	1472233	-	WP_000794156.1	aminopeptidase F family protein	527.7794648	1305916544	0.18919475	3.384630027	6.31E-21	3.26E-20	19.48878274
ABUW_RS05550	ABUW_1643	NZ_CP008706.1	1657060	1658035	-	WP_000121011.1	multidrug efflux SMR transporter AbeS	97.71160511	1303334149	0.244180248	5.537590406	9.42E-08	2.00E-07	6.698707004
ABUW_RS00190	ABUW_1669	NZ_CP008706.1	1666737	1668224	+	WP_000050613.1	NAD-dependent phenylacetaldehyde dehydrogenase	103.6095839	1302669636	0.212229053	6.137655141	8.38E-10	2.08E-09	8.67895374
ABUW_RS01490	ABUW_1709	NZ_CP008706.1	1716374	1716441	+	WP_000789875.1	DUF1191 domain-containing protein	528.0564702	1302110992	0.17466969	7.435557107	9.09E-14	2.98E-13	12.52578374
ABUW_RS02005	ABUW_1495	NZ_CP008706.1	141619	141852	-	WP_000437833.1	hypothetical protein	10.0233212	1300817186	0.372786628	3.489414679	0.000484031	0.000746168	3.21793338
ABUW_RS01205	ABUW_3336	NZ_CP008706.1	3369538	3369548	+	WP_000195220.1	hypothetical protein	280.9337715	1298310332	0.177862584	7.29952304	2.89E-10	9.16E-10	12.03810453
ABUW_RS10845	ABUW_2848	NZ_CP008706.1	286148	2861934	+	WP_00140376.1	hypothetical protein	87.98716311	1297933037	0.243774612	6.324318004	1.01E-07	2.16E-07	6.66756164
ABUW_RS00315	ABUW_1708	NZ_CP008706.1	1707738	1710011	+	WP_000698542.1	meliponin-dependent oxidoreductase	442.19198165	1297718931	0.200082457	6.489205059	8.82E-11	2.35E-10	6.928032108
ABUW_RS02075	no	NZ_CP008706.1	192006	192092	-		transposase domain-containing protein	23.5418176	129721627	0.328073739	3.954734846	7.66E-05	0.000127615	3.894098375
ABUW_RS00995	ABUW_2058	NZ_CP008706.1	2036281	2040152	-	WP_000632243.1	hypothetical protein	2580.1471	12968406	0.290181519	4.485108287	8.00E-06	1.45E-05	4.838031908
ABUW_RS11945	ABUW_2089	NZ_CP008706.1	2089797	2071847	-	WP_000918647.1	dienelactone hydrolase family protein	38.94643018	1294962239	0.368015007	5.91775633	8.00E-043543	0.000671009	3.17307753
ABUW_RS02850	ABUW_1580	NZ_CP008706.1	1574468	1575394	-	WP_000950641.1	terminase	79.1794326	1293962751	0.270014919	4.792274499	1.65E-06	3.17E-06	5.498480747
ABUW_RS02820	ABUW_1701	NZ_CP008706.1	1704643	1698653	-	WP_000399241.1	ABC transporter/substrate-binding protein	125.2668217	1291755618	0.216592793	6.101090999	8.73E-07	2.17E-05	8.663540206
ABUW_RS00385	ABUW_1909	NZ_CP008706.1	1921257	1921214	+	WP_000094258.1	hypothetical protein	8.29206261	1287524379	0.411233643	1.038828898	0.001074296	0.002585559	2.59710698
ABUW_RS02815	ABUW_1573	NZ_CP008706.1	157460	1574019	-	WP_001059843.1	phage witt morphogenesis protein	93.373641	128621974	0.346107606	3.716235688	0.000210272	0.000322096	3.492016609
ABUW_RS15550	ABUW_3204	NZ_CP008706.1	3232147	3233534	-	WP_001033441.1	amidohydrolase	486.4521068	128454181	0.200209229	6.140197454	8.24E-10	2.06E-09	8.68613271
ABUW_RS13410	ABUW_2762	NZ_CP008706.1	2752566	2753915	+	WP_000126169.1	metal-dependent hydrolase	85.38504811	128203824	0.23003838	5.574777382	2.45E-08	5.51E-08	7.25848041
ABUW_RS11450	ABUW_2354	NZ_CP008706.1	2336883	2337728	-	WP_000535318.1	ArcZ family transcriptional regulator	652.4444105	1281913677	0.234560161	5.442595808	5.25E-08	1.16E-07	6.93930216
ABUW_RS1805	ABUW_3327	NZ_CP008706.1	3363235	3364166	+	WP_001067742.1	CopJ family protein	77.418595	1279958534	0.19424872	6.589276554	4.42E-11	1.20E-10	9.92018754
ABUW_RS10575	ABUW_2176	NZ_CP008706.1	2169559	2167385	-	WP_000249278.1	2'-5' RNA ligase family protein	350.0841259	1271916357	0.217948192	8.869235609	4.38E-09	1.03E-08	7.98719277
ABUW_RS01385	ABUW_1627	NZ_CP008706.1	1629535	1626687	-	WP_000364261.1	LyxR family transcriptional regulator	98.41129267	1278476995	0.19231984	6.081463374	1.16E-09	2.93E-09	5.53132328
ABUW_RS01975	ABUW_1669	NZ_CP008706.1	1671894	1671898	-	WP_001436202.1	alpha/beta fold hydrolase	26.55957796	127801958	0.428369752	2.983451164	0.002816021	0.004059237	2.391955952
ABUW_RS10440	ABUW_3119	NZ_CP008706.1	3206785	3207108	+	WP_001047855.1	hypothetical protein	501.851081	1277853636	0.32604176	3.918716046	8.90E-05	0.000146936	3.83287187
ABUW_RS02840	ABUW_1578	NZ_CP008706.1	1573882	1574091	-	WP_000056474.1	tail protein X	37.2391165	1277625074	0.302950539	4.216653439	2.48E-05	4.32E-05	4.364516203
ABUW_RS01740	ABUW_1605	NZ_CP008706.1	1619388											

ABLUW_RS09685	ABLUW_0931	NZ_CP008706.1	693732	1694033	+	WP_000907899.1	DUF2523 domain-containing protein	13.5451287	1.230529355	0.2102299	5.803754381	6.48E-09	1.91E-08	7.82123035
ABLUW_RS06335	ABLUW_0303	NZ_CP008706.1	1318254	1318568	+	WP_000247952.1	hypothetical protein	26.68477425	1.229384637	0.340594271	3.609528226	0.000306754	0.000480713	3.3191E13
ABLUW_RS1855	ABLUW_3667	NZ_CP008706.1	3725597	3726031	+	WP_00075666.1	anS	440.2054857	1.228844101	0.10871426	8.858816698	8.09E-19	3.633E-18	1.470490337
ABLUW_RS1840	ABLUW_2433	NZ_CP008706.1	2420869	2422164	-	WP_000242222.1	stress-induced protein	100.2571252	1.228318005	0.527887812	2.326850472	0.01973225	0.025875281	1.58718492
ABLUW_RS07330	ABLUW_0607	NZ_CP008706.1	1402349	1403752	+	WP_000190549.1	heavy metal sensor histidine kinase	84.9329031	1.225878477	0.141930862	6.638424874	5.78E-18	2.48E-17	16.60554832
ABLUW_RS0555	ABLUW_3205	NZ_CP008706.1	3233548	3234933	-	WP_010192249.1		78.33217242	1.22384433	0.2444455	0.004979149	5.59E-07	1.15E-06	5.960781977
ABLUW_RS1080	ABLUW_2095	NZ_CP008706.1	268187	2682328	+	WP_00185369.1	LexA family transcriptional regulator	690.1779384	1.219092237	0.1033094	9.303702927	1.36E-20	8.85E-20	18.9430943
ABLUW_RS08950	ABLUW_9339	NZ_CP008706.1	1834541	1835070	+	WP_001807206.1	pcaG	72.8596559	1.217502134	0.327802296	3.718404075	0.000202078	0.000322096	3.49214669
ABLUW_RS0320	ABLUW_3155	NZ_CP008706.1	318185	3183094	+	WP_000071499.1	NAD(P)/FAD-dependent oxidoreductase	697.7787244	1.214726328	0.21648045	5.637300483	1.73E-08	3.92E-08	7.406710933
ABLUW_RS1800	ABLUW_2425	NZ_CP008706.1	241666	241950	-	WP_001025680.1	N-acetyltransferase	284.1577172	1.210631846	0.241024465	5.033217786	4.82E-07	9.68E-07	6.01426463
ABLUW_RS04450	ABLUW_0827	NZ_CP008706.1	803489	805138	+	WP_001891057.1	phosphoethanolamine-lypid A transferase	438.1037165	1.210381817	0.142118417	8.523442579	1.55E-17	6.50E-17	16.8708664
ABLUW_RS04445	ABLUW_1110	NZ_CP008706.1	113168	1133389	+	WP_000469453.1	alpha-keto acid decarboxylase family protein	4938.377473	1.210901443	0.423822296	2.857092603	0.004275411	0.000599871	2.221858087
ABLUW_RS0775	ABLUW_2633	NZ_CP008706.1	2631185	2631362	+	WP_001090072.1	LipA/Cst family transcriptional regulator	228.551362	1.210637277	0.10701452	6.144915967	8.00E-10	2.00E-09	6.688970004
ABLUW_RS1918	ABLUW_3658	NZ_CP008706.1	3717569	3719365	+	WP_001184958.1	hypothetical protein	2025.442237	1.209954487	0.204299456	5.922455798	3.17E-09	7.56E-09	8.11478204
ABLUW_RS03625	ABLUW_0736	NZ_CP008706.1	740318	740527	-	WP_000028947.1	hypothetical protein	73.36062456	1.208040054	0.248320193	4.864849407	1.16E-06	2.24E-06	5.649751982
ABLUW_RS0360	ABLUW_3226	NZ_CP008706.1	3254665	3254668	-	WP_001131888.1	cation transporter	160.4718579	1.207915017	0.2147687	6.637924469	1.72E-08	3.91E-08	7.407823243
ABLUW_RS07185	ABLUW_1470	NZ_CP008706.1	1459304	1459948	+	WP_000680470.1	glycoyltransferase	1075.612586	1.205743319	0.41103429	2.932943958	0.003357645	0.004753321	2.323002896
ABLUW_RS07180	ABLUW_1431	NZ_CP008706.1	1423557	1423880	+	WP_000673007.1	hypothetical protein	218.142004	1.205462365	0.212163521	5.182746114	2.07E-07	4.25E-07	6.367542708
ABLUW_RS01760	ABLUW_1469	NZ_CP008706.1	145708	1459307	+	WP_000581827.1	class I/IIAM-dependent methyltransferase	106.371645	1.204074184	0.349234371	2.741002384	0.00619698	0.009420745	2.074649484
ABLUW_RS11880	ABLUW_2441	NZ_CP008706.1	2429496	2429717	-	WP_000498474.1	hypothetical protein	84.122427	1.203966017	0.428105371	2.825318499	0.004723438	0.006570374	2.82014566
ABLUW_RS09240	ABLUW_0997	NZ_CP008706.1	1898480	1898483	+	WP_000056614.1	SCR family oxidoreductase	24.40784	1.200869501	0.320955068	3.741850209	0.000182889	0.000292636	3.536722448
ABLUW_RS00240	ABLUW_0278	NZ_CP008706.1	2006097	2006097	+	WP_000971688.1	modB	68.94161077	1.198857237	0.280106263	4.61418214	3.98E-06	7.44E-06	5.84627064
ABLUW_RS0690	ABLUW_3410	NZ_CP008706.1	3410933	3410073	+	WP_001077277.1	taIC	45.2005497	1.198680884	0.167188789	3.809054622	0.00019499	0.00022356	3.645207889
ABLUW_RS052	ABLUW_0622	NZ_CP008706.1	617198	6172703	+	WP_000744219.1	LipA/Cst family transcriptional regulator	673.6837546	1.197180314	0.195101462	6.153010307	8.00E-10	2.20E-09	8.673664199
ABLUW_RS03800	no	NZ_CP008706.1	760708	761898	+		terminase family protein	42.00885199	1.193723222	0.262849745	4.538473603	5.67E-06	1.04E-05	4.982866601
ABLUW_RS08010	ABLUW_0641	NZ_CP008706.1	6317480	6317818	+	WP_001043508.1	hypothetical protein	2614524357	1.192664756	0.271819765	4.392568429	1.12E-05	2.00E-05	4.688970004
ABLUW_RS07905	ABLUW_0620	NZ_CP008706.1	6103356	614792	-	WP_001075431.1	eat	85.2975536	1.19342872	0.36196939	3.271895719	0.00186829	0.00187342	2.10188887
ABLUW_RS02845	ABLUW_0579	NZ_CP008706.1	574502	574544	-	WP_000015691.1	head complementin/tilization protein	50.45212328	1.182890779	0.295627973	4.00281834	6.30E-05	0.000105762	3.975670345
ABLUW_RS02440	ABLUW_2933	NZ_CP008706.1	2947306	2948451	+	WP_000731756.1	galactose mutarotase	43.91777044	1.182673224	0.21454108	4.307818795	1.65E-05	2.91E-05	4.53610701
ABLUW_RS01780	ABLUW_0900	NZ_CP008706.1	9093925	9093925	+	WP_000098635.1	hypothetical protein	74.74005412	1.181728597	0.269116588	4.387560453	1.14E-05	2.04E-05	4.900368833
ABLUW_RS03635	ABLUW_1951	NZ_CP008706.1	197901	1980365	+	WP_001033624.1	FAD-dependent oxidoreductase	67.6374377	1.17940493	0.210929653	5.530429155	3.16E-08	7.16E-08	7.145741851
ABLUW_RS03230	ABLUW_0596	NZ_CP008706.1	614234	614476	+	WP_000004363.1	hypothetical protein	65.45291858	1.179144329	0.272832269	4.309403484	1.84E-05	2.89E-05	4.539162167
ABLUW_RS02395	ABLUW_0488	NZ_CP008706.1	500331	501164	+	WP_000755011.1	enoyl-CoA hydratase/isomerase family protein	167.7730424	1.173899923	0.322555524	3.638730337	0.000273964	0.000430836	3.366880815
ABLUW_RS04845	ABLUW_0950	NZ_CP008706.1	1950553	1952100	+	WP_001032988.1	DHA2 family efflux MFS transporter permease subunit	232.8890705	1.17311073	0.443933302	2.642538246	0.00822817	0.01102808	1.953356981
ABLUW_RS04805	ABLUW_1226	NZ_CP008706.1	1212523	1214800	+	WP_010252916.1	D-amino acid dehydrogenase	5.989389265	1.172775324	0.256178094	5.177968812	4.70E-06	8.71E-06	5.95991845
ABLUW_RS02320	no	NZ_CP008706.1	3371498	3378620	+	WP_001884441.1	hypothetical protein	12.8169254	1.172748835	0.462542783	2.55343867	0.01020681	0.01848243	1.825409851
ABLUW_RS01820	ABLUW_3459	NZ_CP008706.1	3505261	3505668	+	WP_001028070.1	hypothetical protein	289.656229	1.170581726	0.194163253	6.028853085	1.65E-09	4.03E-09	5.394849454
ABLUW_RS01800	ABLUW_1188	NZ_CP008706.1	1121942	1120581	+	WP_000983826.1	basJ	15.9262843	1.17054259	0.493197931	3.273463345	0.01922142	0.022962358	1.68898316
ABLUW_RS05500	ABLUW_2790	NZ_CP008706.1	2786649	2788007	+	WP_000369468.1	MFS transporter	114.927611	1.170372641	0.252505044	4.63421195	6.75E-06	1.15E-06	7.05686227
ABLUW_RS01810	ABLUW_2326	NZ_CP008706.1	2309738	2310281	+	WP_000710973.1	1-acyl-sn-glycerol-3-phosphate acyltransferase	352.2496348	1.170360073	0.308498866	3.79371339	0.00014811	0.000240433	3.69719054
ABLUW_RS03450	ABLUW_1027	NZ_CP008706.1	1023719	1023021	-	WP_000485787.1	basD	538.1236882	1.170275077	0.418591431	2.795745502	0.005198017	0.00717655	2.14048285
ABLUW_RS02435	ABLUW_0863	NZ_CP008706.1	843547	843753	+	WP_000099358.1	hypothetical protein	132.530459	1.169607842	0.210932863	5.544929432	2.94E-08	6.54E-08	7.44422252
ABLUW_RS01978	ABLUW_2244	NZ_CP008706.1	2233311	2233754	+	WP_001046675.1	SRMP3 family protein	318.431188	1.169403177	0.223509285	5.222664963	1.76E-07	3.68E-07	6.434182181
ABLUW_RS01345	ABLUW_2109	NZ_CP008706.1	2114268	2116821	-	WP_001089728.1	2-oxo acid dehydrogenase subunit E2	734.8421235	1.169321434	0.428662872	2.727834621	0.000375156	0.00874549	2.058215852
ABLUW_RS01235	ABLUW_2932	NZ_CP008706.1	2946668	2947114	-	WP_001019633.1	hypothetical protein	939.014503	1.168692764	0.205932869	4.676118803	1.39E-08	3.16E-08	7.550312997
ABLUW_RS08990	ABLUW_0447	NZ_CP008706.1	1843497	1844363	+	WP_001870208.1	MBL fold metallo-hydrolase	316.535403	1.168010958	0.241937948	4.83372322	1.34E-06	2.60E-06	5.588026652
ABLUW_RS0395	ABLUW_3778	NZ_CP008706.1	3838235	3839260	+	WP_001091033.1	enoyl-CoA hydratase/isomerase family protein	119.231998	1.165719397	0.243887754	4.779737309	1.76E-06	3.36E-06	5.473607023
ABLUW_RS03075	ABLUW_0812	NZ_CP008706.1	8124	81899	+	WP_000571167.1	HsdY family protein	722.0750193	1.165605379	0.25250846	4.63282472	3.91E-06	7.32E-06	5.15848891
ABLUW_RS08010	ABLUW_1418	NZ_CP008706.1	1410544	1418657	+	WP_000729218.1	hypothetical protein	6.532604237	1.163584895	0.66039208	1.764681826	0.077620668	0.093492877	1.029221476
ABLUW_RS07315	ABLUW_0500	NZ_CP008706.1	1486833	1487450	+	WP_000768153.1	paraquat-inducible protein A	231.0089717	1.161918122	0.170250761	6.752143737	1.40E-11	4.10E-11	10.38404995
ABLUW_RS02590	ABLUW_2591	NZ_CP008706.1	2582744	2586349	-	WP_000457282.1	uca	121.925481	1.161018934	0.211889969	5.480259193	4.25E-08	9.30E-08	7.209188389
ABLUW_RS02000	ABLUW_2507	NZ_CP008706.1	2502388	2503581	+	WP_000050378.1	Cox transferase	94.1036442	1.160552493	0.207194554	5.574919568	2.48E-08	5.56E-08	7.242520508
ABLUW_RS03915	ABLUW_0799	NZ_CP008706.1	778171	774248	-	WP_000041780.1	Acr family DNA-binding protein	360.341468	1.15995824	0.228273931	5.079370024	3.79E-07	7.66E-07	6.11671123
ABLUW_RS03900	ABLUW_0751	NZ_CP008706.1	748948	748941	+	WP_000062004.1	GntR family transcriptional regulator	196.831477	1.158063498	0.207376629	5.584349117	2.35E-08	5.27E-08	7.278199385
ABLUW_RS01790	ABLUW_2507	NZ_CP008706.1	2002192	2002096	-	WP_000367699.1	hypothetical protein	95.0864005	1.1547355	0.243479606	4.742037465	2.11E-06	4.02E-06	5.395773947
ABLUW_RS03260	ABLUW_2841	NZ_CP008706.1	2851951	2853362	+	WP_000203777.1	APC family permease	119.8800197	1.152711901	0.296785068	8.831995611	0.000162754	0.000183222	3.774172708
ABLUW_RS0695	ABLUW_1855	NZ_CP008706.1	181350	181414	+	WP_000097918.1	Mec family protein	57.83939205	1.151865205	0.204586665	5.630206656	1.80E-08	4.07E-08	7.390405591
ABLUW_RS08020	ABLUW_0643	NZ_CP008706.1	183879	1839040	+	WP_000661051.1	hypothetical protein	88.82470643	1.151655002	0.3675182	3.133344879	0.01072862	0.00251015	2.600229946
ABLUW_RS03270	ABLUW_0664	NZ_CP008706.1	670429	671253	-	WP_000734697.1	self-repair family protein	43.19565547	1.151602381	0.160971479	7.62834721	8.50E-13	2.62E-12	1.158169871

ABUW_RS1140	ABUW_2290	NZ_CP008706.1	2278041	2278271	+	WP_0001679.1		hypothetical protein	696.482719	1.10349846	0.249928	4.45536124	8.386-06	152E-05	4.88166412
ABUW_RS1210	ABUW_2500	NZ_CP008706.1	2466075	2466677	-	WP_0004204.5.1		amino acid synthase family protein	63.6305126	1.02970727	0.3778627	2.94525347	0.00322605	0.004576276	2.339487791
ABUW_RS0700	ABUW_819	NZ_CP008706.1	618954	619339	-	WP_0001242.12		ethanodamine ammonia-lyase subunit EutB	51.48723832	1.10212104	0.32591544	3.412574923	0.000643522	0.00080617	3.00805005
ABUW_RS1600	ABUW_2384	NZ_CP008706.1	237196	237262	-	WP_00010765.1		MF5 transporter	48.41250282	1.11024041	0.29035879	3.82718408	0.000109642	0.000212785	3.676160298
ABUW_RS0430	ABUW_0944	NZ_CP008706.1	950665	953073	+	WP_000370435.1		FdhF/YdeP family oxidoreductase	111.842605	1.03844319	0.25094631	4.622636538	9.75E-06	175E-05	4.756061951
ABUW_RS0516	ABUW_0211	NZ_CP008706.1	925851	925051	+	WP_000082790.1		hypothetical protein	86.0240553	1.08495137	0.293362816	3.778189639	0.00015558	0.000251034	3.600267454
ABUW_RS0230	ABUW_0433	NZ_CP008706.1	445900	447390	+	WP_000416103.1		NAD(P)FAD-dependent oxidoreductase	1601.571082	1.05378587	0.80169706	6.15158677	1.92E-09	1.92E-09	8.76688771
ABUW_RS1235	ABUW_3342	NZ_CP008706.1	3375650	3376648	+	WP_024432485.1	dusA	rRNA hydriouridine[20(20a)] synthase DusA	1015.587121	1.07110726	0.228397006	4.847308409	125E-06	2.43E-06	5.614393726
ABUW_RS0350	ABUW_0807	NZ_CP008706.1	784297	784659	+	WP_000835166.1		hypothetical protein	42.63624352	1.06778105	0.342809003	3.228632406	0.001243837	0.001827651	2.738106732
ABUW_RS1685	ABUW_3492	NZ_CP008706.1	3541254	3541834	-	WP_000291731.1	crcB	fluoride efflux transporter CrcB	329.3183734	1.06512762	0.218479699	5.064602196	4.09E-07	8.26E-07	6.083019953
ABUW_RS1808	ABUW_3716	NZ_CP008706.1	3774775	3775371	-	WP_001233437.1		TerR family transcriptional regulator	45.85125873	1.05729389	0.295368125	3.743563698	0.000181429	0.000290415	3.536980956
ABUW_RS1705	ABUW_3516	NZ_CP008706.1	3564335	3564664	+	WP_000207459.1		MerR family transcriptional regulator	624.2330037	1.04106642	0.325941875	3.387434183	0.000705496	0.00169795	2.970099436
ABUW_RS0860	ABUW_0784	NZ_CP008706.1	178188	1782362	+	WP_012305084.1		DUF2750 domain-containing protein	902.0149776	1.02825051	0.238436064	4.624321461	3.76E-06	7.06E-06	5.578195299
ABUW_RS1695	ABUW_3213	NZ_CP008706.1	3243718	3245400	-	WP_001568249.1		MF5 transporter	81.68467794	1.02376666	0.30589899	3.604381518	0.000310897	0.000489578	3.31071916
ABUW_RS1250	ABUW_2110	NZ_CP008706.1	2094188	2095022	-	WP_000097108.1		ABC transporter permease	84.18385386	1.01856616	0.20339639	5.416303679	6.06E-08	132E-07	6.879426069
ABUW_RS1695	ABUW_3674	NZ_CP008706.1	3730894	3732342	-	WP_00518093.1		hypothetical protein	631.7560912	1.01301655	0.54977801	7.10618973	1.9E-12	3.64E-12	11.43889862
ABUW_RS03610	ABUW_0733	NZ_CP008706.1	739688	739888	-	WP_001291625.1		Alpa family page regulatory protein	914862411	1.01242609	0.276394256	3.984318003	6.77E-05	0.000103325	3.945674272
ABUW_RS0585	ABUW_0711	NZ_CP008706.1	777297	777370	+	WP_0007142419.1		hypothetical protein	79.17377996	1.00119227	0.23706606	6.640559798	3.47E-06	6.55E-06	8.1637587
ABUW_RS1215	ABUW_2493	NZ_CP008706.1	2488825	2490094	-	WP_000750378.1		hypothetical protein	32.88457375	1.08821802	0.3186573	3.532772876	0.000411226	0.000638223	3.95027549
ABUW_RS1095	ABUW_2483	NZ_CP008706.1	2481931	2482068	-	WP_000816406.1	putative 2-aminocetylphosphonate ABC transporter substrate-binding protein	13120424454	1.097886441	0.329740066	3.329551226	0.000689861	0.001500918	0.888570549	
ABUW_RS1790	ABUW_3252	NZ_CP008706.1	3281966	3282304	+	WP_001674611.1	raIA	ribosome-associated translation inhibitor RaIA	3509.359416	1.097481684	0.238633833	4.599016217	1.42E-06	7.91E-06	5.01235173
ABUW_RS1660	ABUW_3894	NZ_CP008706.1	3962180	3963235	+	WP_000991659.1		aromatic-rmp hydrolyzing dyogynase subunit alpha	61.0666413	1.02719933	0.22717702	4.829708987	1.37E-06	2.64E-06	5.578196073
ABUW_RS1880	ABUW_3898	NZ_CP008706.1	3865532	3865793	+	WP_000269732.1		GabY/YeaQ/YngJ family stress response membrane protein	865.088656	1.092651684	0.35040823	3.188223237	0.000181449	0.000263594	2.57093682
ABUW_RS1695	ABUW_3414	NZ_CP008706.1	3460247	3462247	+	WP_000205448.1		DUF839 domain-containing protein	270.5251623	1.090431266	0.163332339	6.676160436	2.45E-11	6.84E-11	9.184939
ABUW_RS1320	ABUW_2534	NZ_CP008706.1	2525290	2525290	-	WP_000389648.1	paalB	1,2-phenylethyl-CoA epoxide subunit B	2333.557698	1.087025329	0.603231867	1.802020494	0.071645013	0.086719271	1.061884362
ABUW_RS03640	ABUW_0739	NZ_CP008706.1	721964	721964	-	WP_000993558.1		hypothetical protein	228.6016204	1.085597217	0.220492676	4.92306892	8.50E-07	1.68E-06	1.5747890718
ABUW_RS1840	ABUW_2230	NZ_CP008706.1	221964	222045	+	WP_00201828.1		MotA/TolQ/EabB proton channel family protein	65.5740238	1.084648737	0.201617342	5.38240892	7.35E-08	1.58E-07	6.801342913
ABUW_RS1740	ABUW_3587	NZ_CP008706.1	3648893	3648249	-	WP_001304851.1		hypothetical protein	928.7108039	1.083059203	0.305279039	3.547899015	0.00038837	0.000604532	3.218580705
ABUW_RS1740	ABUW_2626	NZ_CP008706.1	2625823	2623453	+	WP_001303905.1		exo-alpha-sialidase	59.15551667	1.07918694	0.280382347	3.848732648	0.000118731	0.000193513	3.912289854
ABUW_RS0640	ABUW_1425	NZ_CP008706.1	1419623	1419623	+	WP_002034965.1		hypothetical protein	14.26543835	1.078944207	0.542005304	1.990652488	0.046519105	0.057006981	1.237314078
ABUW_RS1610	ABUW_0311	NZ_CP008706.1	972825	9724039	+	WP_000160408.1		MF5 transporter	85.5646256	1.07721168	0.179683875	5.989035683	2.1E-09	5.1E-09	6.292423824
ABUW_RS1770	ABUW_3649	NZ_CP008706.1	3716277	3716495	+	WP_000354164.1		hypothetical protein	293.5266817	1.076982229	0.201440812	5.346356378	8.97E-08	1.91E-07	6.718966633
ABUW_RS1405	ABUW_2894	NZ_CP008706.1	2901938	2902486	+	WP_001092989.1		DUF2239 family protein	1012.105045	1.07613201	0.280022932	3.842929463	0.000121574	0.000187908	3.70335665
ABUW_RS0895	ABUW_1828	NZ_CP008706.1	1824553	1825230	-	WP_000366062.1		DUF421 domain-containing protein	137.842117	1.07575408	0.237496889	4.529505196	5.91E-06	1.08E-05	6.676160436
ABUW_RS05450	ABUW_1114	NZ_CP008706.1	113330	113409	+	WP_000383013.1		amino acid permease	1086.508443	1.074659297	0.283504073	3.790618859	0.001500272	0.000242859	3.616454758
ABUW_RS06470	ABUW_1526	NZ_CP008706.1	153831	1539385	+	WP_000208716.1		lysosyme	312.5601936	1.074400006	0.105754943	6.897813949	5.28E-12	1.54E-11	10.81247928
ABUW_RS0895	ABUW_1846	NZ_CP008706.1	1843079	1843492	+	WP_000789128.1		YeeE/YeeJ family protein	86.70647978	1.074048175	0.26855306	4.029397286	5.59E-05	9.43E-05	4.025488307
ABUW_RS1905	ABUW_3677	NZ_CP008706.1	3734405	3736315	+	WP_000573062.1		ODG-type type-1 integrase/transposase/recombinase	2025.29116	1.07214039	0.245174341	4.37820706	123E-05	2.9E-05	6.469558885
ABUW_RS1215	ABUW_2085	NZ_CP008706.1	2067195	2067105	+	WP_000843216.1		transporter	47.6862662	1.07033773	0.31276872	3.42193629	0.000521762	0.000949263	3.022618022
ABUW_RS06870	ABUW_1409	NZ_CP008706.1	1407736	1408392	+	WP_000826376.1		hypothetical protein	64.29230816	1.069466782	0.275899201	3.876259323	0.000106059	0.000173422	3.76895891
ABUW_RS1870	ABUW_3773	NZ_CP008706.1	3831637	3833526	-	WP_000279948.1		fatty acyl-AMP ligase	87.32734642	1.068786406	0.27021708	3.955288102	7.64E-05	8.00E-07425	3.894743558
sRNA38	no	no	no	no	no	no	no	no	19.3977967	1.068505206	0.391304703	2.726232705	0.006406162	0.00878506	2.066255069
ABUW_RS04565	ABUW_0930	NZ_CP008706.1	938217	938306	+	WP_0001679.1		RNA-Ser	61.02538289	1.06813771	0.414888556	2.574517174	0.01003801	0.01427338	1.872010078
sRNA58	no	no	no	no	no	no	no	no	205.2040006	1.06756158	0.321679888	3.318709565	0.000904344	0.00150483	2.869510878
ABUW_RS1070	ABUW_2338	NZ_CP008706.1	2322218	2322048	+	WP_000078420.1		methionine transporter	17.42487562	1.066386286	0.206083515	5.174592903	2.28E-07	4.7E-07	6.326977603
ABUW_RS04575	ABUW_0932	NZ_CP008706.1	912519	914523	+	WP_001017162.1		non-ribosomal peptide synthetase	296.006442	1.064404809	0.99639147	5.334345019	9.59E-08	2.04E-07	6.690366338
ABUW_RS04090	ABUW_0835	NZ_CP008706.1	839711	839397	+	WP_000512921.1		hypothetical protein	587.5925793	1.064900692	0.157808018	6.082355237	1.9E-09	2.93E-09	8.53312328
ABUW_RS1625	ABUW_3299	NZ_CP008706.1	333308	3333178	+	WP_001000111.1		ComEA family DNA-binding protein	356.6646255	1.062485511	0.159670756	6.54227235	2.85E-11	7.88E-11	10.1347378
ABUW_RS0716	ABUW_0757	NZ_CP008706.1	752595	752774	+	WP_000606269.1		hypothetical protein	14.34490396	1.060999693	0.415707007	2.522256204	0.010702765	0.019278623	1.045310673
ABUW_RS02160	ABUW_0440	NZ_CP008706.1	452140	454335	+	WP_001616895.1		TRAP transporter large permease subunit	1682.852946	1.058881848	0.21975434	4.184801243	1.61E-06	2.79E-06	5.554395977
ABUW_RS06990	ABUW_1435	NZ_CP008706.1	1427029	1427343	+	WP_001024063.1		hypothetical protein	45.5931899	1.057999169	0.281009271	3.764997344	0.000166551	0.000267451	3.737577574
ABUW_RS07895	ABUW_1638	NZ_CP008706.1	161128	161143	-	WP_000774022.1	eutC	ethanodamine ammonia-lyase subunit EutC	92.5151749	1.056418074	0.217670373	3.890026966	0.000100023	0.000164497	3.783424018
ABUW_RS05895	ABUW_1964	NZ_CP008706.1	191614	1916507	-	WP_000203149.1		GODF domain-containing protein	967.921872	1.05364472	0.202312687	5.207996059	1.91E-07	3.97E-07	6.401029493
ABUW_RS1020	ABUW_2470	NZ_CP008706.1	2483483	2484006	+	WP_000220505.1		3-hydroxyacyl-CoA dehydrogenase	1817.547632	1.053542873	0.26912244	3.914737246	9.05E-05	0.000148985	3.826274841
ABUW_RS02205	ABUW_0449	NZ_CP008706.1	461097	463520	+	WP_000473568.1		hypothetical protein	13463.87897	1.052764544	0.267129185	3.94102302	8.11E-05	0.000134809	3.870687761
ABUW_RS07975	ABUW_1834	NZ_CP008706.1	1832229	1833348	+	WP_000055706.1		spore coat protein U domain-containing protein	1453.557127	1.051467687	0.288156106	3.648951611	0.000203310	0.00041922	3.819721236
ABUW_RS09570	ABUW_1968	NZ_CP008706.1	197093	1971053	+	WP_000872857.1		SDR family NAD(P)-dependent oxidoreductase	6.75599531	1.049136388	0.481419007	2.179281433	0.020931068	0.037347591	1.427714066
ABUW_RS1716	ABUW_2821	NZ_CP008706.1	2826194	2826283	-	WP_000292337.1		ammonium transporter</							

Table S14. RNA-seq data: Absolute and relative expression (Tet/MEP > 2-fold down)

ABLW_RS08880	ABLW_R25	N2_CP008706.1	925095	922232	+	WP_0008668.1	CTP synthase	18781.20588	-1.0048427	0.1605432 E	-6.2380800 E	4.43E-10	1.13E-09	8.948921557
ABLW_RS08940	ABLW_1001	N2_CP008706.1	912570	91910	-	WP_0043708.1	deoxyguanosinetriphosphate triphosphohydrolase	1234.419366	-1.100175987	0.164380641	-6.489000045	8.64E-11	2.30E-10	9.638274554
ABLW_RS08945	ABLW_0920	N2_CP008706.1	928268	926788	+	WP_0007329.2	MBL fold metallo- hydrolase	2247.770997	-1.100880434	0.177933566	-5.630014445	1.80E-08	4.07E-08	7.380400961
ABLW_RS190	ABLW_2386	N2_CP008706.1	2374626	2375921	-	WP_00018277.1	monooxygenase	608.1380311	-1.00227812	0.19107207	-5.243958183	1.57E-07	3.29E-07	6.482804102
ABLW_RS00175	ABLW_0036	N2_CP008706.1	44788	41965	+	WP_000529425.1	hydroethanol synthase	935.8497236	-1.002601563	0.202063412	-4.961816446	6.98E-07	1.39E-06	5.8569885
ABLW_RS01075	ABLW_0280	N2_CP008706.1	297514	298515	+	WP_001985598.1	sulfate ABC transporter substrate-binding protein	290.2902415	-1.002905105	0.200912677	-4.991474256	5.98E-07	1.16E-06	5.924453039
ABLW_RS05165	ABLW_0500	N2_CP008706.1	658748	6562025	+	WP_000031228.1	glycerolacetylhydrolase-3-phosphate dehydrogenase	47029.24808	-1.005182511	0.179993934	-5.984535477	2.34E-08	5.27E-08	7.728189385
ABLW_RS08435	ABLW_1732	N2_CP008706.1	1728754	1730247	+	WP_000089272.1	glnK nitrogen regulation protein (NR)	1841.680835	-1.00568441	0.173602027	-5.79395391	6.9E-09	1.6E-08	7.793174124
ABLW_RS08435	ABLW_3888	N2_CP008706.1	3954163	3954665	+	WP_00094663.1	puE 5-(carboxyamino)imidazole ribonucleotide mutase	2690.694069	-1.00583311	0.173235566	-5.8739731	4.25E-09	1.00E-08	8
ABLW_RS16065	ABLW_3307	N2_CP008706.1	3341993	3342781	+	WP_01196724.1	crotonase/tenoyl-CoA hydratase family protein	339.0483809	-1.008899472	0.173703328	-5.729799083	1.0E-08	2.31E-08	7.63038802
ABLW_RS16040	ABLW_3302	N2_CP008706.1	3333223	3335729	+	WP_000259109.1	ctoninal (gppGpp synthetase)guanosine-3',5'-bis(diphosphate) 3'-pyr	14608.86713	-1.009234603	0.163238867	-6.5859798	4.52E-11	1.23E-10	9.92094889
ABLW_RS1790	ABLW_3859	N2_CP008706.1	3926609	3927175	+	WP_00190743.1	5'-nucleotidase	44194394	-1.013339882	0.16307869	-8.947507832	8.95E-10	4.00E-10	17.39794040
ABLW_RS17575	ABLW_3410	N2_CP008706.1	3468884	3469404	-	WP_00061569.1	acyl-CoA thioesterase	414.978217	-1.01987163	0.166305599	-5.62639581	2.57E-07	5.26E-07	6.279014256
ABLW_RS16045	ABLW_3404	N2_CP008706.1	3451081	3451944	+	WP_001884475.1	FadB-dependent dioxygenase	759.4841598	-1.010282875	0.162973735	-7.619342277	2.75E-10	9.18E-10	15.03716732
ABLW_RS00000	ABLW_3731	N2_CP008706.1	737470	738468	+	WP_001653074.1	zinc-binding dehydrogenase	1517.920871	-1.012191506	0.16599844	-5.967802778	2.40E-09	5.78E-09	8.238072192
ABLW_RS00435	ABLW_0624	N2_CP008706.1	799457	800063	-	WP_000434847.1	1-acyl-sn-glycerol-3-phosphate acyltransferase	495.1285035	-1.019606282	0.165067278	-5.96198197	2.03E-07	4.2E-07	6.375717904
ABLW_RS16035	ABLW_3261	N2_CP008706.1	3319067	3319047	-	WP_000050951.1	phenylalanine-tRNA ligase subunit alpha	4182.571047	-1.019765255	0.165727523	-6.965600579	3.49E-10	1.03E-11	19.98716278
ABLW_RS00150	ABLW_0165	N2_CP008706.1	16679	18237	+	WP_000737388.1	phoR phosphate (phage) sensor/histidine kinase PhoR	973.405025	-1.01947186	0.174410424	-5.804176971	5.2E-09	1.32E-08	7.915840169
ABLW_RS1915	ABLW_2289	N2_CP008706.1	2276707	2277192	+	WP_000204682.1	tRNA (pseudine)54(C)-methyltransferase TmaA	181.12959	-1.022417749	0.1716643	-6.765760594	1.33E-11	3.77E-11	16.42365885
ABLW_RS19175	ABLW_0320	N2_CP008706.1	344168	344339	+	WP_000260334.1	30S ribosomal protein S16	29373.41621	-1.023552943	0.263203956	-3.88631165	0.000191609	0.000167022	3.77722632
ABLW_RS16340	ABLW_3795	N2_CP008706.1	3846462	3847892	+	WP_00077999.1	amino acid permease	584.638181	-1.02398094	0.22183411	-4.418050392	3.9E-06	7.33E-06	5.04866025
ABLW_RS01810	ABLW_0235	N2_CP008706.1	254146	254745	+	WP_004458293.1	LydE family translocator	88.5974979	-1.025019688	0.25087219	-4.08816077	4.39E-05	7.47E-05	4.03673938
ABLW_RS18070	ABLW_3816	N2_CP008706.1	3878627	3879997	+	WP_00029987.1	phosphomannosyl transferase/phosphoglucomylase	299.99525	-1.0258823	0.165071903	-5.242481968	1.58E-07	3.3E-07	6.480172708
ABLW_RS18015	ABLW_058	N2_CP008706.1	603730	603838	-	WP_00055193.1	ribitolase monooxygenase	663.2602768	-1.027263358	0.22359776	-6.894247098	3.34E-06	8.09E-06	5.092051976
ABLW_RS1815	ABLW_2842	N2_CP008706.1	2855958	2857401	+	WP_00189231.1	hydroethanol synthase	174.662033	-1.027897094	0.16888926	-5.81870724	2.36E-07	4.85E-07	6.314256261
ABLW_RS02435	ABLW_0496	N2_CP008706.1	50197	507979	+	WP_000284347.1	adenine (5'-N)-adenine (5'-N)-dimethyltransferase	4622.731277	-1.02819189	0.16164831	-6.358470983	2.04E-10	5.29E-10	9.276543228
ABLW_RS02400	ABLW_0490	N2_CP008706.1	503227	503883	+	WP_000863320.1	hydroethanol synthase	1672.86062	-1.029054761	0.171845505	-6.857571842	1.9E-08	2.32E-06	5.634510015
ABLW_RS16060	ABLW_3306	N2_CP008706.1	3339069	3341896	+	WP_000045434.1	response regulator	2622.601572	-1.030057863	0.16596884	-8.9303766	5.43E-10	2.46E-10	17.60906489
ABLW_RS08215	ABLW_1887	N2_CP008706.1	1862531	1863565	+	WP_01166920.1	UDP-N-acetylmannan dehydrogenase	1265.344704	-1.031900506	0.17375253	-8.7946611	1.46E-10	6.5E-10	17.98641901
ABLW_RS07105	ABLW_577	N2_CP008706.1	565692	566990	+	WP_00073963.1	AarF/ABC/UVR kinase family protein	3225.658773	-1.032230601	0.164149078	-6.288372842	3.2E-10	8.2E-10	9.085566843
ABLW_RS10755	ABLW_2212	N2_CP008706.1	219040	2199972	+	WP_001225564.1	Dpp-type penicillinase	193.264251	-1.032334447	0.16308483	-6.330045645	2.45E-10	6.32E-10	9.99282922
ABLW_RS08080	ABLW_1782	N2_CP008706.1	1780187	1791865	+	WP_00010940.1	aspartate aminotransferase family protein	118.314044	-1.033756346	0.165052277	-6.263053834	3.78E-10	9.63E-10	9.01373713
ABLW_RS04040	ABLW_0819	N2_CP008706.1	795616	796527	+	WP_000097110.1	polymyosin synthase family protein	1389.930379	-1.034778145	0.127401889	-8.12229191	4.58E-10	1.73E-10	14.7619339
ABLW_RS04040	ABLW_0987	N2_CP008706.1	1000905	1001225	-	WP_00105071.1	hydroethanol synthase	942.79193	-1.034970109	0.203848157	-5.077181955	3.83E-07	7.74E-07	6.110190339
ABLW_RS02575	ABLW_074	N2_CP008706.1	1180885	1189341	+	WP_000542117.1	icd NADP-dependent succinate dehydrogenase	2004.382013	-1.03181089	0.162814193	-5.678502722	1.36E-08	3.16E-08	7.508633068
ABLW_RS18175	ABLW_3085	N2_CP008706.1	310206	3102763	+	WP_000397522.1	pgeF peptidoglycan editing factor PgeF	719.2215165	-1.038235106	0.13936668	-7.748389537	9.3E-10	3.25E-10	13.4881664
ABLW_RS04215	ABLW_0859	N2_CP008706.1	838466	838999	+	WP_000626045.1	hydroethanol synthase	2200.79021	-1.038480323	0.16161645	-6.429771825	1.28E-10	3.36E-10	9.473860723
ABLW_RS16420	ABLW_3379	N2_CP008706.1	3348466	3341066	+	WP_00516889.1	type IV plus biogenesis/stability protein PW	2000.678642	-1.040873242	0.16476278	-7.722058684	1.0E-10	3.93E-10	15.40507645
ABLW_RS01900	ABLW_0387	N2_CP008706.1	412556	412843	+	WP_000250997.1	STAS domain-containing protein	879.2771853	-1.041663339	0.16508872	-5.338999325	3.95E-08	1.99E-07	6.701946024
ABLW_RS08810	ABLW_1811	N2_CP008706.1	1806264	1807319	+	WP_000558174.1	N-acetyl-gamma-glutamyl-phosphate reductase	2280.618007	-1.041604206	0.165656102	-7.627653755	2.39E-10	8.09E-10	10.0905148
ABLW_RS12800	ABLW_2638	N2_CP008706.1	2638607	2637475	+	WP_011668337.1	O-methyltransferase	184.588333	-1.042701928	0.163038235	-4.73160914	1.07E-10	3.49E-10	12.45717452
ABLW_RS16015	ABLW_2363	N2_CP008706.1	2347942	2348724	+	WP_000257212.1	Paik family protein	2370.24718	-1.042741877	0.16521526	-6.549370867	5.78E-11	1.56E-10	9.808875402
ABLW_RS04040	ABLW_0909	N2_CP008706.1	601983	603605	+	WP_001643188.1	hydroethanol synthase	1317.17272	-1.043484817	0.169944869	-5.2196254	1.76E-07	3.74E-07	6.42718398
ABLW_RS02080	no	N2_CP008706.1	2881956	2882194	-		hydroethanol synthase	55.44343002	-1.043896681	0.23816148	-4.420452462	8.85E-06	1.77E-05	5.02206734
ABLW_RS19115	ABLW_2327	N2_CP008706.1	2310443	2311192	+	WP_000907230.1	YdcP/Php family DNA-binding transcriptional regulator	8240.275071	-1.04424924	0.218643395	-8.89249408	9.96E-07	1.96E-06	5.077143929
ABLW_RS16030	ABLW_3461	N2_CP008706.1	3506833	3507423	-	WP_01814507.1	hydroethanol synthase	3418.82578	-1.044700879	0.17054195	-7.642304421	2.0E-10	7.25E-10	13.0966199
ABLW_RS17995	ABLW_3897	N2_CP008706.1	3755581	3766572	+	WP_00094593.1	mtid multidrug transporter subunit Mtd	806.191478	-1.044712369	0.16067847	-5.49444969	3.9E-08	8.84E-08	7.063486258
ABLW_RS18175	ABLW_3897	N2_CP008706.1	3964832	3965359	+	WP_000214880.1	hydroxanthone phosphotransferase	2927.386254	-1.044737681	0.17166478	-6.992745609	1.1E-09	2.75E-09	8.560676638
ABLW_RS16070	ABLW_3409	N2_CP008706.1	3456690	3457316	+	WP_000106715.1	SHAM1 family non-canonical putative NTP pyrophosphatase	504.245295	-1.045832225	0.16991959	-5.273500148	1.34E-07	2.82E-07	6.549750892
ABLW_RS01950	ABLW_0355	N2_CP008706.1	411956	411876	+	WP_000842362.1	outer membrane lipid asymmetry maintenance protein Mta	4540.319454	-1.051444793	0.163719056	-6.837439805	8.06E-10	2.33E-11	15.6234460
ABLW_RS15885	ABLW_2656	N2_CP008706.1	2667900	2669012	-	WP_000775471.1	pppP Xaa-Pro aminopeptidase	2647.10751	-1.051933646	0.155677274	-8.365333892	5.99E-10	2.41E-10	15.61962966
ABLW_RS16050	ABLW_2911	N2_CP008706.1	276421	2716723	+	WP_001865715.1	hydroethanol synthase	532.5219793	-1.054211915	0.288609373	-3.640518148	0.000272069	0.000428022	3.588330368
ABLW_RS09415	ABLW_1933	N2_CP008706.1	191494	1933071	-	WP_000152473.1	aldehyde dehydrogenase (NADP+)	264.469188	-1.056196105	0.308572385	-3.40282845	0.000653766	0.000999507	3.002104583
ABLW_RS04665	ABLW_0911	N2_CP008706.1	919954	919100	+	WP_000070815.1	amino acid permease	5173.80012	-1.058822321	0.173875488	-6.06231862	1.34E-09	3.29E-09	8.482804102
ABLW_RS16035	ABLW_3368	N2_CP008706.1	3406821	3406679	+	WP_01173998.1	rigA ribosome small subunit-dependent GTPase A	447.7335511	-1.060495022	0.218854164	-4.431107036	9.37E-06	1.69E-05	4.77215295
ABLW_RS16010	ABLW_1229	N2_CP008706.1	126998	126139	-	WP_000444328.1	hydroethanol synthase	975.747879	-1.060219671	0.261274858	-4.9199516	2.73E-05	4.72E-05	4.326058601
ABLW_RS16060	ABLW_2334	N2_CP008706.1	2321720	2323885	-	WP_000109961.1	malate synthase G	9216.426337	-1.060902336	0.178419141	-5.948104192	2.75E-09	6.57E-09	8.16343463
ABLW_RS04765	ABLW_0972	N2_CP008706.1	982999	983494	+	WP_001885338.1	TadE/gcd family protein	782.883986	-1.061278657	0.169064109	-6.672018377	2.52E-11	7.03E-11	15.93304467
ABLW_RS04765	ABLW_1014	N2_CP008706.1	1025500	1026321	+	WP_000809887.1	dapD 3-oxo-2-hydroxybutyrate-2,6-dicarbonyltransferase N-succinyltransferase	7006.66181	-1.0					

ABUW_RS10655	ABUW_292	NZ_CP008706.1	217660	217833	+	WP_000070796.1		AarF/ABC1UbB kinase family protein	3451086926	-1.020292578	0.141837625	-7.89841806	2.82E-5	1.02E-14	13.99109983
ABUW_RS20335	ABUW_3839	NZ_CP008706.1	3907041	3907208	-	WP_000938939.1		hyetrical protein	37239661024	-1.0229945	0.342254468	-3.28168123	0.00033781	0.00029004	2.8588163
ABUW_RS0445	ABUW_086	NZ_CP008706.1	826186	828226	-	WP_00054789.1		site-specific recombinase	2124.79079	-1.023564321	0.02262542	-8.470617497	2.44E-7	1.0E-16	16.99967803
ABUW_RS09005	ABUW_0249	NZ_CP008706.1	042924	050172	+	WP_000205474.1	ubA	4-hydroxybenzoate octaprenyltransferase	8916006074	-1.023768864	0.19186467	-5.838218319	1.36E-7	5.73E-17	16.243438
ABUW_RS20595	ABUW_0426	NZ_CP008706.1	44333	442652	+	WP_002000592.1	secY	proteome translocase subunit SecY	174538.7486	-1.024851701	0.024070091	-1.50479615	6.64E-06	1.22E-05	4.9350499
ABUW_RS04850	ABUW_0889	NZ_CP008706.1	90989	902785	-	WP_000268346.1		RNA methyltransferase	12217776	-1.025718657	0.168835636	-6.67484392	2.80E-11	7.24E-11	10.1626143
ABUW_RS20325	ABUW_0781	NZ_CP008706.1	763564	766119	+	WP_001078744.1		hyetrical protein	99.10703954	-1.02695442	0.256172564	-4.399360433	1.09E-05	1.94E-05	4.7018927
ABUW_RS17775	ABUW_3630	NZ_CP008706.1	371054	371210	-	WP_000493866.1		riboflavin synthase	3978.301555	-1.029056154	0.162453684	-6.950018732	3.65E-12	1.08E-11	10.96657674
ABUW_RS02280	ABUW_0484	NZ_CP008706.1	475506	476957	-	WP_000216141.1	msB	(S-isopentenyl)adenosine(37)-C(2)-methylthio transferase	9619.885016	-1.030375129	0.147899708	-7.638200933	2.20E-14	7.46E-14	13.0726107
ABUW_RS00725	ABUW_0146	NZ_CP008706.1	160572	161669	+	WP_000124355.1	murG	(rho-pho-muramoyl)pentapeptide beta-N-acetylglucosaminidase	502.390055	-1.032231995	0.184090551	-9.561993812	1.16E-21	6.20E-21	20.20149435
ABUW_RS1400	ABUW_2904	NZ_CP008706.1	291825	2912769	+	WP_001083350.1		beta-ha family hydrolase	9338.433977	-1.034071071	0.14988818	-7.567631859	3.80E-14	1.27E-13	12.8969628
ABUW_RS12850	ABUW_2648	NZ_CP008706.1	2646817	2647356	-	WP_000179337.1		beta-ha family hydrolase	1691592417	-1.034969592	0.176884068	-6.541491859	1.4E-10	3.69E-10	9.432973634
ABUW_RS107405	ABUW_1446	NZ_CP008706.1	136778	143319	+	WP_000334670.1	puF	amidophosphoribosyltransferase	6489.507365	-1.038893384	0.133749875	-8.518444486	1.67E-17	6.96E-17	16.10739076
ABUW_RS10040	ABUW_2067	NZ_CP008706.1	204283	204447	-	WP_000147274.1	pgqE	pyrimidoquinone biosynthesis protein PgqE	549.5050651	-1.040623819	0.21991077	-5.98072448	2.14E-07	4.42E-07	6.354577731
ABUW_RS20325	ABUW_0716	NZ_CP008706.1	722376	722323	+	WP_001182097.1	rncC	rod shape-determining protein RncC	4557.864125	-1.043475576	0.254387689	-4.495011464	6.96E-06	1.27E-05	4.88616279
ABUW_RS04760	ABUW_0952	NZ_CP008706.1	161141	161085	+	WP_001055198.1		hyetrical protein	785.4073993	-1.043512473	0.224894028	-5.084672506	3.68E-07	7.46E-07	13.0726107
ABUW_RS20850	ABUW_0127	NZ_CP008706.1	90061	91136	+	WP_001028416.1		MS-RNA (murAC(498)-ND3)-methyltransferase	682.1074966	-1.04425268	0.12418621	-9.218080483	3.06E-20	1.52E-19	18.9185641
ABUW_RS1470	ABUW_3830	NZ_CP008706.1	296905	297035	-	WP_000359621.1		YbaH family protein	34.31636574	-1.044590925	0.388835489	-2.944554396	0.003234201	0.004580509	2.33860896
ABUW_RS21290	ABUW_2583	NZ_CP008706.1	361290	361290	+	WP_000175011.1		DMT family transporter	723.2407591	-1.045946484	0.166074051	-7.845299549	4.33E-15	1.53E-14	11.8130887
ABUW_RS1010	ABUW_2204	NZ_CP008706.1	2248746	2249378	-	WP_000563183.1	rnmG	16S rRNA (guanine(527)-N(7))-methyltransferase RnmG	1707.59547	-1.046443464	0.16620065	-7.36693871	1.75E-10	5.61E-10	12.25103714
ABUW_RS00518	ABUW_0135	NZ_CP008706.1	1345762	1349441	-	WP_001027069.1	adeG	ribulose biphosphate reductase permease subunit AdeG	137.5027374	-1.047052168	0.251641702	-4.563716081	5.03E-06	9.29E-06	5.03186428
ABUW_RS00305	ABUW_0236	NZ_CP008706.1	1036320	1037963	-	WP_000367533.1	nadB	L-aspartate oxidase	2852.686532	-1.04710106	0.128006299	-8.961560703	3.21E-19	1.48E-19	17.8271387
ABUW_RS16335	ABUW_3302	NZ_CP008706.1	3401281	3402168	+	WP_001024213.1		MacA family efflux pump subunit	816.247614	-1.047144429	0.19284098	-6.271386534	3.58E-10	9.14E-10	9.03903804
ABUW_RS107405	ABUW_0610	NZ_CP008706.1	614147	614800	+	WP_001022019.1		glycylphosphoglycerate phosphodiesterase	9384.957469	-1.047138793	0.20910636	-9.489310104	2.33E-21	1.24E-20	19.90087831
ABUW_RS00550	ABUW_104	NZ_CP008706.1	187018	189207	+	WP_000428308.1		MFJ transporter	426.803168	-1.047143661	0.146257171	-7.845330161	4.32E-15	1.53E-14	11.8130887
ABUW_RS107405	ABUW_3230	NZ_CP008706.1	323013	323659	-	WP_000357166.1	muA	UDP-N-acetylglucosamine 6-carboxyvinyltransferase	9301652407	-1.047176002	0.172975435	-6.63393581	3.24E-11	8.91E-11	10.001223
ABUW_RS10960	ABUW_2234	NZ_CP008706.1	2240285	2241058	-	WP_000497300.1		TatD family hydrolase	3090.423944	-1.048171643	0.17302975	-9.01402348	6.02E-19	9.47E-19	16.0236050
ABUW_RS20325	ABUW_0051	NZ_CP008706.1	57168	57530	+	WP_000101010.1		HT family protein	869.365297	-1.048256503	0.1676195	-6.847430465	7.52E-12	2.18E-11	10.6614351
ABUW_RS20440	ABUW_0497	NZ_CP008706.1	507980	508083	+	WP_000167234.1		symmetrical/ub(5'-nucleosyl)-tetraphosphatase	3176.031275	-1.048182697	0.17580461	-6.697631498	2.12E-11	5.93E-11	10.2294531
ABUW_RS1765	ABUW_2214	NZ_CP008706.1	2201439	2201439	-	WP_000168826.1	raA	ribonucleic acid synthetase activity regulator Raa	1700.377994	-1.052707949	0.202237496	-6.699773648	1.20E-08	2.75E-08	7.60607660
ABUW_RS20795	ABUW_1436	NZ_CP008706.1	1447795	1445303	+	WP_000461855.1		DUF3333 domain-containing protein	1204.678672	-1.05335514	0.19077079	-8.817825464	1.97E-18	5.85E-18	17.2867604
ABUW_RS1790	ABUW_3048	NZ_CP008706.1	3074477	3075199	+	WP_000763673.1	rncC	septum site-determining protein RncC	856.052093	-1.05364944	0.18345944	-6.11445526	1.68E-19	7.38E-19	17.0176434
ABUW_RS18555	ABUW_3812	NZ_CP008706.1	3874865	3875816	-	WP_000587286.1	ldd	FMN-dependent L-lactate dehydrogenase Ldd	2830.650457	-1.05467123	0.339754189	-3.398148845	0.000878435	0.001930699	2.986868145
ABUW_RS04775	ABUW_0974	NZ_CP008706.1	984651	985886	+	WP_00108436.1		lipotein-releasing ABC transporter permease subunit AdeC	2705.1887096	-1.055194439	0.16648191	-7.386345673	1.91E-10	4.87E-10	12.3124764
ABUW_RS10075	ABUW_3309	NZ_CP008706.1	3343675	3344449	+	WP_000532989.1		TbmA family protein	5887.98601	-1.056052051	0.218954968	-6.464093333	4.65E-08	1.02E-07	16.9999828
ABUW_RS16335	ABUW_3188	NZ_CP008706.1	3226652	3227638	+	WP_00013155.1		DUF1852 domain-containing protein	3257.508537	-1.058187164	0.146341974	-7.281139026	0.005418643	0.00749815	2.12494494
ABUW_RS00550	ABUW_030	NZ_CP008706.1	642206	643033	+	WP_000344900.1	kpB	signal peptidase I	3787.850848	-1.0591188	0.14085169	-8.229314651	1.88E-16	7.33E-16	15.13489603
ABUW_RS10185	ABUW_0384	NZ_CP008706.1	41947	411956	+	WP_00109147.1	mde	ymmetry maintenance ABC transporter permease subunit	4235.638467	-1.061026355	0.18305167	-6.343879499	2.24E-10	5.78E-10	9.237321346
ABUW_RS00550	ABUW_105	NZ_CP008706.1	100210	105611	+	WP_001024251.1	glaA	lactoylcholine lyase	2824.570661	-1.061861931	0.179063237	-6.488480755	8.67E-11	2.31E-10	9.63638802
rRNA5															
ABUW_RS00550	ABUW_101	NZ_CP008706.1	182314	183144	+	WP_000505750.1		peptidoglycan DD-metalloendopeptidase family protein	6898.61918	-1.06517556	0.20610031	-5.65169317	1.59E-08	3.61E-08	7.442492798
ABUW_RS1025	ABUW_3500	NZ_CP008706.1	3547353	3548219	-	WP_000125346.1		glutamate racemase	1363.340622	-1.066888343	0.16045454	-7.285179276	3.21E-13	1.01E-12	11.99957680
ABUW_RS1340	ABUW_2748	NZ_CP008706.1	2773731	2773949	+	WP_000194507.1	alsA	alanine-ubA family ligase	9486.18599	-1.069032229	0.198368689	-5.881957392	4.05E-09	9.58E-09	8.91634491
ABUW_RS17355	ABUW_3566	NZ_CP008706.1	3623182	3623739	-	WP_000208041.1	pgsA	xylylglycine- glycerol-3-phosphate 3-phosphatidyltransferase	764.6545968	-1.070463235	0.18314879	-7.891739866	2.98E-15	1.07E-14	13.97019322
ABUW_RS00595	ABUW_0196	NZ_CP008706.1	1856074	1857012	+	WP_001168539.1		multifunctional RNA adenosine cap protein	2287.923548	-1.071649193	0.154343773	-8.051024457	8.16E-16	1.61E-16	14.81710642
ABUW_RS12885	ABUW_2651	NZ_CP008706.1	2650336	2650111	+			RNA-Gly	477.887967	-1.071889596	0.342923416	-3.418834382	0.000835869	0.000970555	3.010203641
rRNA6															
ABUW_RS1485	ABUW_3392	NZ_CP008706.1	3433426	3434784	-	WP_000450961.1		permease	8442.530602	-1.071981958	0.253669983	-4.619710796	3.84E-06	7.21E-06	5.42064741
ABUW_RS10155	ABUW_0236	NZ_CP008706.1	130635	130717	+	WP_001183997.1	aroB	3-dehydroquinate synthase	3734.07106	-1.072402976	0.218231674	-5.372286012	1.67E-07	6.777283259	
ABUW_RS17935	ABUW_0236	NZ_CP008706.1	130635	130717	+	WP_001183997.1		5-carboxymethyl-2-hydroxymuconate Delta-isomerase	3338.954343	-1.074418762	0.1203501	-10.48260004	1.04E-25	7.26E-25	24.03960338
ABUW_RS1040	ABUW_0390	NZ_CP008706.1	414680	416081	+	WP_000849702.1		NiLX domain-containing protein	857.1003485	-1.076471188	0.147897878	-7.955592071	1.78E-15	6.63E-15	14.80586802
ABUW_RS1040	ABUW_2890	NZ_CP008706.1	2897941	2899266	+	WP_000239953.1		HyCoC family transporter	2343.28336	-1.07809774	0.176623793	-8.086116	2.83E-14	10.5421056	
ABUW_RS10760	ABUW_3629	NZ_CP008706.1	3687522	3688718	-	WP_000907680.1	ftsW	putative lipid II flippase FtsW	2168.674001	-1.078661604	0.199442025	-5.909795106	3.43E-09	8.14E-09	8.089735595
ABUW_RS1700	ABUW_2616	NZ_CP008706.1	2607400	2608008	-	WP_000873472.1		hyetrical protein	777.8748284	-1.079101768	0.131716561	-7.358050839	0.000709301	0.00074266	3.56828027
ABUW_RS10825	ABUW_114	NZ_CP008706.1	180586	180682	+	WP_000952702.1	clpA	YTP-dependent Clp protease ATP-binding subunit ClpA	1541.19663	-1.079310395	0.176463273	-6.68108835	2.34E-11	6.54E-11	10.844225
ABUW_RS10820	ABUW_0185	NZ_CP008706.1	183164	183134	+	WP_000161610.1	recJ	single-stranded DNA-specific exonuclease RecJ	2689.826037	-1.081864295	0.1951724	-8.471098563	2.43E-17	1.01E-16	15.99697683
ABUW_RS10105	ABUW_0631	NZ_CP008706.1	633688	634998	-	WP_000446411.1		MSB family MSB transporter	2834.822118	-1.083889005	0.1862327	-7.784080427	7.38E-14	2.43E-13	12.6139373
ABUW_RS17380	ABUW_3611	NZ_CP008706.1	3616942	3617005	+	WP_000817711.1		hyetrical protein	1647.171691	-1.085105443	0.189737008	-8.481292335	2.		

ABUW_RS0830	ABUW_0167	NZ_CP008706.1	86519	16764	+	WP_096640204.1	prfB	peptide chain release factor 2	8124	137348	-1232922849	0.198718593	-8.824455416	1.10E-18	4.90E-18	17.30803930
ABUW_RS06560	ABUW_0445	NZ_CP008706.1	156538	1337908	-	WP_000848561.1	yegQ	tRNA S-hydroxymethyl modification protein YegQ	1612	726209	-123381471	0.300798312	-4.1010064	4.10E-05	7.00E-05	4.16401896
ABUW_RS1070	ABUW_3104	NZ_CP008706.1	3120065	3108739	-	WP_000985168.1		HAD-1A family hydrolase	9688	1784691	-1234725575	0.52899093	-0.06303754	8.05E-24	4.93E-23	22.30716308
ABUW_RS1835	ABUW_3663	NZ_CP008706.1	3722859	3723771	-	WP_000219268.1		signal peptidase II	237	5434184	-1235386025	0.318972547	-3.8729984	0.000175704	0.355196616	
ABUW_RS1043	ABUW_1110	NZ_CP008706.1	107737	1920629	-	WP_000227394.1		aspartate aminotransferase family protein	24107	59039	-123705652	0.179457479	-6.89336666	5.45E-12	1.59E-11	10.78802688
ABUW_RS1045	ABUW_2968	NZ_CP008706.1	204444	2049728	-	WP_001031363.1	pqiQ	alloquoline quinoxaline biosynthesis peptide chaperone P	314	5337947	-1238350309	0.178301995	-6.946097803	3.76E-12	1.1E-11	10.95467702
ABUW_RS0190	ABUW_0557	NZ_CP008706.1	1065251	1067276	+	WP_000275424.1	dusB	tRNA dHcydihydrolyase synthase DusB	564	8490088	-123925754	0.18992221	-0.13355686	4.87E-25	3.21E-24	23.49349407
ABUW_RS7735	ABUW_3842	NZ_CP008706.1	3702434	3703618	+	WP_000593169.1		peptidase S41	944	6518007	-1239912201	0.146589488	-8.468404599	2.71E-17	1.10E-16	10.95078768
ABUW_RS0340	ABUW_0618	NZ_CP008706.1	619721	620233	+	WP_001059542.1		DUF1543 domain-containing protein	980	7346771	-1239929429	0.178195671	-6.966246621	3.45E-12	1.02E-11	10.91919893
ABUW_RS0510	ABUW_1216	NZ_CP008706.1	114848	1149013	-	WP_00107195.1		gamma carboxic anhydride family protein	627	1749455	-124059148	0.12547401	-9.887238626	4.73E-23	2.77E-22	21.55072503
ABUW_RS1118	ABUW_1118	NZ_CP008706.1	103284	1140186	+	WP_001091973.1		phosphate ABC transporter ATP-binding protein	187	485707	-1241276072	0.147054948	-8.440899746	3.15E-17	1.29E-16	16.88941829
ABUW_RS0740	ABUW_0228	NZ_CP008706.1	151379	151474	-	WP_001005190.1		ABC transporter permease	2875	540059	-1243687895	0.17632326	-7.051890962	1.77E-12	5.31E-12	11.274190548
ABUW_RS16705	ABUW_3436	NZ_CP008706.1	3471863	3480102	-	WP_002038961.1		RNA-binding protein	440	1732554	-1243740996	0.172077082	-7.227819148	4.91E-13	1.533E-12	11.81530857
ABUW_RS02540	ABUW_0517	NZ_CP008706.1	528372	528809	+	WP_000876469.1	tnxC	thioesteron TnC	618	681384	-1245412706	0.141881467	-8.777828079	1.67E-18	7.31E-18	17.0608267
ABUW_RS19005	ABUW_3903	NZ_CP008706.1	3969443	3971023	+	WP_001188090.1	yscC	membrane protein insertase YscC	33583	20947	-1246377639	0.218873741	-5.747019586	9.08E-09	2.10E-08	7.877710705
ABUW_RS10670	ABUW_0327	NZ_CP008706.1	314937	315013	+	WP_000525222.1		TSUP family transporter	490	371832	-1247164247	0.161289916	-7.732437816	1.06E-14	3.67E-14	13.43533394
ABUW_RS16716	ABUW_3835	NZ_CP008706.1	3903094	3903789	+	WP_000724221.1		FKBP-type peptidyl-prolyl-cis-trans isomerase	2235	995508	-1248377816	0.143407162	-8.707922651	3.09E-18	1.34E-17	16.8728952
ABUW_RS1000	ABUW_3455	NZ_CP008706.1	345553	3544191	-	WP_012300756.1		SAM-dependent methyltransferase	404	1235928	-124833077	0.20212402	-6.178280956	6.49E-10	1.64E-09	8.78516612
ABUW_RS16416	ABUW_0940	NZ_CP008706.1	947003	947608	-	WP_010107011		ribonucleoside family protein	104	955494	-1248241418	0.239625027	-4.163551399	3.05E-05	5.25E-05	4.279616262
ABUW_RS16995	ABUW_2261	NZ_CP008706.1	2246373	2247008	-	WP_002064044.1		MeOAToUEd68 protein channel family protein	1024	525071	-1249787463	0.171651654	-7.280839801	3.32E-13	1.04E-12	11.98236666
ABUW_RS33445	ABUW_0700	NZ_CP008706.1	703595	705769	-	WP_001990324.1	yccS	TIGR6185 family membrane protein	2435	136888	-1249974042	0.148448469	-8.420255517	3.78E-17	1.53E-16	15.81630857
ABUW_RS30715	ABUW_0598	NZ_CP008706.1	1594951	1595745	+	WP_001080978.1		DUF4189 domain-containing protein	336	1456267	-1250046878	0.354166836	-3.432716673	0.000917501	0.3391959	
ABUW_RS18525	ABUW_3806	NZ_CP008706.1	3861636	3880462	-	WP_001083583.1	acnD	Fe/S-dependent 2-methylsuccinate dehydrogenase AcnD	4507	335954	-1251532322	0.318600878	-3.916343757	9.02E-05	0.000148765	3.627499233
ABUW_RS19655	ABUW_3438	NZ_CP008706.1	3534387	3535733	+	WP_000073358.1	abeM	multidrug efflux MATE transporter AbeM	1680	788869	-12538514983	0.237381058	-6.282027937	1.28E-07	2.69E-07	16.57047762
ABUW_RS18600	ABUW_0821	NZ_CP008706.1	3887000	3888175	-	WP_000935236.1		DegT/DnaJ/ErpY/CitY58 aminotransferase family protein	1058	69027	-1256029814	0.152123242	-6.256659535	1.50E-16	5.85E-16	15.23244184
ABUW_RS18045	ABUW_3284	NZ_CP008706.1	336786	316025	+	WP_001010740.1		type IV pilus secretin PilQ family protein	3155	444185	-1259545267	0.160696258	-7.824940129	5.08E-15	1.79E-14	13.74714697
ABUW_RS17180	ABUW_3531	NZ_CP008706.1	3589334	3589107	+	WP_001066569.1		unctional phosphoribosyl-AMP cyclophosphoryltransferase family protein	2095	742044	-1259666871	0.198461891	-6.64840932	2.96E-11	8.18E-11	10.0872467
ABUW_RS071490	ABUW_02409	NZ_CP008706.1	1520409	1521251	+	WP_001030277.1		zinc-ribon and DUF3426 domain-containing protein	115	5105053	-1265415354	0.127678373	-9.910608032	3.73E-23	2.20E-22	21.65757732
ABUW_RS04470	ABUW_0911	NZ_CP008706.1	905428	906936	+	WP_000063780.1	gdpK	glycylglycine GlycK	1219	319478	-1265478621	0.175708486	-7.202148566	5.93E-13	1.64E-12	11.73518218
ABUW_RS18000	ABUW_0355	NZ_CP008706.1	1043358	1043604	+	WP_000895101.1	recO	DNA repair protein RecO	884	467807	-1267059197	0.17263544	-7.335058019	2.14E-13	6.66E-13	12.93671588
ABUW_RS18054	ABUW_0347	NZ_CP008706.1	828241	829218	-	WP_000234081.1		poly(ADP-ribose) synthase family protein	1242	319027	-1267095972	0.169909693	-9.923858347	2.30E-15	4.10E-15	14.073055
ABUW_RS18660	ABUW_0281	NZ_CP008706.1	344409	344957	+	WP_000192336.1	rmlK	ribonucleic maturation factor RmlK	59620	40753	-1267481474	0.262355994	-4.831023746	1.36E-06	2.63E-06	5.800444252
ABUW_RS18325	ABUW_3360	NZ_CP008706.1	3399655	3400164	+	WP_000549818.1		hypothetical protein	459	1596572	-1268365658	0.137184963	-9.244939369	2.35E-20	1.18E-19	16.9281979
ABUW_RS02416	ABUW_0492	NZ_CP008706.1	504336	504989	-	WP_000101061.1		glutathione S-transferase N-terminal domain-containing protein	484	812293	-1270225323	0.184241778	-6.893237487	5.45E-12	1.59E-11	10.78960282
ABUW_RS06060	ABUW_0231	NZ_CP008706.1	943057	943134	+	WP_00124039.1		DUF4845 domain-containing protein	1440	244316	-1270548952	0.105551111	-8.180320087	3.15E-16	1.20E-16	14.92081975
ABUW_RS181616	ABUW_3418	NZ_CP008706.1	3466642	3467001	+	WP_000889270.1		hypothetical protein	288	823438	-1274064438	0.1849808	-6.887549636	5.68E-12	1.65E-11	10.78251906
ABUW_RS071455	ABUW_0217	NZ_CP008706.1	1510889	151620	-	WP_001270556.1	glbB	hydroxyacylglutathione hydrolase	876	456012	-1275880484	0.119893316	-7.101975018	2.37E-12	7.08E-12	11.14916674
ABUW_RS14040	ABUW_2966	NZ_CP008706.1	2971902	297577	-	WP_011424681.1		acyl-CoA thioesterase	855	3062696	-1276551977	0.178738158	-7.142021662	9.20E-13	2.62E-12	11.54975089
ABUW_RS14044	ABUW_2148	NZ_CP008706.1	213222	2133551	-	WP_001024697.1		YbaB/EBIC family nucleoside-associated protein	2580	8911971	-1277156979	0.168824494	-7.567539204	3.80E-14	1.27E-13	16.9861628
ABUW_RS071485	ABUW_0333	NZ_CP008706.1	1519763	1520032	-	WP_001868304.1	fs	DNA-binding transcriptional regulator Fts	5561	157505	-1278739592	0.214206063	-5.966670399	2.38E-09	5.73E-09	8.241845378
ABUW_RS17435	ABUW_3036	NZ_CP008706.1	3062430	3063497	-	WP_000092403.1		hypothetical protein	3869	652455	-1279275309	0.160238912	-7.983649303	1.42E-15	5.24E-15	14.28066871
ABUW_RS04000	ABUW_0170	NZ_CP008706.1	88145	189203	+	WP_000819049.1		alkene reductase	913	5455979	-1279377387	0.175526993	-7.288402074	3.10E-13	9.87E-13	12.00582685
ABUW_RS18580	ABUW_1140	NZ_CP008706.1	116063	1160979	+	WP_000618791.1	epnB	EF-P beta-lyticin protein EpnB	1740	719242	-1279816858	0.114061321	-11.20222259	3.24E-29	2.73E-28	27.56387335
ABUW_RS181940	ABUW_0347	NZ_CP008706.1	8354773	8356794	+	WP_001004884.1	uvrB	endonuclease ABC subunit UvrB	3746	387079	-128033018	0.274690098	-5.171492152	2.32E-07	4.78E-07	16.32097332
ABUW_RS181960	ABUW_0382	NZ_CP008706.1	1394785	1395240	+	WP_001779591.1		histidine phosphatase family protein	877	3377208	-1281116358	0.122480308	-8.466070542	1.91E-25	24.04381867	
ABUW_RS08045	ABUW_0711	NZ_CP008706.1	186372	186664	+	WP_0002224849.1		3-deoxy-D-manno-6-phosphonic acid transferase	1107	524757	-1281035623	0.121871877	-0.504688716	8.23E-26	5.79E-25	24.23732144
ABUW_RS02225	ABUW_0453	NZ_CP008706.1	465765	466406	+	WP_000857682.1		fumaroylcoenzyme A:glutamate hydrolase family protein	257	125978	-1281981788	0.145533719	-6.1807166667	1.27E-18	5.64E-18	17.2447209
ABUW_RS107035	ABUW_3502	NZ_CP008706.1	3540066	3550778	+	WP_000400008.1		electron transfer flavoprotein-ubiquinone oxidoreductase	10857	30397	-1283355966	0.193353519	-6.631097024	3.33E-11	9.16E-11	10.0300538
ABUW_RS180105	ABUW_0266	NZ_CP008706.1	283550	284565	-	WP_000516306.1		TocE family protein	359	6077373	-1283842779	0.241985534	-5.300452803	1.02E-07	2.38E-07	6.62342034
ABUW_RS180165	ABUW_2187	NZ_CP008706.1	219388	2194953	+	WP_00043421.1		SukN N-terminal domain-containing protein	6601	1254243	-1285272756	0.133408923	-9.583038889	5.74E-22	3.17E-21	20.49894074
ABUW_RS020725	ABUW_0056	NZ_CP008706.1	608283	62088	+	WP_001825403.1		replication-associated recombination protein A	2015	765876	-1285687708	0.175455396	-7.32771826	2.34E-13	7.44E-13	12.026984
ABUW_RS10570	ABUW_2794	NZ_CP008706.1	2791324	2793324	+	WP_000446079.1		confinery alcohol dehydrogenase	726	2226881	-12860719467	0.19334145	-6.651855918	2.89E-11	7.99E-11	10.09745322
ABUW_RS07200	ABUW_1477	NZ_CP008706.1	1465281	1466516	+	WP_000397471.1	gltS	sodium/glutamate symporter	4470	134707	-1287134621	0.234403592	-5.492384349	3.97E-08	8.75E-08	17.05791947
ABUW_RS01360	ABUW_1400	NZ_CP008706.1	1403464	1404411	+	WP_000068615.1		helicase-helicase domain-containing protein	348	211844	-1287807857	0.185198686	-6.953993422	3.55E-12	1.05E-11	10.9781807
ABUW_RS10005	ABUW_3091	NZ_CP008706.1	3102182	3107400	+	WP_000398824.1	lobB	outer membrane lipoprotein LobB	753	7535776	-1288347446	0.168278495	-8.063821987	7.39E-16	2.77E-15	14.55720253
ABUW_RS013650	ABUW_0622	NZ_CP008706.1	621565	624368	+	WP_000088559.1		hypothetical synthase subunit alpha	237	1316939	-12891962739	0.252467949	-5.19787521	3.26E-07	6.64E-07	6.17831921
ABUW_RS180130	ABUW_0311	NZ														

ABUW_RS01845	ABUW_0376	NZ_CP008706.1	401038	401926	-	WP_000166013.1	aroE	shikimate dehydrogenase	1233.789617	-1.354956335	0.244038167	-5.552231052	2.826E-08	6.296E-08	7.201493955
ABUW_RS10710	ABUW_2918	NZ_CP008706.1	2928360	2928977	+	WP_000029241.1		rhomboid family intramembrane serine protease	365.023804	-1.358141711	0.206031263	-6.591820537	4.346E-11	1.8E-10	9.928117993
ABUW_RS00475	ABUW_0096	NZ_CP008706.1	107610	108920	-	WP_001_985281.1		hypothetical protein	4.865.661078	-1.3600474728	0.200048008	-13.337358889	1.406E-40	2.306E-39	38.63282776
ABUW_RS19100	ABUW_2486	NZ_CP008706.1	2442159	2442881	-	WP_000434319.1		UTRA domain-containing protein	329.3203418	-1.360519018	0.166397251	-8.176307036	2.936E-10	1.0E-10	14.9507898
ABUW_RS14940	ABUW_2169	NZ_CP008706.1	2140243	2140656	+	WP_000312749.1		HTF family protein	3536.865902	-1.361313411	0.107405440	-8.469744225	2.466E-17	1.023E-16	59.9919993
ABUW_RS10600	ABUW_2181	NZ_CP008706.1	2162783	2163076	+	WP_000018791.1		hypothetical protein	60.8669129	-1.36155106	0.483558717	-2.81543019	0.004070397	0.006766493	2.96836363
ABUW_RS17260	ABUW_3547	NZ_CP008706.1	3604440	3604749	-	WP_000555570.1	secG	preprenin translocase subunit SecG	3223.024936	-1.362606174	0.22840885	-6.14781087	7.866E-10	1.975E-09	8.70553374
sRNA62	no	no	no	no	no	no	no	no	1268.471058	-1.3641980546	0.412107384	-3.312166444	0.000925665	0.001937905	2.86018476
ABUW_RS06620	ABUW_0557	NZ_CP008706.1	1569381	1569932	-	WP_000918439.1		tetrasiticopeptide repeat protein	625.418508	-1.366425371	0.234847085	-5.826878248	5.655E-09	1.325E-08	7.87942609
sRNA62	no	no	no	no	no	no	no	no	9675.922477	-1.37271914	0.280878905	-4.887227628	1.025E-06	2.016E-06	5.696803943
ABUW_RS10380	ABUW_2136	NZ_CP008706.1	212292	2124003	-	WP_000918444.1	aroC	chotomate synthase	3097.526888	-1.373084269	0.190085929	-7.223492416	5.075E-13	1.08E-12	11.8014291
ABUW_RS10500	ABUW_2161	NZ_CP008706.1	2142124	2142714	-	WP_000183456.1		DUF377 domain-containing protein	1954.584944	-1.373373139	0.132870454	-10.33618291	4.836E-25	3.205E-24	23.49485002
ABUW_RS18800	ABUW_3861	NZ_CP008706.1	3928598	3929599	+	WP_000771825.1	rbF	bifunctional riboflavin kinase/FAD synthetase	849.4024723	-1.376166814	0.144673616	-9.552219667	1.875E-21	1.0E-20	19.99967863
ABUW_RS15515	ABUW_3196	NZ_CP008706.1	3224910	3225401	-	WP_0002249482.1		flavin reductase	1472.464774	-1.37701423	0.31018636	-4.440267791	9.986E-06	1.633E-05	4.787812396
ABUW_RS08520	ABUW_1749	NZ_CP008706.1	1747163	1747583	-	WP_000040963.1		RNA-binding protein	1677.096827	-1.37703783	0.22763289	-6.049379897	1.455E-09	3.555E-09	8.449771647
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001290065.1		hypothetical protein	845.1754442	-1.37781977	0.104189274	-12.23300943	5.656E-40	8.866E-39	38.05256628
ABUW_RS04550	ABUW_0927	NZ_CP008706.1	935673	936056	+	WP_001110719.1		SCP2 sterol-binding domain-containing protein	4098.045421	-1.379264039	0.173380811	-7.9551053	1.786E-15	4.837E-14	8.837587
ABUW_RS02300	ABUW_0047	NZ_CP008706.1	54563	55153	-	WP_000657011.1		DNA-3'-phosphogluconate glycosylase I	278.1901554	-1.379340396	0.190564971	-7.238163338	4.555E-13	1.425E-12	11.8471196
ABUW_RS02990	ABUW_0609	NZ_CP008706.1	609901	610087	+	WP_000680574.1		response regulator	1011808953	-1.380459871	0.17252649	-8.001637197	1.235E-13	4.566E-15	14.34193516
ABUW_RS01900	ABUW_2309	NZ_CP008706.1	2870334	2870619	+	WP_000003719.1		cell division protein ZapA	9265.800498	-1.381992449	0.146899632	-9.281095102	1.675E-20	8.441E-20	10.97365715
ABUW_RS17340	ABUW_3603	NZ_CP008706.1	3662700	3662710	-	WP_000209090.1	tpiE	anthranilate synthase component I	2457.581762	-1.383396053	0.163868884	-8.849633578	8.786E-19	3.93E-18	17.45056075
ABUW_RS00460	ABUW_0950	NZ_CP008706.1	957717	959105	-	WP_000048860.1	adaA	DNA repair protein AdaA	774.8793501	-1.384912891	0.140773171	-9.246735434	2.31E-20	1.16E-19	16.93564201
ABUW_RS01880	ABUW_0341	NZ_CP008706.1	303864	304508	-	WP_000481451.1		Park family protein	2233.874121	-1.385117272	0.263561951	-5.254895432	1.486E-07	3.16E-07	6.50808306
ABUW_RS14860	ABUW_3062	NZ_CP008706.1	3098882	3099352	-	WP_001138055.1	pspG	30S ribosomal protein S7	68711.14624	-1.386894257	0.209754878	-6.18976191	3.796E-11	1.040E-10	9.08266661
ABUW_RS04455	ABUW_1643	NZ_CP008706.1	1642281	1643714	+	WP_000162982.1		nicotinate phosphoribosyltransferase	3526.543565	-1.388882655	0.339787525	-3.402396384	0.000478706	0.000738797	3.131474877
ABUW_RS04880	ABUW_0995	NZ_CP008706.1	907534	907986	+	WP_000107564.1	tolR	protein TolR	338.660339	-1.390379788	0.20900718	-6.652306337	2.896E-11	7.978E-11	10.0854858
ABUW_RS18885	ABUW_3432	NZ_CP008706.1	3474774	3478483	+	WP_001189081.1		cation proton antiporter	4610.097036	-1.392272385	0.242902447	-5.73191042	9.946E-09	2.295E-08	7.64614518
ABUW_RS01950	ABUW_0030	NZ_CP008706.1	31596	316491	-	WP_000173454.1		pyrimidine permease	752.005083	-1.393267908	0.198791904	-7.004558485	2.466E-12	7.35E-12	11.19311266
ABUW_RS04425	ABUW_1609	NZ_CP008706.1	162631	1627734	+	WP_00117543.1		diaminobutyrate-2-oxoglutarate transaminase	17067.2937	-1.392815949	0.16038162	-7.721916009	1.165E-14	3.98E-14	10.4001893
ABUW_RS04640	ABUW_1844	NZ_CP008706.1	1843335	1844602	+	WP_000105308.1		NADH hydrolase	812.155289	-1.393731466	0.31875078	-4.46887733	7.865E-06	1.431E-05	4.84466393
ABUW_RS16535	ABUW_3402	NZ_CP008706.1	3447165	3448510	-	WP_00198432.1		trigger factor	29043.31763	-1.393615574	0.15406664	-8.440625862	3.16E-17	1.295E-16	5.8884192
ABUW_RS01755	ABUW_1554	NZ_CP008706.1	1559262	1560149	-	WP_001167811.1		RCD family protein	9556.146815	-1.393701477	0.163555587	-9.380030824	1.095E-19	5.19E-19	18.28433204
ABUW_RS02180	ABUW_0444	NZ_CP008706.1	457364	459781	-	WP_00165350.1	mr	ribonuclease R	5030.403583	-1.397201408	0.17001741	-12.69985197	5.926E-37	7.905E-36	35.82237291
ABUW_RS10805	ABUW_2840	NZ_CP008706.1	2810997	2814212	+	WP_000277832.1		LysM peptidoglycan-binding domain-containing protein	8102.430189	-1.398371788	0.14141984	-9.907597015	3.866E-23	2.27E-22	21.64139714
ABUW_RS18185	ABUW_0242	NZ_CP008706.1	259682	260321	-	WP_00105588.1		DUF1294 domain-containing protein	355.1900212	-1.399170248	0.162908925	-9.150350406	5.67E-20	2.78E-19	15.9559552
ABUW_RS00495	ABUW_0100	NZ_CP008706.1	111721	112164	-	WP_00102027.1		D-tyrosyl-tRNA(Ty) decarboxylase	504.6645882	-1.399606871	0.153024261	-10.34428105	4.446E-25	2.956E-24	23.53017798
ABUW_RS15790	ABUW_3610	NZ_CP008706.1	3671463	3672210	-	WP_000897420.1		uroporphyrogen-III synthase	582.3561972	-1.400643902	0.18147009	-7.444412299	9.746E-14	3.18E-13	4.01757288
ABUW_RS00870	ABUW_1655	NZ_CP008706.1	1648022	1650178	+	WP_001189921.1		TorB-dependent adenosine receptor	351.6875437	-1.402668554	0.541760555	-2.58909137	0.009622905	0.01910651	1.889051859
ABUW_RS00885	ABUW_1626	NZ_CP008706.1	1622264	1623191	+	WP_000800538.1	kdsA	3-deoxy-8-phosphotriculonate kinase	8760.735662	-1.402807375	0.176023786	-7.969419398	1.595E-15	5.86E-15	13.62427036
ABUW_RS00570	ABUW_1158	NZ_CP008706.1	118187	1183305	+	WP_00201737.1		EAL domain-containing protein	3168.7544	-1.403663357	0.19876537	-9.433440999	3.97E-21	2.09E-20	19.87853371
ABUW_RS18605	ABUW_3416	NZ_CP008706.1	3448477	3446556	-	WP_000335018.1		NRDE family protein	867.5403768	-1.405653393	0.228678778	-6.146846695	7.906E-10	1.98E-09	8.70333481
ABUW_RS18890	ABUW_3272	NZ_CP008706.1	3304809	3305545	+	WP_081915948.1		pyrimidine-5-carboxylate reductase	3423.24779	-1.406955321	0.11820101	-12.58230991	2.646E-36	3.404E-35	34.46602108
ABUW_RS13335	ABUW_1712	NZ_CP008706.1	171049	1712927	-	WP_00079986.1		bifunctional nucleoside-5-phosphoribosyltransferase protein MucC	9332.311466	-1.407254933	0.16716882	-8.953886286	3.43E-19	1.58E-18	17.80142421
ABUW_RS18450	ABUW_3385	NZ_CP008706.1	3423495	3425678	-	WP_000776302.1		carboxy-terminal processing peptidase	19534.41889	-1.408028797	0.15706158	-8.964838397	3.16E-19	1.445E-18	17.84193751
ABUW_RS17725	ABUW_3846	NZ_CP008706.1	3914859	3915476	+	WP_000737570.1		thiol disulfide interchange protein DsbA/DsbL	7985.484719	-1.408497941	0.24058419	-5.854460961	4.796E-09	1.96E-08	9.640021657
ABUW_RS18870	ABUW_3268	NZ_CP008706.1	3297518	3298435	+	WP_000785635.1		mechanosensitive ion channel family protein	804.323744	-1.409857479	0.22095587	-6.380719723	1.765E-10	4.59E-10	9.338187314
ABUW_RS02055	ABUW_0418	NZ_CP008706.1	437990	438526	-	WP_000115197.1	tpiE	50S ribosomal protein L5	24190.0444	-1.411800156	0.26380263	-5.435172888	8.71E-08	1.86E-07	6.730478058
ABUW_RS01945	ABUW_0288	NZ_CP008706.1	300264	300308	+	WP_001190541.1		methyltransferase domain-containing protein	183.0014	-1.412228546	0.199537301	-10.12079958	4.47E-24	2.79E-23	22.55493958
ABUW_RS02820	ABUW_0533	NZ_CP008706.1	541450	542583	+	WP_000667229.1	tgt	tRNA guanosine(34)transylase Tgt	5028.588603	-1.415308044	0.244804307	-5.78185379	7.41E-09	1.725E-08	7.764471953
ABUW_RS01360	ABUW_0723	NZ_CP008706.1	726845	729262	-	WP_000406996.1	thrH	phosphoserine phosphatase/homoserine phosphatase	600.050949	-1.419138373	0.185522879	-7.638647485	2.205E-14	7.44E-14	13.62427036
ABUW_RS17560	ABUW_3607	NZ_CP008706.1	3665331	3667367	-	WP_000870031.1		general secretion pathway protein	1068.70002	-1.4197148654	0.193436058	-9.489026147	2.33E-21	1.25E-20	19.90038999
ABUW_RS19160	ABUW_2718	NZ_CP008706.1	2702466	2706323	-	WP_000931798.1	hspA	ATP-dependent RNA helicase HspA	5359.575327	-1.417292033	0.2026217	-6.994799686	2.66E-12	7.93E-12	11.90172681
ABUW_RS00575	ABUW_1634	NZ_CP008706.1	1645148	1645348	+	WP_001185517.1		NF08103 family lipoprotein	6753.609057	-1.417445923	0.19042129	-7.443731148	9.79E-14	3.20E-13	12.49485002
ABUW_RS00815	ABUW_1769	NZ_CP008706.1	1766667	1770173	-	WP_000734811.1		PIGA domain-containing protein	206.5046345	-1.419787315	0.27554337	-5.220584328	1.785E-07	3.72E-07	4.629456706
ABUW_RS01830	ABUW_1184	NZ_CP008706.1	1254758	1257909	-	WP_001021055.1		class C Extended-ink spectrin beta-lactamase ADC-11	759.119548	-1.417799356	0.21935954	-6.658223559	2.77E-11	7.68E-11	10.1463878
ABUW_RS17015	ABUW_3498	NZ_CP008706.1	354138	3545154	-	WP_000007331.1	henH	fenicolase	549.1805789	-1.418671679	0.163009239	-13.6661907	1.625E-42	2.96E-41	40.5287829
ABUW_RS04905	ABUW_1000	NZ_CP008706.1	101879	101478	-	WP_000578663.1	ruvA	Holliday junction branch migration protein RuvA	1265.10194	-1.418857227	0.188642738	-10.23393603	1.405E-24	8.95E-24	23.04879616
ABUW_RS02320	ABUW_1890	NZ_CP008706.1	1845764	1846734	-	WP_000167981.1	</								

ABUW_RS0456	ABUW_3378	NZ_CP008706.1	347684	348475	-	WP_000405163.1	helic-tum-hells domain-containing protein	2785.549389	-1.500491898	0.133408422	-1.124735513	2.395-29	2.045-28	27.6903693
ABUW_RS0450	ABUW_0295	NZ_CP008706.1	350373	356606	+	WP_00064372.1	adok	5590.021092	-1.500694632	0.134075335	-1.1929935	4.42E-29	3.68E-28	27.4341628
ABUW_RS0400	ABUW_0817	NZ_CP008706.1	792355	793890	-	WP_002204084.1	amino acid permease	6941.947382	-1.501662535	0.134090176	-1.130197553	8.95E-29	7.28E-28	27.13786862
ABUW_RS0390	ABUW_0309	NZ_CP008706.1	333929	333934	-	WP_001175590.1	ic tonal (p)ppCp synthetase (guanosine-3'-5'-bis(diphosphate)3'-pyr	4235.696217	-1.503810373	0.126793329	-1.186032724	1.90E-32	1.96E-31	30.70774393
ABUW_RS0500	ABUW_9239	NZ_CP008706.1	940398	942435	+	WP_000033781.1	hspA	9644.403319	-1.505656493	0.134055667	-7.90991109	2.58E-15	9.29E-15	14.0338494
ABUW_RS0405	ABUW_9311	NZ_CP008706.1	929051	930638	-	WP_001626286.1	MF3 transporter	204.72777776	-1.509523265	0.125893093	-0.996232508	1.34E-12	4.06E-12	11.39147397
ABUW_RS1490	ABUW_2352	NZ_CP008706.1	2348451	2349206	+	WP_000976598.1	cysE	864.256811	-1.509816594	0.147781274	-0.21671509	1.70E-24	1.05E-23	22.96557624
ABUW_RS1035	ABUW_2269	NZ_CP008706.1	225556	2256163	+	WP_001074011.1	fructose-bisphosphate aldolase class II	9851.12851	-1.510597828	0.13747878	-0.69497516	3.49E-19	1.51E-17	16.8213025
ABUW_RS1085	ABUW_2717	NZ_CP008706.1	270265	2702371	-	WP_000512361.1	beta-keetoacyl-ACP synthase II	2294.787525	-1.510599863	0.140695493	-0.71679268	8.58E-27	6.31E-26	25.9997064
ABUW_RS0505	ABUW_0322	NZ_CP008706.1	943403	944095	+	WP_000160699.1	mc	2696.635898	-1.512523414	0.187943312	-0.048982289	8.29E-16	3.09E-16	14.51004152
ABUW_RS0640	ABUW_3222	NZ_CP008706.1	325135	3252200	-	WP_001278262.1	nadA	1924.969616	-1.512937567	0.1332265	-1.135613084	6.91E-30	6.07E-29	28.268191
ABUW_RS0860	ABUW_3266	NZ_CP008706.1	329510	3296590	-	WP_001166321.1	gapE	925.675695	-1.513431914	0.19993919	-8.91091025	5.06E-19	2.30E-18	17.63827216
ABUW_RS1770	ABUW_3637	NZ_CP008706.1	3696263	3697402	+	WP_000063593.1	threonine synthase	13469.92852	-1.51435043	0.197300224	-0.767360927	1.65E-14	5.64E-14	13.2487209
ABUW_RS0260	ABUW_0419	NZ_CP008706.1	438536	438841	+	WP_001074624.1	rpsN	43389.76961	-1.515024864	0.245624853	-6.18043858	6.91E-10	1.74E-09	8.759450752
ABUW_RS0920	ABUW_3479	NZ_CP008706.1	3528492	3530333	+	WP_000084318.1	long-chain-acyl-CoA synthetase	1039.346738	-1.51831974	0.202743376	-0.747910026	7.49E-14	2.46E-13	12.6906469
ABUW_RS1785	ABUW_3532	NZ_CP008706.1	3589197	3590619	+	WP_000065140.1	AAA family ATPase	2004.641716	-1.519383924	0.196772483	-0.678891926	3.7E-22	2.06E-21	26.0861278
ABUW_RS1925	ABUW_2666	NZ_CP008706.1	261781	261810	+	WP_000091760.1	hypothetical protein	94.97048432	-1.519450036	0.150179574	-0.326032106	0.00247786	0.00355111	2.449586636
ABUW_RS0740	ABUW_3645	NZ_CP008706.1	631147	632592	-	WP_000075491.1	dnaB	837.621275	-1.51952475	0.193232329	-1.746727673	7.34E-32	7.28E-31	30.13768662
ABUW_RS0760	ABUW_3647	NZ_CP008706.1	3709962	3709964	+	WP_001516590.1	DNA polymerase β subunit chi	1918.43198	-1.51977885	0.160244478	-0.83235413	2.42E-27	1.84E-26	25.7359218
ABUW_RS1920	ABUW_2246	NZ_CP008706.1	2234334	2235458	-	WP_001983908.1	enoyl-CoA hydratase/isomerase family protein	7394.673035	-1.521984602	0.142310667	-0.61913	1.05E-26	8.05E-26	25.08959045
ABUW_RS0445	ABUW_0590	NZ_CP008706.1	62519	630874	-	WP_000105853.1	ghnU	1618.48632	-1.522039980	0.178752903	-6.520095656	1.59E-17	6.64E-17	16.17763192
ABUW_RS0145	ABUW_0617	NZ_CP008706.1	642400	643410	-	WP_000085721.1	AraC family transcriptional regulator	5251.094685	-1.52235578	0.17322081	-0.768866047	3.33E-22	1.86E-21	20.73048706
ABUW_RS0605	ABUW_854	NZ_CP008706.1	847323	847429	-	WP_001019962.1	N-acetyltransferase	209.810568	-1.526435383	0.341602389	-4.468220962	7.89E-06	1.43E-05	4.844663963
ABUW_RS0485	ABUW_1742	NZ_CP008706.1	974189	974892	+	WP_001037943.1	OmpH family outer membrane protein	5896.748467	-1.526875384	0.198263794	-0.704295456	1.14E-19	5.44E-19	18.26670736
ABUW_RS0470	ABUW_0960	NZ_CP008706.1	968423	971937	+	WP_000184451.1	gprA	18935.58875	-1.527736379	0.147402898	-0.36433779	3.60E-25	2.40E-24	23.61978876
ABUW_RS0335	ABUW_2255	NZ_CP008706.1	224176	224147	-	WP_001183027.1	PZ domain-containing protein	353.9904428	-1.529216258	0.174703192	-0.753791964	2.06E-18	9.00E-18	17.04574549
ABUW_RS0740	ABUW_0330	NZ_CP008706.1	151052	151438	-	WP_000733779.1	hypothetical protein	4499.244611	-1.530039431	0.15428412	-0.917023945	3.91E-23	2.07E-22	21.08429605
ABUW_RS1925	ABUW_3115	NZ_CP008706.1	3195808	3196404	+	WP_000093856.1	scpB	180.246169	-1.531888749	0.139622043	-0.917025025	5.31E-28	4.7E-27	26.13796395
ABUW_RS0295	ABUW_0680	NZ_CP008706.1	64378	64680	-	WP_001177091.1	hypothetical protein	3489.14857	-1.533216745	0.163630877	-0.231283771	2.67E-20	1.54E-19	18.8729952
ABUW_RS1925	ABUW_0432	NZ_CP008706.1	445342	445347	+	WP_001216380.1	gplQ	87978.97395	-1.53341848	0.225071973	-0.109523152	1.75E-09	4.25E-09	8.3718107
ABUW_RS1955	ABUW_2917	NZ_CP008706.1	2927564	2928202	-	WP_000102721.1	nfsA	434.630476	-1.535614611	0.160270999	-0.823956644	5.05E-15	1.85E-14	13.7423243
ABUW_RS1919	ABUW_3278	NZ_CP008706.1	3309597	3309923	+	WP_001077675.1	tnxA	1184.46586	-1.535745894	0.19334961	-0.317607201	5.47E-17	2.21E-16	6.6550773
ABUW_RS1775	ABUW_3045	NZ_CP008706.1	3071469	3072122	-	WP_001002415.1	OmpA family protein	37602.89175	-1.5359563823	0.239324923	-6.432943988	1.25E-10	3.30E-10	9.48186606
ABUW_RS1780	ABUW_3451	NZ_CP008706.1	3497362	3498480	+	WP_000682762.1	asd	5789.966197	-1.540482677	0.249978009	-6.92472774	7.16E-10	1.80E-09	8.744727495
ABUW_RS0335	ABUW_0617	NZ_CP008706.1	618482	619111	+	WP_000327732.1	tpdR	4653.874164	-1.541267431	0.207276317	-0.433810595	1.04E-13	3.39E-13	12.4681803
ABUW_RS0300	ABUW_0610	NZ_CP008706.1	610651	612093	-	WP_001160220.1	YnfU family protein	1001.585155	-1.54219361	0.1911108	-0.80689156	7.21E-16	2.70E-16	14.56883624
ABUW_RS0725	ABUW_3682	NZ_CP008706.1	369758	371797	+	WP_012305657.1	kdpB	246.724029	-1.542706614	0.194060434	-0.1494619533	1.87E-15	6.83E-15	14.505793
ABUW_RS0303	ABUW_0603	NZ_CP008706.1	60918	617856	+	WP_001275073.1	bile acid sodium symporter family protein	568.9668358	-1.542878914	0.196389193	-0.280854266	1.22E-16	4.83E-16	15.9105287
ABUW_RS1750	ABUW_3565	NZ_CP008706.1	3664354	3664172	-	WP_000129667.1	FHA domain-containing protein	2193.186051	-1.546185213	0.160443246	-0.127755163	8.89E-25	5.76E-24	23.23957752
ABUW_RS0145	ABUW_0234	NZ_CP008706.1	252970	254049	+	WP_000167028.1	DNA/RNA non-specific endonuclease	898.1026902	-1.547350321	0.165210277	-0.365714632	7.55E-21	3.88E-20	19.416827
ABUW_RS1745	ABUW_3590	NZ_CP008706.1	3655583	3655763	+	WP_000318991.1	poB	15085.9078	-1.553550251	0.162581061	-0.050264773	8.26E-16	3.08E-16	14.5194289
ABUW_RS1925	ABUW_0430	NZ_CP008706.1	344463	3446276	-	WP_001082550.1	cipX	35381.46014	-1.554005994	0.191674835	-0.2366607	8.09E-25	5.27E-24	23.27819398
ABUW_RS0445	ABUW_0518	NZ_CP008706.1	522933	522933	+	WP_001087659.1	acyl-CoA thioesterase	1316.793734	-1.554117694	0.172655894	-0.901238541	2.23E-19	1.04E-18	17.59826666
ABUW_RS0880	ABUW_0254	NZ_CP008706.1	1242291	1242875	-	WP_000256669.1	ammonioacylcholine/serine/threonine synthase component	3340.84241	-1.555328005	0.182293173	-0.137069105	7.90E-47	1.85E-45	44.7302327
ABUW_RS0835	ABUW_0705	NZ_CP008706.1	688336	689202	+	WP_000188359.1	rpsH	4537.974002	-1.558856591	0.185794644	-0.205899719	1.44E-23	8.69E-23	22.06018022
ABUW_RS0305	ABUW_0502	NZ_CP008706.1	66219	66863	+	WP_001985076.1	pncA	465.7607637	-1.558991662	0.144918886	-0.75761933	5.48E-27	4.05E-26	25.39254498
ABUW_RS0430	ABUW_0333	NZ_CP008706.1	944107	945109	+	WP_001985518.1	era	734.134413	-1.559227003	0.164219332	-0.494980084	2.20E-21	1.9E-20	19.9281979
ABUW_RS0480	ABUW_0579	NZ_CP008706.1	991181	992000	+	WP_000140071.1	alpha beta hydrolase	2624.615581	-1.562269604	0.193549333	-0.17438221	2.58E-24	1.63E-23	22.7878194
ABUW_RS0410	ABUW_0854	NZ_CP008706.1	833009	834582	+	WP_000082210.1	RNA (cytidine(34)-2'-O)-methyltransferase	988.8238745	-1.563994049	0.149654427	-0.44867484	1.49E-25	1.01E-24	23.95957863
ABUW_RS1235	ABUW_2127	NZ_CP008706.1	214369	2175085	+	WP_000020860.1	trmB	806.9630589	-1.564318908	0.251772826	-0.60663752	1.28E-09	3.95E-09	15.8099446
ABUW_RS0400	ABUW_1614	NZ_CP008706.1	121708	1202778	+	WP_001417890.1	formate dehydrogenase	1867.40143	-1.565692599	0.252254548	-0.207854291	5.37E-10	1.36E-09	8.86641092
ABUW_RS0370	ABUW_3555	NZ_CP008706.1	3610291	3610247	-	WP_000099685.1	pyrimidine purine nucleoside phosphorylase	2184.914021	-1.566388721	0.181387092	-0.705738167	2.85E-22	1.59E-21	20.79802088
ABUW_RS1785	ABUW_3762	NZ_CP008706.1	3816742	3817134	-	WP_000387256.1	SidB family protein	919.231876	-1.567964478	0.214265897	-0.346622003	2.03E-13	6.15E-13	12.8641901
ABUW_RS1970	ABUW_3691	NZ_CP008706.1	3750199	3751518	-	WP_000366687.1	MF3 transporter	942.4093812	-1.568928077	0.17855318	-0.774166676	1.72E-18	7.53E-18	17.0230502
ABUW_RS1795	ABUW_3654	NZ_CP008706.1	3742603	375660	+	WP_000738515.1	ammonium transporter	3737.422396	-1.570459027	0.172693078	-0.093952618	9.55E-20	4.60E-19	18.33724217
ABUW_RS1975	ABUW_3859	NZ_CP008706.1	3927022	3927949	-	WP_000480809.1	muonL D-transpeptidase	6136.047388	-1.570877385	0.17284669	-0.219033408	2.34E-38	3.31E-37	36.48017201
ABUW_RS1400	ABUW_3375	NZ_CP008706.1	341631	3416229	-	WP_000587188.1	tetranucleotide repeat protein	3481.842702	-1.570896057	0.186322241	-1.152192343	1.02E-30	9.38E-30	29.02779716
ABUW_RS0430	ABUW_0209	NZ_CP008706.1	233219	236044	+	WP_000645059.1	class I SAM-dependent methyltransferase	1820.26502	-1.57185707	0.185677455	-0.483227926	2.47E-21	1.31E-20	19.8827287
ABUW_RS1430	ABUW_0291	NZ_CP008706.1	319881	319822	+	WP_000201229.1	PN domain-containing protein	1612.43845	-1.572805392	0.258677532	-0.680220125	1.20E-09	2.96E-09	8.528708289
ABUW_RS0990	ABUW_2260	NZ_CP008706.1	2245929	2246357	-	WP_000666684.1	leoplymer transporter EabD	188.363632	-1.577061267	0.143208761	-1.101232384</			

ABUW_RS03350	ABUW_0681	NZ_CP008706.1	6648.0	666888	+	WP_000505931.1		methyl-accepting chemotaxis protein	870.1720525	-1.63781593	0.2308342	-7.09586035	1.296-12	3.93E-12	1140660745
ABUW_RS4855	ABUW_3061	NZ_CP008706.1	3087565	3089703	-	WP_00011824.1	fusA	elongation factor G	489559.0235	-1.642809477	0.24895213	-6.998896962	4.4E-11	1.0E-10	9.94602557
ABUW_RS1430	ABUW_2330	NZ_CP008706.1	231025	232322	+	WP_002000338.1	purT	4'-de-phosphorylphosphoribosylglycinamide formyltransferase	2940.672837	-1.644313059	0.18995854	-11.83326991	2.63E-32	2.67E-31	30.57348874
ABUW_RS0210	ABUW_0431	NZ_CP008706.1	4443.6	445323	+	WP_000198631.1	gsoA	DNA-directed RNA polymerase subunit alpha	37291.8397	-1.645591261	0.284724523	-5.779590898	7.49E-09	1.74E-08	7.79460752
ABUW_RS8960	ABUW_3491	NZ_CP008706.1	354064	354076	+	WP_000046492.1		Hsp90 type B effector protein	487.7155219	-1.64723255	0.201341557	-8.18132766	2.8E-16	1.08E-15	14.9603764
ABUW_RS0270	ABUW_0377	NZ_CP008706.1	590956	591968	+	WP_000226912.1		cold-shock protein	3557.87634	-1.648663577	0.258265529	-6.38371972	1.73E-10	4.50E-10	9.34678406
ABUW_RS1474	ABUW_3032	NZ_CP008706.1	3059917	3061635	+	WP_000347036.1		PYTPW family type-4a plus ATPase	995.735821	-1.651659916	0.174434078	-9.465237544	2.93E-21	1.55E-20	19.8056663
ABUW_RS17745	ABUW_3644	NZ_CP008706.1	3705307	3705377	+	WP_000881094.1	lptG	LPS export ABC transporter permease LptG	1712.31878	-1.651819548	0.21084879	-7.825388189	5.06E-16	1.79E-14	13.7474697
ABUW_RS0355	ABUW_0722	NZ_CP008706.1	727256	728460	-	WP_000216076.1		phosphoadenylyl-sulfate reductase	2819.305928	-1.652259886	0.104034839	-12.32709271	6.47E-35	7.81E-34	33.87348937
ABUW_RS0105	ABUW_0350	NZ_CP008706.1	37618	372759	+	WP_001281782.1		GlulEu:PhoVal dehydrogenase	50154.86083	-1.652264943	0.203491465	-8.123018539	4.55E-16	1.72E-15	14.76447155
ABUW_RS4335	ABUW_0292	NZ_CP008706.1	31819	312529	+	WP_000076101.1		type 4a plus biogenesis protein P4O	1434.943211	-1.653494775	0.267696958	-6.176740985	6.54E-10	1.65E-09	6.78258056
ABUW_RS4035	ABUW_2889	NZ_CP008706.1	289628	289817	+	WP_001047610.1		LyxR family transcriptional regulator	2418.581854	-1.65375918	0.108974739	-15.17597745	5.10E-52	1.08E-50	49.80184291
ABUW_RS03260	ABUW_0662	NZ_CP008706.1	668269	669405	+	WP_001006153.1		NADH:flavin oxidoreductase/NADH oxidase	3052.869033	-1.655020463	0.248447749	-6.662184058	2.70E-11	7.49E-11	10.12551918
ABUW_RS03125	ABUW_0635	NZ_CP008706.1	637674	638434	-	WP_000192258.1		patatin family protein	960.087583	-1.656018564	0.146633385	-11.49020263	2.35E-30	2.12E-29	28.67366414
ABUW_RS1010	ABUW_0204	NZ_CP008706.1	229153	230601	+	WP_000016588.1		NAD-dependent succinate: semialdehyde dehydrogenase	4770.024141	-1.656232216	0.3105598	-5.324547088	1.0E-07	2.5E-07	6.66756164
ABUW_RS14345	ABUW_2973	NZ_CP008706.1	2988800	2990530	+	WP_000714073.1	mcp	malate dehydrogenase (sucinate)	19328.92757	-1.656850263	0.27845227	-5.934833285	2.94E-09	7.03E-09	8.19304675
ABUW_RS02560	ABUW_0521	NZ_CP008706.1	530383	530587	+	WP_000019820.1		sulfurtransferase	2343.500924	-1.661144564	0.223291856	-7.439349026	1.0E-13	3.30E-13	12.4818606
ABUW_RS02085	ABUW_0424	NZ_CP008706.1	440667	440463	+	WP_000049088.1	rmsD	50S ribosomal protein L30	58027.65802	-1.666523347	0.265185033	-6.260185831	3.36E-10	8.61E-10	4.904566949
ABUW_RS03335	ABUW_3401	NZ_CP008706.1	3446783	3446993	-	WP_000289452.1	cnpP	Pi-dependent Ctp endonuclease proteolytic subunit Ctp	5074.444145	-1.666274462	0.194049692	-11.9258989	6.95E-29	5.71E-28	27.24326389
ABUW_RS01670	ABUW_0339	NZ_CP008706.1	361932	362507	+	WP_001743885.1		supernatant dehydratase family protein	8222.173678	-1.666499212	0.247505995	-6.73318048	1.65E-11	4.69E-11	10.32079154
ABUW_RS02165	ABUW_0441	NZ_CP008706.1	454483	454519	+	WP_001130889.1		hypothetical protein	651193046	-1.666802632	0.21768166	-7.657068033	1.90E-14	6.47E-14	13.89005572
ABUW_RS0108	ABUW_0858	NZ_CP008706.1	83828	839464	-	WP_000118404.1		iron-containing alcohol dehydrogenase	2203.148335	-1.667120915	0.156848066	-10.50829652	7.9E-26	5.56E-25	24.2533568
ABUW_RS17080	ABUW_3511	NZ_CP008706.1	3597820	3595958	+	WP_000156649.1		pinosilanol protein	525.5293356	-1.668870209	0.160017256	-11.0251819	9.46E-29	7.68E-28	27.11638378
ABUW_RS03260	ABUW_0678	NZ_CP008706.1	668269	669405	+	WP_000108706.1	pilG	twirling motility response regulator P4G	569.1783327	-1.670785879	0.255186421	-6.548114637	5.83E-11	1.08E-10	9.10184210
ABUW_RS14765	ABUW_3042	NZ_CP008706.1	3068759	3069211	+	WP_000668152.1	dut	dUTP diphosphatase	803.3596108	-1.671173126	0.17363308	-9.624864643	6.28E-22	3.45E-21	20.4621890
ABUW_RS1465	ABUW_2357	NZ_CP008706.1	2338870	2340300	+	WP_000018700.1		pyridoxal phosphate-dependent aminotransferase	486.88727	-1.673756957	0.244285798	-6.851634327	7.30E-12	2.12E-11	10.67366414
ABUW_RS1405	ABUW_2761	NZ_CP008706.1	271807	272430	+	WP_000107496.1		TerRACr family transcriptional regulator	57.7599935	-1.678975606	0.306488214	-5.48104714	4.23E-08	9.13E-08	7.31050319
ABUW_RS14740	ABUW_3581	NZ_CP008706.1	3641293	3641293	+	WP_001094933.1	hspG	molecular chaperone HspG	5586.864606	-1.682546655	0.333163301	-5.050367656	4.4E-07	8.88E-07	6.05198704
ABUW_RS0590	ABUW_1842	NZ_CP008706.1	186689	186895	+	WP_000380475.1		carbon starvation protein A	4234.63348	-1.683017822	0.235510457	-5.202455338	1.97E-07	4.08E-07	6.389339837
ABUW_RS02090	ABUW_0425	NZ_CP008706.1	440847	441127	+	WP_000172340.1	gpiO	50S ribosomal protein L15	81988.17951	-1.683824676	0.264762091	-6.359764984	2.02E-10	5.25E-10	9.279840697
ABUW_RS01960	ABUW_0633	NZ_CP008706.1	39647	40270	+	WP_001196530.1		TerRACr family transcriptional regulator	966.5338779	-1.6866869752	0.17666973	-9.547072991	1.33E-21	7.23E-21	20.106817
ABUW_RS04445	ABUW_0826	NZ_CP008706.1	802004	802008	+	WP_000362009.1		putin	2522.8938	-1.687249327	0.210211094	-8.026462355	1.00E-16	3.73E-15	14.42291917
ABUW_RS02040	ABUW_0549	NZ_CP008706.1	55049	55945	+	WP_001024461.1		M23 family metalloproteinase	381299.0773	-1.689394049	0.185494763	-9.102893667	8.02E-20	3.88E-19	9.41188227
ABUW_RS03170	ABUW_0644	NZ_CP008706.1	650519	650995	+	WP_000193247.1		DUF354 domain-containing protein	16213509.18	-1.691285912	0.219535702	-7.703921951	1.32E-14	4.50E-14	34.1319886
ABUW_RS0400	ABUW_0887	NZ_CP008706.1	893880	893705	+	WP_000729551.1	yhbY	ribosome assembly RNA-binding protein YhbY	3358.052065	-1.694049698	0.193768016	-12.66402959	9.36E-37	1.23E-35	34.91094849
ABUW_RS17780	ABUW_3651	NZ_CP008706.1	371256	3712548	+	WP_001083669.1		DNA-adenine methylase	2614.953082	-1.696360706	0.162033937	-10.46881906	1.20E-25	8.37E-25	24.0772454
ABUW_RS17265	ABUW_3548	NZ_CP008706.1	3604782	3605576	-	WP_000101931.1		triose-phosphate isomerase	3180.553632	-1.696410752	0.210404165	-7.892484462	2.96E-15	1.06E-14	13.97469410
rRNA															
ABUW_RS8660	ABUW_3833	NZ_CP008706.1	389944	390210	+	WP_001075962.1		polysaccharide biosynthesis tyrosine autokinase	5688.1294	-1.69773389	0.18180528	-12.9410159	2.64E-38	3.70E-37	36.4319828
ABUW_RS8635	ABUW_3828	NZ_CP008706.1	389434	3895583	+	WP_001065041.1	wecC	UDP-N-acetyl-D-mannosamine dehydrogenase	28873.63592	-1.699903258	0.159958987	-10.89682573	1.19E-27	9.25E-27	26.03385827
ABUW_RS0445	ABUW_2809	NZ_CP008706.1	280886	290255	+	WP_000146092.1		hypothetical protein	604.2149602	-1.703259932	0.18065674	-9.427679342	4.4E-21	2.16E-20	6.65955459
ABUW_RS07595	ABUW_0556	NZ_CP008706.1	542619	543452	+	WP_000004354.1		kinase/phosphorylase	564.3408648	-1.70459225	0.12884442	-13.23266399	5.68E-40	8.88E-39	38.05165703
ABUW_RS0450	ABUW_0701	NZ_CP008706.1	705897	707111	+	WP_000003701.1		multidrug efflux MFS transporter	638.163166	-1.706150167	0.159539486	-10.69421872	1.08E-26	7.89E-26	25.92923
ABUW_RS04705	ABUW_0959	NZ_CP008706.1	967125	968057	+	WP_000295888.1		FAD-binding protein	29476.92568	-1.706708997	0.206695932	-8.257197103	1.49E-16	5.84E-16	52.3528715
ABUW_RS01116	ABUW_0632	NZ_CP008706.1	635183	635774	+	WP_001885920.1		hemerythrin family protein	966.912932	-1.707052368	0.18104593	-8.428905661	4.4E-21	2.19E-20	16.63546207
ABUW_RS0875	ABUW_1798	NZ_CP008706.1	1791542	1791650	+	WP_001034203.1		ResAe (2Fe-2S) protein	2155.927229	-1.707567733	0.180052946	-6.6687679	1.43E-26	1.03E-25	24.9878278
ABUW_RS01825	ABUW_0372	NZ_CP008706.1	395481	395735	+	WP_000101717.1		PuqC domain-containing protein	1948.91657	-1.708617318	0.195145197	-12.88947824	0.003805332	0.005449063	2.263618791
ABUW_RS1610	ABUW_3741	NZ_CP008706.1	3707126	3707173	+	WP_000093181.1		transcriptional repressor	660.4071478	-1.714474356	0.159679103	-10.7370619	9.82E-27	5.04E-26	25.29765946
ABUW_RS0445	ABUW_0992	NZ_CP008706.1	104384	105301	+	WP_000087403.1	thiL	thiamine-phosphate kinase	5439.519303	-1.714974827	0.14857817	-11.542571604	8.05E-31	7.42E-30	29.02959609
ABUW_RS4945	ABUW_3484	NZ_CP008706.1	3532620	3533374	+	WP_000279705.1	hemW	radical SAM family heme chaperone HemW	2448.018589	-1.717785596	0.318177088	-5.398834996	6.71E-08	1.45E-07	6.83803198
ABUW_RS0190	ABUW_0283	NZ_CP008706.1	281663	282166	+	WP_000721434.1		hypothetical protein	4441725076	-1.719797755	0.255299662	-6.729260074	1.7E-11	4.80E-11	18.3915876
ABUW_RS4960	ABUW_0111	NZ_CP008706.1	1023569	1023985	+	WP_000711345.1		hypothetical protein	3004.248416	-1.721438329	0.202462568	-8.502019785	1.86E-17	7.71E-17	16.1204562
ABUW_RS02335	ABUW_0548	NZ_CP008706.1	51564	51589	+	WP_001287365.1		hypothetical protein	398.987744	-1.726278693	0.15041627	-11.47668624	1.73E-30	1.57E-29	28.80410035
ABUW_RS03320	ABUW_0675	NZ_CP008706.1	671814	681182	+	WP_001885939.1		efflux RND transporter permease subunit	2165.323271	-1.732057731	0.143356391	-10.08218012	1.31E-33	1.45E-32	33.838632
ABUW_RS01790	ABUW_0189	NZ_CP008706.1	176219	176375	+	WP_001840851.1		TonB-dependent siderophore receptor	5668.21991	-1.733966493	0.37654314	-6.410268276	4.02E-06	7.52E-06	51.9237892
ABUW_RS02025	ABUW_0615	NZ_CP008706.1	616607	617469	+	WP_000463364.1		TonB-dependent receptor	5184.836293	-1.7371805701	0.193447434	-12.48004639	9.58E-36	1.20E-34	33.92081875
ABUW_RS0795	ABUW_0307	NZ_CP008706.1	800210	800384	+	WP_000061059.1	rpiA	ribose-5-phosphate isomerase RpiA	2847.905191	-1.738980814	0.19061487	-9.121709463	7.39E-20	3.58E-19	18.44418507
ABUW_RS0970	ABUW_2876	NZ_CP008706.1	288001	288719	+	WP_000809154.1	rmdA	penicillin-binding protein 2	977.553938	-1.742098968	0.174191825	-10.00535434	1.44E-23	8.72E-23	22.05483352

ABLUW_RS3375	ABLUW_3370	NZ_CP008706.1	341024	341041	+	WP_000729828.1	gncC	glutaredoxin 3	4240.510412	-1.81937839	0.21896823	-8.542287628	1326.17	5.555E-17	16.25570702
ABLUW_RS3455	ABLUW_3020	NZ_CP008706.1	304584	304692	-	WP_000028703.1	EnvA/EnvK family multiting effector transporter/periplasmic adaptor		6410.020321	-1.81182266	0.28308617	-6.397992887	1576.10	4.1E-10	9.38656878
ABLUW_RS3595	ABLUW_3634	NZ_CP008706.1	3672235	367352	+	WP_031844408.1	hemC	hydromethylglutathione synthase	9233.302183	-1.82151018	0.18587924	-9.080327288	1866.23	1.02E-22	21.9507878
ABLUW_RS3615	ABLUW_3058	NZ_CP008706.1	307540	3080572	-	WP_000027837.1		DNA topoisomerase Flak	9183.75782	-1.81932434	0.19589586	-9.28395338	1516.38	2.8E-37	36.6654331
ABLUW_RS3700	ABLUW_0341	NZ_CP008706.1	85034	85585	-	WP_000023651.1	xih	exodeoxyribonuclease II	934.719568	-1.819289512	0.175423979	-9.36485839	3586.25	2.39E-24	23.8216021
ABLUW_RS3703	ABLUW_0442	NZ_CP008706.1	454626	455195	-	WP_000745523.1		YheY family putative metal-binding protein	1766.887067	-1.819466817	0.207535778	-8.767894327	1916.98	8.86E-16	17.07778372
ABLUW_RS3940	ABLUW_016	NZ_CP008706.1	93135	933761	-	WP_000208082.1		isopenicillin diaminase	14965.48078	-1.818956664	0.253751878	-7.178016	7.410E-13	2.29E-12	11.64018452
ABLUW_RS3335	ABLUW_0852	NZ_CP008706.1	687035	691655	+	WP_000588892.1		Hpt domain-containing protein	6681.92919	-1.820399949	0.202916022	-6.87166255	2946.19	136E-19	17.8664819
ABLUW_RS1810	ABLUW_3729	NZ_CP008706.1	378761	378816	+	WP_000184680.1		glutathione peroxidase	3340.40201	-1.820587097	0.224705647	-8.92097662	5.40E-16	2.04E-16	6.69036883
ABLUW_RS3895	ABLUW_3273	NZ_CP008706.1	3305617	3307020	-	WP_010300732.1	MS	RNA lysidine[34] synthetase TIS	6971043029	-1.821631481	0.165419745	-9.52618609	5.37E-36	6.80E-35	34.16749109
ABLUW_RS3075	ABLUW_2075	NZ_CP008706.1	2056937	2057578	-	WP_000026856.1		isochromatase family protein	469.7438181	-1.823876175	0.565706585	-3.224067428	0.001263836	0.001854332	2.731812507
ABLUW_RS0418	ABLUW_0852	NZ_CP008706.1	832220	833491	+	WP_000566842.1	serS	serine--tRNA ligase	4697.708007	-1.826599124	0.201179597	-9.094655468	9.49E-20	4.57E-19	18.3400388
ABLUW_RS0960	ABLUW_0184	NZ_CP008706.1	218563	219237	-	WP_000899418.1	lenA	thiaminase II	726.0604883	-1.83216808	0.166917723	-11.67560163	1.70E-31	1.65E-30	29.78251066
ABLUW_RS03475	ABLUW_0706	NZ_CP008706.1	711793	710228	+	WP_000615951.1		threonine ammonia-lyase	1004.432457	-1.83524309	0.16620302	-11.44330049	3.38E-41	5.78E-40	39.23807216
ABLUW_RS0165	ABLUW_0278	NZ_CP008706.1	295193	296701	-	WP_000865422.1		glutamate--tRNA ligase	3986.287169	-1.836375585	0.132185827	-11.89448116	6.84E-44	1.37E-42	41.86327943
ABLUW_RS0490	ABLUW_0489	NZ_CP008706.1	509390	510064	-	WP_000480818.1		LigII family protein	2318015899	-1.841830581	0.209593391	-8.787636716	1.53E-18	6.17E-18	17.97327448
ABLUW_RS1750	ABLUW_3505	NZ_CP008706.1	3551831	3552670	+	WP_011548081.1		CBS domain-containing protein	4603.487446	-1.842365689	0.162338516	-9.00462493	1.79E-72	1.50E-70	69.82390874
ABLUW_RS1950	ABLUW_0786	NZ_CP008706.1	766298	766823	+	WP_00043392.1		hyphenal protein	384.781428	-1.84533548	0.246267851	-7.145225162	8.98E-13	2.76E-12	11.55090902
ABLUW_RS1025	ABLUW_2267	NZ_CP008706.1	2251289	2253727	+	WP_000682628.1		LPS-associated protein LipD	3685.775373	-1.847532242	0.200616007	-9.209296257	3.28E-20	1.62E-19	18.79044649
ABLUW_RS1490	ABLUW_3390	NZ_CP008706.1	3434980	3435600	-	WP_000024253.1	eda	γ -2-oxoglutarate decarboxylase, 2-dehydro-3-deoxy-phospho	3031.339621	-1.847816921	0.239537627	-7.714067311	1.02E-14	4.21E-14	10.3707179
ABLUW_RS0280	ABLUW_0423	NZ_CP008706.1	440163	440660	+	WP_001141025.1	rpsE	50S ribosomal protein S5	92110.7173	-1.84955144	0.278851879	-6.632737955	3.30E-11	9.06E-11	10.0428781
ABLUW_RS0170	ABLUW_1797	NZ_CP008706.1	1791708	1791916	+	WP_000175306.1		DUF1449 family protein	397.914551	-1.852391925	0.1620001	-9.1276824	3.84E-34	4.38E-33	32.58552589
ABLUW_RS08160	ABLUW_1799	NZ_CP008706.1	1791867	1792671	-	WP_000246611.1		adenosine kinase	2785.749359	-1.854189487	0.132943217	-9.195291935	3.02E-44	6.27E-43	42.20273246
ABLUW_RS1815	ABLUW_2387	NZ_CP008706.1	237040	238058	-	WP_000471020.1		hypothetical protein	610.4540051	-1.85533665	0.149118642	-6.34429764	1.07E-07	2.27E-07	6.043974143
ABLUW_RS18125	ABLUW_3724	NZ_CP008706.1	3782664	378323	+	WP_000633612.1		thymidylate/uracil-AMP synthase	424.335862	-1.856009862	0.13227468	-11.02826761	1.05E-44	2.11E-43	42.6560773
ABLUW_RS0808	ABLUW_3310	NZ_CP008706.1	3344561	3344952	+	WP_010417580.1	rnfS	ribosome silencing factor	10029.26628	-1.857512819	0.241430757	-6.793770425	1.43E-14	4.91E-14	13.30891851
ABLUW_RS01840	ABLUW_0395	NZ_CP008706.1	419703	422276	+	WP_000045400.1	plsB	glycerol-3-phosphate 1-O-acyltransferase PlsB	6411.142166	-1.859509511	0.16611804	-11.9279162	4.42E-29	3.68E-28	27.3416218
ABLUW_RS0900	ABLUW_0182	NZ_CP008706.1	200589	204066	-	WP_000188740.1		hybrid sensor/histidine kinase/response regulator	9255.530751	-1.860716908	0.114745103	-11.9271871	2.30E-39	3.47E-38	37.45967073
ABLUW_RS01700	ABLUW_3841	NZ_CP008706.1	391011	391827	-	WP_010217232.1	rph	ribonuclease PH	4069.856881	-1.860860906	0.146233903	-9.25047189	1.93E-33	2.09E-32	31.67963071
ABLUW_RS12225	ABLUW_2725	NZ_CP008706.1	2710666	2711677	-	WP_000781042.1		glutathione S-transferase N-terminal domain-containing protein	215184348	-1.864183674	0.218283791	-8.54021209	1.34E-17	5.63E-17	16.2449181
ABLUW_RS1325	ABLUW_2745	NZ_CP008706.1	2733192	2734511	-	WP_000517792.1		adenosylsuccinate synthase	30542.30006	-1.865376957	0.16353265	-11.403735758	3.84E-30	3.43E-29	28.64470508
ABLUW_RS11960	ABLUW_2916	NZ_CP008706.1	292510	2927394	-	WP_000041166.1		TorB-dependent adenosine receptor	8611762005	-1.870531024	0.549690467	-3.403507244	0.000616266	0.001011638	2.9848901
ABLUW_RS0395	ABLUW_3374	NZ_CP008706.1	3413386	3414531	+	WP_010172116.1	bamB	outer membrane protein assembly factor BamB	7757.92466	-1.872233437	0.168329735	-11.83121692	2.89E-32	2.73E-31	30.56383735
ABLUW_RS03020	ABLUW_0614	NZ_CP008706.1	61993	61511	+	WP_000509973.1		cofactor:acetic acid-N ⁶ -dimethyladenosyltransferase	311305136	-1.87591058	0.19958496	-9.89430401	4.38E-23	2.57E-22	21.59006668
ABLUW_RS01990	ABLUW_2057	NZ_CP008706.1	2030482	2035051	-	WP_000042181.1	S	hydroxymethylglutathione dehydrogenase/class II alcohol dehydrogenase	1718.705206	-1.878186209	0.222182952	-8.454092798	2.81E-17	1.96E-16	15.93540201
ABLUW_RS18280	ABLUW_3755	NZ_CP008706.1	3811807	381875	-	WP_000210750.1	guaA	glutamine-hydrolyzing GMP synthase	9208.384194	-1.878270732	0.227881958	-8.236818447	1.74E-16	6.78E-16	16.16817031
ABLUW_RS02605	ABLUW_0420	NZ_CP008706.1	438583	439248	+	WP_000062618.1	rpsH	50S ribosomal protein S8	1452.66771	-1.879695927	0.253596059	-7.41027683	1.24E-13	4.02E-13	9.39577395
ABLUW_RS0865	ABLUW_3267	NZ_CP008706.1	3260687	3273205	+	WP_000462729.1		hypothetical protein	603.7451977	-1.881165101	0.239951034	-7.248864282	4.20E-13	1.32E-12	11.87942607
ABLUW_RS18975	no	NZ_CP008706.1	332374	3321878	+	WP_010297364.1	infC	translation initiation factor F-3	19105.63424	-1.883846382	0.188718466	-9.862502294	1.82E-23	1.09E-22	1.96267535
ABLUW_RS0695	ABLUW_0172	NZ_CP008706.1	187849	188634	+	WP_00154366.1		thiazole synthase	2794.139684	-1.884887102	0.14706675	-9.81722466	11.1E-37	1.79E-36	35.74714697
ABLUW_RS01250	ABLUW_0457	NZ_CP008706.1	437657	437874	+	WP_010062685.1	rpsK	50S ribosomal protein L24	44858.95409	-1.885291642	0.229661798	-8.208944883	2.23E-16	8.65E-16	16.06298389
ABLUW_RS10390	ABLUW_2342	NZ_CP008706.1	2325711	2326802	+	WP_000056572.1	ychF	redox-regulated ATPase YchF	3.981.90602	-1.887309231	0.28775327	-7.061292384	1.65E-12	4.98E-12	11.93271066
ABLUW_RS01975	ABLUW_0187	NZ_CP008706.1	222145	222225	+	WP_010216080.1	sab	single-strand DNA-binding protein	5401256462	-1.888084984	0.158720376	-9.61072558	3.46E-42	6.22E-41	40.20620692
ABLUW_RS01740	ABLUW_0149	NZ_CP008706.1	84196	84950	+	WP_000057904.1		cell division protein PsaQ/CwhB	2277.998777	-1.89051927	0.16383564	-9.28909089	1.04E-34	9.26E-33	32.9109489
ABLUW_RS02990	ABLUW_0628	NZ_CP008706.1	629273	629914	-	WP_000175332.1		permease	919.481628	-1.891925734	0.376533887	-8.030288651	4.77E-07	1.38E-07	6.18634401
ABLUW_RS0815	ABLUW_1874	NZ_CP008706.1	1861636	1867604	+	WP_000047940.1		acetyl-CoA C acetyltransferase	3287.91078	-1.892571636	0.161584797	-9.25071653	7.30E-36	9.16E-35	34.03686449
ABLUW_RS14475	ABLUW_0581	NZ_CP008706.1	2997394	2997993	-	WP_002003811.1		biliverdin-producing heme oxygenase	78.74481961	-1.8931901	0.386442371	-6.16834692	2.36E-07	4.85E-07	6.31425661
ABLUW_RS02340	ABLUW_2998	NZ_CP008706.1	595379	597167	-	WP_000086451.1	aspS	aspartate--tRNA ligase	26296.28745	-1.899835101	0.193356962	-9.820532438	8.74E-23	5.02E-22	21.29926628
ABLUW_RS0490	ABLUW_0999	NZ_CP008706.1	101866	101870	+	WP_01154002.1	rvrB	Holliday junction branch migration DNA helicase RvrB	7373.298355	-1.900000886	0.174074271	-9.19183318	9.42E-28	7.34E-27	26.13430394
ABLUW_RS04950	ABLUW_0209	NZ_CP008706.1	1022713	1022774	-	WP_010139329.1		permease	665.622038	-1.903493987	0.172886367	-11.01156109	3.37E-28	2.67E-27	26.57348874
ABLUW_RS02075	ABLUW_0422	NZ_CP008706.1	438610	440160	+	WP_01003194.1	rplR	50S ribosomal protein L18	42395.18474	-1.90651071	0.28233061	-6.752781814	1.45E-11	4.1E-11	10.3850278
ABLUW_RS07190	ABLUW_0555	NZ_CP008706.1	554082	5542469	+	WP_000853480.1	ppsA	phosphoenolpyruvate synthase	51889.22276	-1.908237893	0.14451869	-11.20409074	8.31E-40	1.28E-38	37.89279003
ABLUW_RS1835	ABLUW_0714	NZ_CP008706.1	720871	721185	+	WP_000107699.1	galC	γ -RNA[Asn] Glu-tRNA[Asn] amidotransferase subunit G	1794.461068	-1.90854376	0.166170195	-11.48498982	1.57E-30	1.43E-29	28.84463396
ABLUW_RS07875	ABLUW_2638	NZ_CP008706.1	263467	2635147	+	WP_085920603.1		GlutN1 family N-acetyltransferase	865.569034	-1.90866715	0.203182167	-9.393817107	5.78E-21	3.00E-20	19.52878775
ABLUW_RS01940	ABLUW_1871	NZ_CP008706.1	186330	1864419	+	WP_000141843.1	tal	transaldolase	4363.726706	-1.918717416	0.201104649	-9.507100365	1.96E-21	1.05E-20	19.878197
ABLUW_RS14650	ABLUW_3019	NZ_CP008706.1	304311	3045834	-	WP_000857095.1		DNA2 family effluor motif transducer permease subunit	462.2073541	-1.919737383	0.280781694	-8.828700111	8.57E-12	2.47E-11	10.60730305
ABLUW_RS18880	ABLUW_3723	NZ_CP008706.1	330387	3304198	+	WP_010154663.1	polA	DNA polymerase I	4650.070165	-1.919102931	0.093914054	-10.6219689	1.74E-94	8.78E-92	91.05650548
ABLUW_RS18100	ABLUW_3723	NZ_CP008706.1	3718483	3782610	+	WP_010091425.									

ABUW_RS03345	ABUW_0680	NZ_CP08706.1	684227	684763	+	WP_000729762.1		putme-binding chemotaxis protein CheW	2.86.743622	-2.002990.83	0.26038022	-7.67379408	1.686E-14	5.73E-14	13.24.84538
ABUW_RS3350	ABUW_3385	NZ_CP08706.1	3408.02	3406905	-	WP_002027450.1		enoyl-ACP reductase	24203.58424	-2.0077026334	0.21618922	-9.484324534	2.44E-21	1.30E-20	9.8860565
ABUW_RS3240	ABUW_3747	NZ_CP08706.1	380323	3805023	-	WP_00_000284.1		arginine- tRNA ligase	5864.76431	-2.0090660674	0.19704286	-8.93077265	5.56E-76	6.59E-76	75.811459
ABUW_RS3985	ABUW_2239	NZ_CP08706.1	2244205	2245932	-	WP_00_070729.1	msbA	Ispid A export membrane-ATP-binding protein MsbA	5249.734235	-2.010926543	0.140036066	-14.38148475	6.76E-47	1.59E-45	44.7980208
sRNA3	no	no	no	no	no	no	no	no	16.1261918	-2.017988779	0.23898822	-9.238845601	3.05E-20	1.49E-19	18.8281973
ABUW_RS3730	ABUW_3441	NZ_CP08706.1	3486500	3486949	-	WP_000368721.1		hypothetical protein	5337.968844	-2.0279079373	0.163572748	-13.20468873	8.22E-40	1.27E-38	37.89819628
ABUW_RS32	ABUW_3742	NZ_CP08706.1	3797896	3798474	+	WP_00_110501.1	znuC	zinc ABC transporter ATP-binding protein ZnuC	924.76048	-2.032008989	0.16326873	-13.2578761	4.07E-40	6.47E-39	38.8909572
ABUW_RS3190	ABUW_3737	NZ_CP08706.1	3794371	3794616	+	WP_000424060.1	atpE	RF1-1ATP synthase subunit C	45828.50385	-2.033902.07	0.271336819	-7.495857493	6.59E-14	2.18E-10	12.66.64351
ABUW_RS3240	ABUW_3116	NZ_CP08706.1	316446	317359	+	WP_00_029249.1	ruB	23S-rRNA pseudouridine(205) synthase RuB	3305.748487	-2.03817208	0.12100731	-16.84416543	1.16E-63	7.41E-62	61.9180879
ABUW_RS00805	ABUW_0162	NZ_CP08706.1	179993	181459	+	WP_000956023.1	guaB	MP dehydrogenase	16935.60974	-2.03965651	0.152410564	-13.38270493	7.63E-41	1.28E-39	38.89278003
ABUW_RS1685	ABUW_2279	NZ_CP08706.1	2264179	2264715	+	WP_000240330.1		DUF2058 domain-containing protein	546.2726127	-2.044178632	0.251648236	-8.123169009	4.54E-16	1.72E-15	14.7647155
ABUW_RS1760	ABUW_3453	NZ_CP08706.1	3500553	3503115	+	WP_000987566.1		hypothetical protein	124.585304	-2.051552385	0.21080407	-9.718343005	5.25E-22	1.42E-21	20.8477186
sRNA91	no	no	no	no	no	no	no	no	255.279932	-2.052932.02	0.224275198	-9.153630028	5.9E-20	2.70E-19	18.6863624
ABUW_RS00720	ABUW_0145	NZ_CP08706.1	159390	160334	+	WP_00_0265491.1	gshB	glutathione synthase	1141209668	-2.053803086	0.19334134	-12.57352862	2.95E-36	3.79E-35	34.42.05079
ABUW_RS3660	no	NZ_CP08706.1	3106461	310815	-		mpB	Rhase P RNA component class A	207814.1666	-2.054763706	0.289068444	-7.105225572	1.18E-12	3.59E-12	14.44490555
ABUW_RS1415	ABUW_2910	NZ_CP08706.1	292249	2927263	-	WP_00_1014.892.1		carbonic anhydrase	14023.18559	-2.056260288	0.19702636	-12.07700997	1.40E-33	1.53E-32	31.8180857
ABUW_RS02580	ABUW_0525	NZ_CP08706.1	533465	534079	+	WP_000645707.1		separation protein lpfZ	1089.803164	-2.056288305	0.19460737	-15.23619643	2.03E-52	6.40E-51	50.9382003
ABUW_RS01790	ABUW_806	NZ_CP08706.1	806564	803131	-	WP_00_983729.1	avaA	threonine ammonia-lyase, biosynthetic	2218.808516	-2.0570452	0.116973471	-17.585336	6.75E-66	4.95E-64	63.3053948
ABUW_RS017875	ABUW_810	NZ_CP08706.1	8077393	8077393	-	WP_0002321672.1		UDP-2'-3'-bisphosphogluconate dehydrogenase	774.8059653	-2.058034271	0.176491336	-11.65017669	9.02E-31	1.94E-30	29.72.98817
ABUW_RS1641	ABUW_3377	NZ_CP08706.1	3416547	3417062	-	WP_000572095.1	lpdIG	pendent (E)-4-hydroxy-3-methylbut-2-enyl diphosphat	5804.401255	-2.0599595429	0.169943453	-12.1699385	3.44E-34	3.94E-33	32.40450378
ABUW_RS00905	ABUW_0183	NZ_CP08706.1	204270	204802	+	WP_000372518.1		DUF485 domain-containing protein	608.7444296	-2.06332039	0.376809001	-15.522673105	3.34E-08	7.14E-08	7.100.8192
ABUW_RS00500	ABUW_0408	NZ_CP08706.1	433778	434098	+	WP_00_058538.1	rlpW	50S ribosomal protein L23	57055.10386	-2.064149106	0.295563352	-6.98377144	2.87E-12	8.55E-12	10.68803799
ABUW_RS150	ABUW_3120	NZ_CP08706.1	3109984	3114164	+	WP_000131442.1	bioA	nosylmethionine-8-amino-7-oxanonanoate transaminase	3760.010881	-2.069671853	0.25927699	-12.70300083	5.69E-37	7.62E-36	35.1804053
ABUW_RS1780	ABUW_2421	NZ_CP08706.1	2488441	2493031	-	WP_000476792.1		transporter substrate-binding domain-containing protein	276.3937033	-2.0747434	0.21188385	-9.79281981	1.2E-22	6.89E-22	21.91.78078
ABUW_RS3455	ABUW_3336	NZ_CP08706.1	3425871	3426890	+	WP_000578593.1	napZ	beta-N-acetylhexosaminidase	1649.255862	-2.077189627	0.161970332	-15.25954215	1.42E-52	4.52E-51	50.34486197
ABUW_RS00200	ABUW_0407	NZ_CP08706.1	433179	433781	+	WP_00_910525.15	rlpD	50S ribosomal protein L4	19424.3185	-2.078541279	0.332400524	-16.25199426	4.05E-10	1.03E-09	8.88782775
ABUW_RS0200	ABUW_0428	NZ_CP08706.1	442897	443253	+	WP_000908015.1	rpmM	30S ribosomal protein S13	81939.95891	-2.079783212	0.27179778	-7.433607728	1.06E-10	3.44E-10	42.4634456
ABUW_RS00000	ABUW_0041	NZ_CP08706.1	48599	48789	+	WP_00_0397146.1		MF3 transporter	339.720582	-2.081343666	0.23481922	-8.85125545	7.91E-19	3.56E-18	17.44855
ABUW_RS1850	ABUW_0377	NZ_CP08706.1	402100	403050	-	WP_00_164614.1	hanF	oxygen-dependent coproporphyrinogen oxidase	3819.627263	-2.081736319	0.30058787	-16.925556674	4.34E-12	1.27E-11	10.8961892
ABUW_RS19000	ABUW_0334	NZ_CP08706.1	3396957	3397778	+	WP_000714003.1		acyl-CoA carboxylase carboxyltransferase subunit alpha	3396.1407	-2.090493318	0.184474489	-11.33216401	9.05E-30	2.99E-29	28.09632387
ABUW_RS17940	ABUW_0643	NZ_CP08706.1	3723375	3724271	+	WP_000041615.1		cation transporter	432.566502	-2.092574296	0.320505173	-11.626035147	6.75E-11	1.82E-10	9.73982962
ABUW_RS02185	ABUW_0364	NZ_CP08706.1	648874	650517	+	WP_000281764.1		nitrite/beta reductase	3884.623421	-2.095722282	0.242449997	-18.880226646	9.47E-18	4.02E-17	16.39577335
ABUW_RS04700	ABUW_0938	NZ_CP08706.1	966358	967187	+	WP_000646180.1		electron transfer flavoprotein subunit beta/FixA family protein	24391.33267	-2.096872301	0.180109159	-11.6422314	2.51E-31	2.39E-30	29.62.8021
ABUW_RS04310	ABUW_0881	NZ_CP08706.1	862134	863147	+	WP_000723411.1	tpS1	tryptophan-tRNA ligase	4321733557	-2.097169947	0.199022231	-15.54088882	5.59E-26	3.98E-25	24.4001893
ABUW_RS02225	ABUW_0639	NZ_CP08706.1	6164694	6183722	+	WP_00_090021.1		alpha-beta hydrolase	9031.400649	-2.09879602	0.108635859	-19.31955066	3.68E-83	7.41E-81	10.9101879
ABUW_RS1985	ABUW_3895	NZ_CP08706.1	3963292	3964617	+	WP_000552288.1	guaD	guanine deaminase	1380.433526	-2.098931492	0.194400095	-10.71691799	3.58E-27	2.08E-26	25.57.86521
ABUW_RS16710	ABUW_3237	NZ_CP08706.1	3265230	3265757	+	WP_081920611.1		gamma carboxyl anhydride family protein	1649.345481	-2.10272184	0.21050468	-10.45820532	1.34E-25	2.43E-24	24.03262608
ABUW_RS18940	ABUW_0890	NZ_CP08706.1	3918282	3918878	+	WP_000510318.1		undecaprenyl-diphosphate	367.9492863	-2.102859251	0.208814956	-10.0790148	5.64E-24	3.51E-23	22.45469288
ABUW_RS04385	ABUW_3834	NZ_CP08706.1	819229	823268	+	WP_00064445.1	caaA	ine-hydrolyzing carboxyl-phosphate synthase small subunit	8564.721879	-2.10070043	0.266181688	-7.924012774	2.30E-15	8.33E-15	14.079355
ABUW_RS02975	ABUW_0605	NZ_CP08706.1	603670	604541	+	WP_00_123422.1	secY	acyl-CoA dehydrogenase C-terminal domain-containing protein	4097.43123	-2.104070537	0.14842868	-10.85082223	1.98E-27	1.52E-26	25.8185641
ABUW_RS18380	ABUW_3371	NZ_CP08706.1	3410439	3410947	+	WP_00_028260.1	sefB	protein-export chaperone SecB	6508.510349	-2.11042343	0.20366662	-10.36699023	3.51E-25	2.34E-24	23.6307814
ABUW_RS02030	ABUW_0140	NZ_CP08706.1	436322	436735	+	WP_000941215.1	rlpP	50S ribosomal protein L16	174795.373	-2.117797611	0.31931679	-16.69764847	2.12E-11	5.93E-11	10.22495431
ABUW_RS05515	ABUW_1027	NZ_CP08706.1	1149113	1150251	-	WP_000197255.1	dacC	D-alanyl-D-alanine carboxypeptidase PBP5/6	2881057605	-2.118146884	0.188610344	-11.20927219	3.67E-29	3.07E-28	27.12.98682
ABUW_RS16510	ABUW_3337	NZ_CP08706.1	3414952	3414378	+	WP_000207467.1		lumarate hydratase	8764.720097	-2.11873315	0.188652324	-11.23207851	3.24E-29	2.73E-28	27.5636735
ABUW_RS17720	ABUW_3639	NZ_CP08706.1	3688770	3699405	+	WP_000633799.1		response regulator	3946.0716941	-2.120201643	0.163116933	-12.89777798	1.26E-38	1.82E-37	36.73992611
ABUW_RS16555	ABUW_3406	NZ_CP08706.1	3454184	3455344	+	WP_000009638.1		homocysteine D-acetyltransferase	1319.018919	-2.123342836	0.160427898	-12.23549622	5.47E-40	8.65E-39	38.06298389
ABUW_RS18630	ABUW_3280	NZ_CP08706.1	3219054	3220262	+	WP_000273589.1	gpgA	Rbf1 family protein phosphatase G1gA	1692.807185	-2.125232712	0.12453861	-17.06418459	1.92E-63	6.21.766877	
ABUW_RS13375	ABUW_2755	NZ_CP08706.1	2744837	2746166	+	WP_000729860.1		NC23 family permease	1374.321845	-2.12547227	0.189270089	-11.22683714	2.91E-29	2.47E-28	27.60730305
ABUW_RS01730	ABUW_0147	NZ_CP08706.1	161881	163129	+	WP_000075472.1	mucC	UDP-N-acetylmuramate-L-alanine ligase	4193.051849	-2.129480768	0.158831764	-10.432518	3.90E-41	6.60E-40	39.8045606
ABUW_RS01255	ABUW_0256	NZ_CP08706.1	269192	270639	-	WP_000051217.1		HAMP domain-containing protein	3163.322235	-2.131917327	0.175516939	-12.14579654	6.04E-34	3.21.677031	
ABUW_RS01875	ABUW_800	NZ_CP08706.1	8192909	1975008	+	WP_000832326.1		TonB-dependent siderophore receptor	1697.479374	-2.131890078	0.266638801	-7.99539665	1.29E-15	4.77E-15	14.32.84862
ABUW_RS1210	ABUW_0429	NZ_CP08706.1	443273	443659	+	WP_00_104016.1	rpmK	30S ribosomal protein S11	59266.30441	-2.13307055	0.273838485	-7.65312635	1.81E-14	6.18E-14	10.2001052
ABUW_RS05085	ABUW_0236	NZ_CP08706.1	614085	614610	+	WP_000729408.1	pdjA	pyridoxal 5'-phosphate synthase	2201247449	-2.133400971	0.149667585	-14.2543205	4.21E-46	9.54E-45	44.02045163
ABUW_RS04795	ABUW_0978	NZ_CP08706.1	91859	919172	+	WP_00_028615.1	sppA	signal peptide peptidase SppA	5972.536788	-2.1346837	0.17350337	-12.29724998	9.37E-35	1.91E-33	32.95078898
ABUW_RS01900	ABUW_0642	NZ_CP08706.1	641632	641870	+	WP_00_175596.1	glucose/galactose/biomolecule family membrane-bound PQQ-dependent C	31415.73592	-2.135991939	0.18713358	-11.39977449	4.16E-30	3.74E-29	28.427284	
ABUW_RS18585	ABUW_3878	NZ_CP08706.1	3945577	3946131	+	WP_00_062789.1	gpeE	nucleotide exchange factor GpeE	6974.534365	-2.140289824	0.221781974	-19.650422808	4.90E-22	2.72E-21	30.5604311
ABUW_RS05620	ABUW_0358	NZ_CP08706.1	1699953	1727349	-	WP_000667410.1	mrcB	penicillin-binding protein B	760.1218097	-2.144508875	0.18438066	-14.4519377	2.46E-47	5.99E-46	45.22257318
ABUW_RS19235	ABUW_0748	NZ_CP08706.1	3810540	3822737	+	WP_000623184.1		NAD-dependent malic enzyme	8849.816192	-2.145318671	0.227271668				

ABUW_RS0465	ABUW_0314	NZ_CP008706.1	336833	337393	+	WP_002194578.1	pIv	type IV plus modification protein PIV	167.2603096	-2.270862996	0.308574459	-7.359205953	1.85E-13	5.93E-10	12.22694531
ABUW_RS02020	ABUW_0411	NZ_CP008706.1	435235	435564	+	WP_001982638.1	pIv	S05 ribosomal protein L22	52252.33271	-2.271536778	0.380856569	-7.10693951	9.27E-13	2.84E-12	115466866
ABUW_RS1080	ABUW_2319	NZ_CP008706.1	230479	230466	-	WP_001918759.1		PAACE efflux transporter	486.7408237	-2.272198317	0.53404885	-4.254217597	2.10E-05	3.67E-05	4.43533936
ABUW_RS005	ABUW_0203	NZ_CP008706.1	227864	229156	+	WP_000369668.1	gabT	4-aminobutyrate--2-oxoglutarate transaminase	1012.526494	-2.273801979	0.36519183	-6.257606984	4.74E-10	1.20E-09	8.020818754
ABUW_RS0585	ABUW_1461	NZ_CP008706.1	161653	196722	+	WP_000035053.1	efp	elongation factor P	337.0106363	-2.274232313	0.207018282	-10.98706015	4.4E-28	3.48E-27	26.45842076
ABUW_RS1990	ABUW_3695	NZ_CP008706.1	3754749	3755372	+	WP_001081658.1		TGROD735 family Rossmann fold protein	2141.923166	-2.280589482	0.218923017	-10.4682893	2.04E-25	1.38E-24	23.86015091
ABUW_RS1915	ABUW_2285	NZ_CP008706.1	2246466	2250185	-	WP_000546460.1		nucleotidyltransferase family protein	1294.664029	-2.287761035	0.166198836	-10.76520493	4.10E-43	7.96E-42	41.09908693
ABUW_RS0430	ABUW_3381	NZ_CP008706.1	3420637	3421058	-	WP_000963851.1	ndk	nucleoside-diphosphate kinase	10827.97567	-2.288597367	0.21085022	-10.84206421	2.18E-27	1.66E-26	25.77989191
ABUW_RS0270	ABUW_3145	NZ_CP008706.1	3170193	3171795	-	WP_001165880.1		5'-methylthioadenosine-S-adenosylhomocysteine nucleosyl	878.1772599	-2.289166955	0.196669255	-11.64323804	2.48E-31	2.37E-30	29.62525195
ABUW_RS0605	ABUW_1975	NZ_CP008706.1	1976929	1980039	+	WP_000987602.1	adeB	multidrug efflux RND transporter permease subunit AdeB	5514.271404	-2.291070772	0.292779026	-17.827431526	4.08E-15	1.70E-14	13.75448731
ABUW_RS1470	ABUW_3031	NZ_CP008706.1	3058852	3059889	+	WP_000355491.1		type IV plus twitching motility protein PIT	604.5924693	-2.297640776	0.252982195	-10.82223251	1.00E-19	5.10E-18	8.29242982
ABUW_RS04470	ABUW_1739	NZ_CP008706.1	1736031	1737227	+	WP_00184643.1		1-deoxy-D-xylulose-5-phosphate reductoisomerase	5527.045313	-2.305549301	0.195625635	-10.92024433	4.77E-44	9.71E-43	42.0178077
ABUW_RS0270	ABUW_2734	NZ_CP008706.1	2721559	2723563	+	WP_001098022.1	rimKL	89(N)-7(N)-methyltransferase RimK/23S-rRNA [guanine2	2486.357841	-2.305608227	0.144638046	-10.94053776	3.31E-57	1.38E-55	54.86010091
ABUW_RS05405	ABUW_165	NZ_CP008706.1	102791	102385	+	WP_001057073.1		acyl-CoA desaturase	19300.02931	-2.308129009	0.271164397	-10.52282794	1.7E-17	7.1E-17	16.148104
ABUW_RS0320	ABUW_3359	NZ_CP008706.1	3397003	3399627	+	WP_000155773.1		leucine--rRNA ligase	9365.46306	-2.308442974	0.187519585	-12.3141001	7.96E-35	8.57E-34	33.01908806
ABUW_RS0405	ABUW_3376	NZ_CP008706.1	3419258	3416550	+	WP_000095254.1	hisS	histidine--rRNA ligase	7992.91816	-2.31001957	0.192079717	-10.25231977	4.34E-46	9.76E-45	44.0155019
ABUW_RS1940	ABUW_3685	NZ_CP008706.1	3742844	3744100	+	WP_000910004.1		OpcD family outer membrane porin	6457.825232	-2.31024229	0.23348995	-10.896179947	4.22E-23	2.47E-22	21.60730305
ABUW_RS1915	ABUW_3558	NZ_CP008706.1	3659338	3660528	-	WP_001029610.1	tuf	elongation factor Tu	18728.81966	-2.314716374	0.220196366	-10.51599007	7.29E-26	5.55E-25	24.8819277
ABUW_RS1705	ABUW_3635	NZ_CP008706.1	3694906	3696302	+	WP_000805827.1		homoserine dehydrogenase	5192.586541	-2.318562225	0.225333293	-10.28947963	7.81E-25	5.43E-24	23.29073004
ABUW_RS0255	ABUW_0502	NZ_CP008706.1	57716	58452	-	WP_000107671.1		dienelactone hydrolase family protein	802.252445	-2.322764581	0.269895843	-10.83736719	3.95E-19	1.62E-18	17.73923261
ABUW_RS0810	ABUW_3863	NZ_CP008706.1	3932491	3933201	+	WP_001933879.1	lepA	signal peptidase I	3212.069427	-2.323799336	0.1069189	-10.97270205	13.1E-64	8.93E-63	62.04914854
ABUW_RS1076	ABUW_2296	NZ_CP008706.1	2283653	2284819	+	WP_001009541.1		methionine adenosyltransferase	10102.90254	-2.328225016	0.148177882	-10.71236532	1.24E-55	4.73E-54	53.52510886
ABUW_RS19410	ABUW_3578	NZ_CP008706.1	3636064	3636768	+	WP_001081850.1		DabA family oxidoreductase	100147480.1	-2.330887739	0.19102029	-10.42390897	1.10E-53	3.81E-52	51.4907502
ABUW_RS1060	ABUW_2274	NZ_CP008706.1	2299015	2290178	+	WP_000103301.1		cupin domain-containing protein	1620.87493	-2.333446034	0.1474904	-10.33852007	1.38E-40	2.27E-39	38.6439741
ABUW_RS0070	ABUW_0143	NZ_CP008706.1	165658	16178	-	WP_00198816.1		TorB1-dependent sensorphore receptor	669.020859	-2.33356607	0.318100621	-10.52483339	9.08E-10	2.26E-09	8.64581951
ABUW_RS1905	ABUW_0308	NZ_CP008706.1	313125	313078	-	WP_000080000.1		RbfA family protein	674.781872	-2.334841078	0.205291462	-10.14841937	5.78E-20	2.62E-19	16.54975080
ABUW_RS1805	ABUW_3862	NZ_CP008706.1	3929661	3932498	+	WP_001081046.1	leS	isoleucine--rRNA ligase	21461.64893	-2.335188085	0.15400999	-10.42359751	1.14E-53	3.81E-52	51.41907502
ABUW_RS1445	ABUW_3584	NZ_CP008706.1	3642842	3644266	+	WP_000994934.1		TRAP transporter-large permease subunit	3010.051945	-2.33820485	0.228375478	-10.2411917	1.30E-24	8.32E-24	23.07897667
ABUW_RS0965	ABUW_0985	NZ_CP008706.1	219500	2202582	+	WP_000608203.1		DUF475 domain-containing protein	634.9550811	-2.340095874	0.193706682	-10.20801616	1.34E-33	1.47E-32	31.83268267
ABUW_RS0305	ABUW_1645	NZ_CP008706.1	1640874	1641344	+	WP_000520701.1		TorB1-dependent receptor	2039.817431	-2.341714744	0.376577761	-10.26758848	5.08E-10	1.29E-09	8.8941029
ABUW_RS1910	ABUW_0409	NZ_CP008706.1	431410	434934	+	WP_001022317.1	rgB	S05 ribosomal protein L2	171697.5468	-2.343751974	0.376408409	-17.410146147	1.23E-13	3.99E-13	62.390271
ABUW_RS1970	ABUW_3733	NZ_CP008706.1	3790776	3791944	+	WP_001084971.1	atpG	FGF1ATP synthase subunit gamma	55467.57216	-2.344301110	0.269354998	-17.86240732	2.83E-19	1.23E-17	16.91091489
ABUW_RS0180	ABUW_0241	NZ_CP008706.1	258729	259679	+	WP_000198180.1		homoserine kinase	6192.207024	-2.350073927	0.181072849	-10.40619494	6.54E-45	1.41E-43	42.85078689
ABUW_RS1910	ABUW_3296	NZ_CP008706.1	3328386	3329195	+	WP_000624763.1	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	3596.919107	-2.350773997	0.17709831	-10.28058823	3.00E-40	4.82E-39	38.31952936
ABUW_RS1790	ABUW_2636	NZ_CP008706.1	2635492	2635166	+	WP_000144889.1		femA domain family protein	1639.22118	-2.3511116	0.195493792	-10.02652774	2.58E-33	2.77E-32	31.55752023
ABUW_RS1955	ABUW_2873	NZ_CP008706.1	2882131	2882784	+	WP_001022044.1	adk	adenylate kinase	10108.67071	-2.351726938	0.193731375	-10.39993864	5.18E-47	1.24E-45	44.90653781
ABUW_RS14045	ABUW_2892	NZ_CP008706.1	2898620	2901157	+	WP_000195679.1		CIM85 family transporter	3737.767202	-2.36018453	0.193493909	-10.5793356	3.20E-34	3.68E-33	32.43416218
ABUW_RS0810	ABUW_0163	NZ_CP008706.1	161809	162946	+	WP_000198870.1	ghnM	phosphogluconate mutase	6879.826909	-2.363943448	0.129008364	-10.323995	5.33E-75	5.11E-73	72.21915791
ABUW_RS1930	ABUW_3888	NZ_CP008706.1	3958453	3958506	+	WP_000501011.1	mpl	muramylase L-alanyl-gamma-D-glutamyl-meso-diamino	1644.723103	-2.367408645	0.200376222	-11.81481822	3.27E-32	3.30E-31	30.48148606
ABUW_RS0805	ABUW_027	NZ_CP008706.1	1623167	1624456	+	WP_000078452.1	eno	phosphoglycerate hydratase	24287.51993	-2.367825621	0.16624136	-10.5607623	6.91E-52	2.11E-50	49.61671754
ABUW_RS0005	ABUW_3295	NZ_CP008706.1	3327634	3328382	-	WP_000184632.1		panthoate--L-alanine ligase	2548.367278	-2.37081827	0.198969685	-10.02918056	1.02E-44	4.56E-43	62.6354027
ABUW_RS1440	ABUW_2352	NZ_CP008706.1	2334599	2336108	+	WP_001919103.1	dapC	succinyl-diaminopimelate transaminase	1670.853439	-2.371648178	0.114323286	-10.23985947	1.51E-95	8.71E-93	92.05998194
ABUW_RS1955	ABUW_0777	NZ_CP008706.1	1776873	1776783	+	WP_001186685.1	bimQ	inched-chain amino acid transport system C carrier prot	4073.025376	-2.374972057	0.235507752	-10.08447509	6.47E-24	4.00E-23	22.39740501
ABUW_RS0930	ABUW_0515	NZ_CP008706.1	529647	527382	-	WP_001093824.1		TGRIE244 family phosphatase	1852.843448	-2.373538454	0.204281764	-11.0327798	2.97E-31	2.70E-30	29.5543958
ABUW_RS1975	ABUW_3734	NZ_CP008706.1	3791722	3793206	-	WP_001186636.1		FGF1ATP synthase subunit alpha	92342.9981	-2.376067987	0.282197798	-14.22564563	3.68E-17	1.55E-16	32.83290874
ABUW_RS1975	ABUW_2379	NZ_CP008706.1	2366167	2366988	-	WP_001099252.1	tauD	taurine dehydrogenase	673.8570798	-2.378328548	0.233544759	-10.8360917	2.35E-24	1.46E-23	22.82681373
ABUW_RS04870	ABUW_0993	NZ_CP008706.1	100490	1006090	+	WP_000165386.1	tblB	Tol-Pal system beta repeat protein receptor TolB	5669.546463	-2.379104761	0.204477271	-11.63520105	2.73E-31	2.58E-30	29.58830269
ABUW_RS1910	ABUW_3510	NZ_CP008706.1	3561692	3562467	+	WP_001081765.1		Hsp33 family molecular chaperone Hsp30	2124.83235	-2.384736752	0.192641966	-10.23791045	3.39E-35	4.11E-34	33.38619518
ABUW_RS1755	ABUW_3646	NZ_CP008706.1	3707621	3709069	+	WP_000673449.1		leucyl aminopeptidase	7421.164913	-2.389480093	0.190933962	-10.39388005	1.47E-75	1.45E-73	72.838632
ABUW_RS04395	ABUW_0986	NZ_CP008706.1	893329	893865	-	WP_000179363.1		DDOMN-like domain-containing protein	886.326452	-2.389792298	0.17548322	-10.84989862	1.27E-43	2.49E-42	61.00380065
ABUW_RS1420	ABUW_0289	NZ_CP008706.1	307106	306961	-	WP_000736662.1	ponA	penicillin-binding protein PBP1a	4162.247066	-2.391616126	0.142827753	-10.62531628	2.00E-77	2.24E-75	74.64975198
ABUW_RS06035	ABUW_0556	NZ_CP008706.1	553239	5533798	+	WP_000884019.1		winged helix-helix transcriptional regulator	605.8195669	-2.392179347	0.14538216	-10.45442163	7.80E-61	4.03E-59	58.39469495
ABUW_RS0445	ABUW_0736	NZ_CP008706.1	1733894	1734448	+	WP_000065428.1	fr	ribosome recycling factor	5586.980737	-2.394263211	0.154040779	-10.48637465	4.29E-54	1.48E-52	51.82973828
ABUW_RS0510	ABUW_0410	NZ_CP008706.1	434948	435223	+	WP_001013819.1	tpsB	S05 ribosomal protein S19	97812.51417	-2.399100016	0.333791475	-17.62319726	1.23E-12	3.74E-12	114271284
ABUW_RS19126	ABUW_3143	NZ_CP008706.1	316047	3168356	+	WP_000460625.1	flh	signal recognition particle protein	6817.362227	-2.399994927	0.180419614	-10.4619115	1.32E-50	3.79E-49	48.42150079
ABUW_RS19240	ABUW_3304	NZ_CP008706.1	3340261	3340145	+	WP_000165005.1		MacB family efflux pump subunit	826.4497942	-2.400100584	0.21133084	-11.33663081	8.68E-30	6.03E-29	28.21686289
ABUW_RS1115	ABUW_3518	NZ_CP008706.1	3566253	3568339	-	WP_001085790.1	prp	polychlorinated nontoxic dihydroxytransferase	41203.49192	-2.400323167	0.182396705	-10.8171199	1.36E-39	2.06E-38	37.88193278
ABUW_RS02290	AB														

ABUW_RS04275	ABUW_0871	NZ_CP080706.1	850933	851643	+	WP_000086385.1		succinate dehydrogenase iron-sulfur subunit	20701.69453	-2.590503314	0.2	6374324	-12.0279164	2.536-33	2.735-32	3150638735
ABUW_RS105	ABUW_2283	NZ_CP080706.1	228551	2288925	+	WP_001016343.1	gcvH	glycine cleavage system protein GcvH	864.1704354	-2.597214079	0	66501181	-15.59034553	8.475-55	3.02E-53	52.5999306
ABUW_RS4850	ABUW_3060	NZ_CP080706.1	3066280	3067470	-	WP_001029610.1	tuf	glycogen elongation factor Tu	23118.7247	-2.603106394	0.214459974	-12.9252592	7.986-35	9.57E-34	33.0480806	
ABUW_RS0070	ABUW_0014	NZ_CP080706.1	19160	17392	+	WP_000335558.1		tyrosine--RNA ligase	3456.523666	-2.607228329	0	61961778	-16.3349738	5.64E-60	2.67E-58	57.5734874
ABUW_RS9930	no	NZ_CP080706.1	3041499	3041858	-		ssaA	transfer-messenger RNA	428436.7419	-2.607700105	0	28824075	-19.046950739	147E-9	6.97E-9	16.1667762
sPN489	no	no	no	no	no	no	no		428458.4734	-2.607719508	0.288230798	-9.947324305	147E-9	6.95E-9	16.168062	
ABUW_RS01550	ABUW_0316	NZ_CP080706.1	337394	338395	+	WP_00070197.1		PF1 family protein	363.5946306	-2.61046526	0.265801962	-9.834186245	8.02E-23	4.62E-22	2.13353902	
ABUW_RS1073	ABUW_2277	NZ_CP080706.1	2262287	2263489	+	WP_000889009.1	tsrT	serine/threonine transporter SerT	4886.714791	-2.616439766	0	9222326	-13.6017117	3.93E-42	6.98E-41	40.1654458
ABUW_RS4880	ABUW_3066	NZ_CP080706.1	3093957	3094409	+	WP_000339889.1	hemJ	protophytylgen oxidase HemJ	5815.195055	-2.633043009	0	168893764	-16.59501838	7.87E-55	2.83E-53	52.54821056
ABUW_RS01610	ABUW_0307	NZ_CP080706.1	330921	331115	-	WP_000289091.1		bacterioferritin-associated ferredoxin	600.0857499	-2.643402022	0.73616271	-13.590833783	0.000326622	0.00051946	3.28069668	
ABUW_RS05825	ABUW_1893	NZ_CP080706.1	124800	125692	+	WP_00055510.1		DUF4105 domain-containing protein	1703.309598	-2.655623686	0.235167517	-11.26247662	143E-29	1.24E-28	27.90657831	
ABUW_RS03315	ABUW_0674	NZ_CP080706.1	676410	678105	-	WP_00102759.1		proline--RNA ligase	7.64.650858	-2.657219326	0	16024757	-16.58196336	9.4E-62	5.1E-60	59.29073004
ABUW_RS02305	ABUW_0489	NZ_CP080706.1	481565	482092	-	WP_00021434.1		hypothetical protein	430.738018	-2.657650688	0.392732955	-16.76068188	1.31E-11	3.74E-11	10.427284	
ABUW_RS1810	ABUW_3735	NZ_CP080706.1	3793310	3793849	-	WP_000819995.1		FOF1-ATP synthase subunit delta	50071.63658	-2.662545376	0.281233603	-19.467388032	2.87E-21	1.62E-20	19.8195641	
ABUW_RS0205	ABUW_0246	NZ_CP080706.1	262407	263108	-	WP_000905538.1	hisA	[5-phosphoribosylamino(methylideneamino)]imidazole-4	3297.61921	-2.672932394	0.17730032	-15.03082672	4.6E-51	1.36E-49	48.8664609	
ABUW_RS04410	ABUW_0899	NZ_CP080706.1	895181	897083	-	WP_001086662.1	ftsH	ATP-dependent zinc metalloprotease FtsH	66757.44407	-2.674200646	0.221871798	-12.05299939	187E-33	2.03E-32	3.169205036	
ABUW_RS07560	ABUW_1549	NZ_CP080706.1	1534055	1534933	+	WP_000191319.1	cyoE	proteobome IX farnesyltransferase	14047.49179	-2.69212296	0.21846657	-12.6481828	1.05E-36	1.50E-35	34.82390874	
ABUW_RS1545	ABUW_3119	NZ_CP080706.1	3198825	3199582	-	WP_000504321.1		8-amino-7-oxononanoate synthase	1340.316106	-2.696324708	0.16345017	-15.02049105	3.16E-61	1.67E-59	56.17728353	
ABUW_RS01480	ABUW_0097	NZ_CP080706.1	906803	910203	+	WP_00026799.1	serB	phosphoenolpyruvate SerB	3787.788393	-2.702950938	0.18435921	-19.82473567	6.77E-85	1.55E-82	1162.92305	
ABUW_RS01795	ABUW_0306	NZ_CP080706.1	387343	389410	+	WP_000333806.1		glycine--RNA ligase subunit beta	1609.34371	-2.716653441	0.21944277	-11.2284289	2.95E-29	2.51E-28	27.60033626	
ABUW_RS17320	ABUW_3509	NZ_CP080706.1	3616267	3616707	+	WP_001075258.1	ruvX	Holliday junction resolvase RuvX	2025.792214	-2.72176474	0.202220352	-12.45840066	2.71E-41	4.69E-40	39.32882716	
ABUW_RS04465	ABUW_0704	NZ_CP080706.1	708980	714555	+	WP_00050337.1		alanine carboxyl symporter family protein	7592.84518	-2.723851626	0.25934321	-15.02086993	6.92E-26	4.90E-25	32.94089302	
ABUW_RS07565	ABUW_1550	NZ_CP080706.1	1534944	1535273	-	WP_000945434.1		cytochrome c ubiquinol oxidase subunit V	3173.014239	-2.728903184	0.218164321	-11.78037086	4.93E-32	4.94E-31	30.30627305	
ABUW_RS1020	ABUW_0228	NZ_CP080706.1	2272272	2276024	+	WP_001049681.1	putA	glutathione peroxidase (GPx)-glutamate gamma-se	28744.34279	-2.73240052	0.20081065	-13.60409211	3.79E-42	10.47096223		
ABUW_RS05975	ABUW_1223	NZ_CP080706.1	1263366	1264472	-	WP_00187010.1	metF	methyltetrahydrofolate reductase (NADPH)	4056.026744	-2.743019195	0.21962144	-13.0024181	1.19E-38	3.76E-44	95.7647155	
ABUW_RS02100	no	NZ_CP080706.1	852077	852211	-	WP_001886360.1		hypothetical protein	723.7178223	-2.744540241	0.17633329	-16.38206597	2.57E-60	1.28E-58	57.89279003	
ABUW_RS06665	ABUW_0166	NZ_CP080706.1	168477	168723	+	WP_000820252.1		functional perphenate dehydrogenase 3-phosphohikimate 1-carbox	5024.58492	-2.743252274	0.18765274	-17.3189125	3.5E-67	2.67E-65	64.57348874	
ABUW_RS04270	ABUW_0870	NZ_CP080706.1	849083	850918	+	WP_000500597.1		succinate dehydrogenase flavoprotein subunit	56104.52344	-2.754505467	0.22418635	-12.28884385	104E-34	32.91009489		
ABUW_RS08620	ABUW_1770	NZ_CP080706.1	1767219	1768937	-	WP_001192460.1		PTS transporter subunit IIC	1353.736865	-2.765102711	0.16606239	-19.6511748	2.97E-62	1.17E-60	59.7700389	
ABUW_RS8980	ABUW_3879	NZ_CP080706.1	3946285	3946225	+	WP_00162607.1	dnaK	molecular chaperone DnaK	66577.33885	-2.774895774	0.20127298	-12.05800646	1.76E-33	3.71666877		
ABUW_RS04255	ABUW_0867	NZ_CP080706.1	846075	847349	+	WP_00187579.1	gltA	citrate (5S)-synthase	34759.78554	-2.777696874	0.22856091	-12.6239975	5.57E-34	6.27E-33	32.20273246	
ABUW_RS08875	ABUW_1824	NZ_CP080706.1	1819883	1900371	-	WP_001844535.1		hypothetical protein	6328.296387	-2.7903003	0.18324604	-17.092364	1.68E-65	1.21E-63	62.9172163	
ABUW_RS1185	ABUW_3736	NZ_CP080706.1	3793862	3794332	-	WP_001024891.1		RF1 ATP synthase subunit B	36085.43341	-2.799510803	0.283326539	-19.54407437	137E-21	7.44E-21	20.12842706	
ABUW_RS17280	ABUW_3501	NZ_CP080706.1	3606835	3606965	+	WP_001162277.1		pepzin peptidase	643.232918	-2.802547616	0.180371667	-15.5371066	1.93E-54	6.75E-53	52.70690035	
ABUW_RS01020	ABUW_0024	NZ_CP080706.1	27683	28667	+	WP_000848730.1	rmbB	16S rRNA cytosine (G87-C)55-methyltransferase RmbB	1775.498883	-2.802716402	0.155697802	-18.00099525	1.91E-72	1.57E-70	69.80410025	
ABUW_RS11695	ABUW_2363	NZ_CP080706.1	2363310	2363311	+	WP_001009738.1		hypothetical protein	4816.071673	-2.813345622	0.191676305	-18.01908262	1.52E-72	1.33E-70	69.87616836	
ABUW_RS00775	ABUW_0166	NZ_CP080706.1	172635	174914	+	WP_00106117.1		2-oxo acid dehydrogenase subunit E2	56104.52344	-2.820384392	0.264002677	-17.70210508	9.95E-27	7.26E-26	53.10063318	
ABUW_RS19715	no	NZ_CP080706.1	851927	852056	+			hypothetical protein	102.199285	-2.835816464	0.185067897	-15.3231089	5.36E-53	1.76E-51	50.75448733	
ABUW_RS00770	ABUW_0165	NZ_CP080706.1	170216	172932	+	WP_000896433.1	aceE	vate dehydrogenase (acetyl-transfering), homodimeric	41950.18742	-2.839954867	0.238882005	-11.88852713	136E-32	1.4E-31	30.85078089	
ABUW_RS01900	ABUW_0367	NZ_CP080706.1	389410	390389	-	WP_00085209.1	glyQ	glycine--RNA ligase subunit alpha	4614.471838	-2.858374338	0.244842611	-11.67433367	1.72E-31	1.67E-30	29.77728353	
ABUW_RS07955	ABUW_1630	NZ_CP080706.1	1625405	1626011	+	WP_00091730.1	pepN	aminopeptidase N	8967.428778	-2.870622429	0.194692872	-14.72652434	4.36E-49	1.9E-47	46.9281979	
ABUW_RS04740	ABUW_3389	NZ_CP080706.1	3429724	3430989	-	WP_00164168.1		glutamate-5-semialdehyde dehydrogenase	4300.65198	-2.878038677	0.13519738	-12.19800148	1.18E-100	1.16E-97	96.92445304	
ABUW_RS01760	ABUW_1651	NZ_CP080706.1	1635273	1635893	-	WP_000852270.1	cyoC	cytochrome c ubiquinol oxidase subunit II	75245.56195	-2.879216494	0.255050586	-11.28878212	1.49E-29	1.29E-28	27.88941027	
ABUW_RS00490	ABUW_0912	NZ_CP080706.1	923186	923476	+	WP_000655579.1		co-chaperone GroES	6377.100597	-2.880369392	0.25544088	-11.27193363	1.82E-29	1.56E-28	37.8068774	
ABUW_RS01585	ABUW_0203	NZ_CP080706.1	279723	281084	+	WP_000190012.1	etfA	energy-dependent translocation thiolate protein B1A	27429.00219	-2.88061601	0.179905328	-18.02057828	9.18E-58	3.98E-56	55.40011903	
ABUW_RS04995	ABUW_1118	NZ_CP080706.1	1129510	1130397	-	WP_001048811.1	cyoW	sulfate ABC transporter permease subunit CyoW	95.9056251	-2.910509528	0.232319761	-12.54094581	4.46E-38	5.68E-35	34.24565166	
ABUW_RS17270	ABUW_3549	NZ_CP080706.1	3605867	3607479	+	WP_001074987.1	pilB	type IV A-pilus assembly ATPase PilB	1238.101225	-2.918919156	0.209595979	-15.83798579	7.49E-44	1.49E-42	4.182681973	
ABUW_RS16655	ABUW_3426	NZ_CP080706.1	3471075	3472104	+	WP_000833866.1		energy transducer TonB	156.1220189	-2.932776675	0.429026986	-16.835879263	8.15E-12	2.36E-11	6.627088	
ABUW_RS17385	ABUW_3572	NZ_CP080706.1	3629099	3632062	-	WP_000580942.1	fadB	fatty acid oxidation complex subunit alpha FadB	10697.51107	-2.953074404	0.284047912	-13.3963054	2.57E-25	1.73E-24	23.7619339	
ABUW_RS14875	ABUW_3005	NZ_CP080706.1	3002709	3009338	+	WP_000832710.1		beta-ketoacyl-ACP synthase I	44223.66246	-2.954779505	0.185085993	-15.96430049	2.26E-57	9.60E-56	55.07728277	
ABUW_RS05545	ABUW_1103	NZ_CP080706.1	1164233	1166851	-	WP_001622279.1		ATP-binding protein	5097.738301	-2.961068616	0.176538198	-16.77409566	3.78E-63	2.30E-61	60.63827216	
ABUW_RS05185	ABUW_2178	NZ_CP080706.1	2160169	2160789	-	WP_000595973.1		acetyltransferase	619.420303	-2.97701857	0.165644841	-15.26454587	1.14E-07	2.95E-07	6.530171984	
ABUW_RS18645	ABUW_3424	NZ_CP080706.1	3470646	3471030	-	WP_000854311.1		biopolymer transporter ExbD	2704.455258	-2.980279614	0.302127545	-19.86430951	5.94E-23	3.46E-22	21.44602929	
ABUW_RS03510	ABUW_0710	NZ_CP080706.1	719939	720817	-	WP_001000558.1	gatA	-tRNA(Lys)(Glu)-RNA(Gln) amidotransferase subunit G	6048.194346	-2.98266176	0.209510011	-14.23575717	5.50E-46	1.23E-44	43.91009489	
ABUW_RS11485	ABUW_2361	NZ_CP080706.1	2347619	2348458	-	WP_001047668.1		RNA methyltransferase	1384.054969	-2.988337569	0.188286178	-15.8711074	1.00E-56	4.03E-55	54.39469495	
ABUW_RS1260	ABUW_2732	NZ_CP080706.1	2719637	2720653	+	WP_000546643.1		aspartate carboxyltransferase catalytic subunit	2349.023416	-2.990779035	0.179075267	-15.7033021	1.28E-62	7.71E-61	60.10164562	
ABUW_RS17440	ABUW_3583	NZ_CP080706.1	3614934	3642015	-	WP_000472947.1		outer membrane beta-barrel protein	1177.011916	-2.999315481	0.175551787	-16.307021783	2.84E-10	7.30E-10	9.38607714	
ABUW_RS16610	ABUW_3417	NZ_CP080706.1	3465790	3466568	+	WP_000599085.1		protoproten diacylglycerol transferase								

ABUW_RS15375	ABUW_1366	NZ_CP008706.1	3191296	3192894	-	WP_000429844.1	nuoM	NADH-quinone oxidoreductase subunit M	36996.21365	-3.570029492	0.251014527	-14.22240191	6.65E-46	148E-44	43.82973828
ABUW_RS15425	ABUW_1376	NZ_CP008706.1	3203608	3204285	-	WP_000878003.1		NADH-quinone oxidoreductase subunit B	8071.788965	-3.58919835	0.289462192	-12.399541	2.63E-35	3.12E-34	33.49340497
ABUW_RS02075	ABUW_0443	NZ_CP008706.1	455176	457230	-	WP_000266455.1		M3 family metalloproteinase	6798.460322	-3.600959717	0.293312661	-12.27686422	1.2E-34	1.41E-33	32.85078089
ABUW_RS05265	ABUW_0272	NZ_CP008706.1	1084741	1086978	+	WP_000806667.1		NADP-dependent isocitrate dehydrogenase	48.69.08892	-3.604507056	0.189152092	-10.056103	5.84E-81	9.8E-79	78.00833099
ABUW_RS15185	ABUW_2381	NZ_CP008706.1	2367863	2368657	-	WP_000114471.1		ATP-binding cassette domain-containing protein	719.963052	-3.608060746	0.452893051	-7.666694864	1.63E-15	5.99E-15	14.22257318
ABUW_RS12115	ABUW_2489	NZ_CP008706.1	2485285	2485881	-	WP_000162863.1		NAD(P)H-dependent oxidoreductase	443.6515256	-3.609445951	0.400948622	-9.002265507	2.21E-19	1.03E-18	17.98716278
ABUW_RS15460	ABUW_1363	NZ_CP008706.1	3210091	3212925	+	WP_000111540.1		ribonucleoside-diphosphate reductase subunit alpha	44162.10903	-3.626404767	0.185697707	-19.5285382	6.28E-85	14.9E-82	81.82681373
ABUW_RS15465	ABUW_1384	NZ_CP008706.1	3212981	3213115	+	WP_000465010.1		hypothetical protein	157.3788477	-3.771500385	0.245817942	-5.34265705	3.97E-53	1.31E-51	50.8827287
ABUW_RS15140	ABUW_2708	NZ_CP008706.1	2691513	2691713	+	WP_000185155.1		heavy-metal-associated domain-containing protein	1418.186303	-3.780307569	0.371376259	-10.17918484	2.46E-24	1.55E-23	22.8096683
ABUW_RS17190	ABUW_2423	NZ_CP008706.1	2410066	2410731	-	WP_000418072.1		amino acid ABC transporter permease	108.8849133	-3.781219079	0.476517086	-7.935117529	2.10E-15	7.63E-15	14.11747546
ABUW_RS07780	ABUW_1593	NZ_CP008706.1	1588486	1591125	+	WP_000888596.1		bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	40018.50632	-3.793605942	0.197024048	-19.25453254	1.29E-82	2.27E-80	79.64397414
ABUW_RS07575	ABUW_1552	NZ_CP008706.1	1535898	1537889	-	WP_000367186.1	cyoB	cytochrome c ubiquinol oxidase subunit I	175014.1556	-3.804925941	0.288308663	-13.19740414	9.08E-40	1.39E-38	37.8569852
sRNA97	no	no	no	no	no	no	no	no	33165.63499	-3.833732226	0.329583918	-11.63203669	2.83E-31	2.67E-30	29.57348874
ABUW_RS00165	ABUW_0034	NZ_CP008706.1	40420	41520	+	WP_0001950643.1		efflux RND transporter periplasmic adaptor subunit	6267.816798	-3.853632664	0.233005602	-16.53879838	1.93E-101	10.2E-99	58.99199883
ABUW_RS15420	ABUW_1375	NZ_CP008706.1	3201736	3203523	-	WP_000852150.1	nuoC	NADH-quinone oxidoreductase subunit C/D	25803.6877	-3.933773307	0.281998984	-13.949556	3.17E-44	6.51E-43	42.18641901
ABUW_RS15415	ABUW_1374	NZ_CP008706.1	3201213	3201722	-	WP_000973142.1	nuoE	NADH-quinone oxidoreductase subunit NuOE	13467.1391	-3.94529915	0.287859524	-13.70565001	9.39E-43	1.75E-41	40.75696195
ABUW_RS04535	ABUW_0924	NZ_CP008706.1	932031	932936	-	WP_000984535.1	htpX	protease HtpX	9940.750187	-3.959291194	0.312388302	-10.67426201	8.21E-37	1.09E-35	34.96257305
ABUW_RS05245	ABUW_1068	NZ_CP008706.1	1079141	1079623	-	WP_000133995.1		peptidylprolyl isomerase	6945.332805	-3.975528978	0.200876338	-19.79092717	3.56E-87	1.20E-84	83.92081875
ABUW_RS08260	ABUW_1696	NZ_CP008706.1	1693467	1694837	-	WP_000939648.1	accC	acetyl-CoA carboxylase biotin carboxylase subunit	23673.18733	-4.004692198	0.220587708	-18.15464804	1.18E-73	1.08E-71	70.96657624
ABUW_RS04300	ABUW_0876	NZ_CP008706.1	859675	859965	+	WP_000114637.1	sucD	succinate--CoA ligase subunit alpha	49529.37226	-4.024177033	0.227417174	-17.69512355	4.57E-70	3.16E-68	67.4424928
ABUW_RS08735	ABUW_1794	NZ_CP008706.1	1787401	1788546	-	WP_000575152.1	cyoB	cytochrome c ubiquinol oxidase subunit II	4867.989219	-4.026741189	0.417343309	-9.648510244	4.99E-22	2.78E-21	20.55909092
ABUW_RS15380	ABUW_1367	NZ_CP008706.1	3192896	3194785	-	WP_000121137.1	nuoL	NADH-quinone oxidoreductase subunit L	34396.29329	-4.03269433	0.257180184	-15.68042041	2.06E-55	7.81E-54	53.11861534
ABUW_RS08265	ABUW_1697	NZ_CP008706.1	1694854	1695273	-	WP_000354611.1	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein	7165.670085	-4.080639424	0.215188621	-18.96484443	3.33E-80	4.97E-78	77.30364361
ABUW_RS04295	ABUW_0875	NZ_CP008706.1	857894	859060	+	WP_000194873.1	sucC	ADP-forming succinate--CoA ligase subunit beta	53007.1766	-4.104629547	0.246012154	-16.68466166	1.69E-62	1.00E-60	60
ABUW_RS05475	ABUW_1119	NZ_CP008706.1	1140333	1141295	+	WP_000897187.1	sohB	protease SohB	9116.465687	-4.11575109	0.252733069	-16.28458595	1.27E-59	5.88E-58	57.23062267
ABUW_RS00170	ABUW_0035	NZ_CP008706.1	41523	44648	+	WP_000671305.1		efflux RND transporter permease subunit	16662.05326	-4.243380898	0.259602594	-16.34567989	4.67E-60	2.24E-58	57.64975198
ABUW_RS05000	ABUW_1019	NZ_CP008706.1	1030394	1031227	-	WP_000083117.1	cysT	sulfate ABC transporter permease subunit CysT	116.0387869	-4.270770556	0.439618573	-19.714762398	2.61E-22	1.46E-21	20.83564714
ABUW_RS15400	ABUW_1371	NZ_CP008706.1	3196169	3197185	-	WP_000107098.1	nuoH	NADH-quinone oxidoreductase subunit NuOH	23369.85271	-4.290147365	0.282188918	-15.2025649	3.40E-52	1.06E-50	49.97469413
ABUW_RS10220	ABUW_2104	NZ_CP008706.1	2086545	2087963	+	WP_000980437.1		aspartate ammonia-lyase	5497.212832	-4.305635571	0.332154627	-12.96274453	1.99E-38	2.82E-37	36.54975089
ABUW_RS15385	ABUW_1368	NZ_CP008706.1	3194782	3195090	-	WP_000529822.1	nuoK	NADH-quinone oxidoreductase subunit NuOK	7618.464258	-4.313886313	0.265031433	-16.276190962	1.44E-59	6.59E-58	57.1811459
ABUW_RS16650	ABUW_3425	NZ_CP008706.1	3417050	3417670	+	WP_000101664.1		MotA/TolQ/ExbB proton channel family protein	4560.680571	-4.330571594	0.349302627	-12.3977641	2.69E-35	3.27E-34	33.48545225
ABUW_RS20210	no	NZ_CP008706.1	2411445	2411558	+	WP_002071921.1		hypothetical protein	7.891497102	-4.352908307	0.851777791	-5.10380142	3.22E-07	6.55E-07	6.837587
ABUW_RS15405	ABUW_1372	NZ_CP008706.1	3197189	3198873	-	WP_000190957.1	nuoG	NADH-quinone oxidoreductase subunit NuOG	61590.78942	-4.393280678	0.293281774	-14.97941977	1.00E-50	2.90E-49	48.537602
ABUW_RS15390	ABUW_1369	NZ_CP008706.1	3195080	3195608	-	WP_012578792.1	nuoJ	NADH-quinone oxidoreductase subunit J	11311.80451	-4.432716358	0.261992546	-16.9192461	3.25E-64	2.14E-62	61.66958623
ABUW_RS15395	ABUW_1370	NZ_CP008706.1	3195608	3196150	-	WP_000276693.1	nuoI	NADH-quinone oxidoreductase subunit Nuol	12274.49772	-4.43298576	0.277076988	-15.9991189	1.30E-57	5.56E-56	55.25492521
ABUW_RS14445	ABUW_2975	NZ_CP008706.1	2991309	2992187	+	WP_000696108.1		homocysteine S-methyltransferase family protein	592.732493	-4.46458552	0.289244154	-15.37268253	2.50E-53	8.31E-52	51.08039898
sRNA48	no	no	no	no	no	no	no	no	160.425978	-4.496214109	0.421471311	-10.68785442	1.44E-26	1.04E-25	24.98206666
ABUW_RS15190	ABUW_2382	NZ_CP008706.1	2368667	2369707	-	WP_000651495.1	tauA	taurine ABC transporter substrate-binding protein	782.0023615	-4.548196245	0.542056598	-8.390629801	4.84E-17	1.96E-16	15.70714393
ABUW_RS15410	ABUW_1373	NZ_CP008706.1	3199885	3201273	-	WP_000109108.1	nuoF	NADH-quinone oxidoreductase subunit Nuof	22232.86764	-4.66334481	0.329812334	-14.1939306	2.17E-45	4.78E-44	43.3205721
ABUW_RS05005	ABUW_1020	NZ_CP008706.1	1031088	1031916	-	WP_000149921.1		alpha/beta hydrolase	280.8572397	-4.737761021	0.542653508	-8.30729738	2.53E-48	1.10E-47	16.95860731
ABUW_RS16540	ABUW_3403	NZ_CP008706.1	3448925	3451156	+	WP_000022885.1		TonB-dependent siderophore receptor	7747.738344	-4.769730842	0.532342277	-8.95984884	3.25E-19	1.50E-18	17.82390874
sRNA100	no	no	no	no	no	no	no	no	3156.530264	-4.792545893	0.27719661	-17.28933805	5.66E-67	4.22E-65	64.37468755
sRNA2	no	no	no	no	no	no	no	no	13880.1352	-5.089718465	0.242324418	-21.00373753	6.08E-98	4.89E-95	94.31069114
sRNA99	no	no	no	no	no	no	no	no	20022.1852	-5.138299095	0.338683364	-15.171195	5.47E-52	1.68E-50	49.77469072
ABUW_RS05010	ABUW_1021	NZ_CP008706.1	1031947	1032954	-	WP_000121600.1		sulfate ABC transporter substrate-binding protein	524.9851564	-5.34676753	0.588663259	-9.02886626	1.06E-19	5.07E-19	18.29499204

Table S15. RNA-seq data: Absolute and relative expression (AT/MEP > 2-fold up)

locus_tag	"old_locus_tag"	chrom	start	stop	strand	refseq_id	symbol	name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
sRNA29	no	no	no	no	no	no	no	no	394.2856283	6.456250197	0.521028838	12.38421841	3.18E-35	2.73E-33
ABUW_RS12725	ABUW_2621	NZ_CP008706.1	2618549	2619007	-	WP_001027311.1		hypothetical protein	4941499428	6.159696675	0.370296495	16.63449901	3.92E-62	2.63E-59
ABUW_RS01140	ABUW_0233	NZ_CP008706.1	252271	252714	-	WP_000581866.1		hypothetical protein	1282.899022	5.810054605	0.340356342	17.07050491	2.46E-65	1.98E-62
ABUW_RS10025	ABUW_2064	NZ_CP008706.1	2045977	2046213	-	WP_000044401.1		hypothetical protein	395.3538908	5.46195431	0.695298673	7.85555181	3.98E-15	4.98E-14
ABUW_RS12975	ABUW_2673	NZ_CP008706.1	2666326	2666784	-	WP_001138417.1		hypothetical protein	4617.200979	5.3318309	0.385549592	13.82917013	1.70E-43	2.75E-41
ABUW_RS07960	ABUW_1631	NZ_CP008706.1	1628562	1629092	+	WP_000750672.1		spore coat protein U domain-containing protein	7973.259285	5.314123614	0.418151905	12.7086142	5.30E-37	5.20E-35
ABUW_RS07180	ABUW_1473	NZ_CP008706.1	1461230	1461556	-	WP_000469224.1		hypothetical protein	1324.7762	5.263456026	0.229949783	22.88959102	5.90E-16	2.38E-12
ABUW_RS20475	ABUW_2443	NZ_CP008706.1	2430503	2430646	-	WP_000251635.1		hypothetical protein	1153.102491	5.227863649	0.889082712	5.889064454	4.10E-09	2.59E-08
ABUW_RS07360	ABUW_1509	NZ_CP008706.1	1494532	1495503	+	WP_000032710.1		acyl-CoA desaturase	82.16500026	5.213719951	0.343475592	15.17930262	4.85E-52	1.63E-49
ABUW_RS07145	ABUW_1466	NZ_CP008706.1	1456445	1456678	-	WP_000194391.1		DUF1711 domain-containing protein	16057.06702	5.172105505	0.628722601	8.226371214	1.93E-16	2.77E-15
ABUW_RS11885	ABUW_2442	NZ_CP008706.1	2429805	2430233	-	WP_001136759.1		hypothetical protein	253.3190753	4.918318934	0.509536453	9.652535964	4.80E-22	1.20E-20
ABUW_RS15330	ABUW_1357	NZ_CP008706.1	3183396	3185072	-	WP_000101666.1		mechanosensitive ion channel	41419.22788	4.899105048	0.301452629	16.25165804	2.17E-59	1.09E-56
ABUW_RS07355	ABUW_1508	NZ_CP008706.1	1493849	1494412	+	WP_000770558.1		lipocalin family protein	97.91582499	4.82963018	0.349241199	13.82892451	1.71E-43	2.75E-41
ABUW_RS07170	ABUW_1471	NZ_CP008706.1	1460237	1460599	+	WP_0007021827.1		NiD/YglW/YdeF family stress tolerance protein	865.07839	4.78292594	0.51620911	9.330337179	1.07E-20	2.29E-9
ABUW_RS11940	ABUW_2454	NZ_CP008706.1	2441852	2442655	+	WP_000121729.1		enoyl-CoA hydratase/isomerase family protein	174.636723	4.682042932	0.322568446	14.514882	9.75E-48	2.46E-45
ABUW_RS16255	ABUW_3346	NZ_CP008706.1	3379744	3382500	-	WP_001185980.1	acnA	aconitate hydratase AcnA	5478.736844	4.651121084	0.264596708	17.57814682	3.62E-69	3.65E-66
ABUW_RS01160	ABUW_0237	NZ_CP008706.1	255242	255931	-	WP_000104986.1	aqpZ	aquaporin Z	107.1219277	4.619125196	0.286666302	16.1324453	2.06E-58	9.22E-56
ABUW_RS00260	ABUW_0053	NZ_CP008706.1	58624	58782	-	WP_000490267.1		DUF1328 domain-containing protein	5808.425003	4.567133833	0.353370835	12.92474869	3.28E-38	3.57E-36
ABUW_RS18870	ABUW_3875	NZ_CP008706.1	3942924	3943354	-	WP_000730315.1		hypothetical protein	2956.891631	4.509271222	0.364193848	13.0273668	8.55E-39	9.84E-37
ABUW_RS10010	ABUW_2061	NZ_CP008706.1	2043221	2043786.1	-	WP_001136786.1		hypothetical protein	1239.277092	4.477199609	0.306246698	14.62216453	2.03E-48	5.45E-46
ABUW_RS03180	ABUW_0646	NZ_CP008706.1	65174	65197	-	WP_00117585.1		VOC family protein	124.266871	4.381108569	0.350863625	12.48864749	8.81E-36	7.75E-34
ABUW_RS20165	ABUW_1657	NZ_CP008706.1	1651777	1651908	-	WP_000181254.1		hypothetical protein	515.538365	4.36827506	0.603304673	7.240578661	4.47E-14	4.53E-12
ABUW_RS11945	ABUW_2455	NZ_CP008706.1	2442667	2444658	+	WP_000046120.1		acetyl(propionyl)methylcrotonyl-CoA carboxylase subunit alpha	3837.508629	4.334663225	0.29188769	16.88E-50	6.87E-48	1.98E-47
ABUW_RS11955	ABUW_2436	NZ_CP008706.1	2424078	2426222	-	WP_000186585.1	katE	catalase HPI	40275.84516	4.313557728	0.38517623	11.95050381	4.12E-29	2.05E-27

ABUW_RS1835	ABUW_2453	NZ_CP008706.1	2440241	2441842	+	WP_007072777.1		methylcrotonyl-CoA carboxylase	2910.262352	4.3106869	0.3378966	0.75943045	2.766-37	2.785-35
ABUW_RS17375	ABUW_612	NZ_CP008706.1	1497572	1498771	+	WP_000598001.1		class ISAM-dependent methyltransferase	132.115013	4.31072006	0.315391067	0.66758993	1.586-42	2.366-40
ABUW_RS00550	ABUW_651	NZ_CP008706.1	645792	646262	+	WP_01023841.1		hypothetical protein	984.5032291	4.257877793	0.53093162	0.342348977	7.286-17	1.161-15
ABUW_RS17365	ABUW_610	NZ_CP008706.1	1495500	1496762	+	WP_0004984184.1		FAD-dependent oxidoreductase	53.3212785	4.25909092	0.404962053	0.499524474	6.686-26	3.816-24
ABUW_RS1405	ABUW_617	NZ_CP008706.1	1503167	1503739	+	WP_000692365.1		nuclear transport factor 2 family protein	82.9493349	4.203367539	0.514508629	1.95677993	5.776-33	4.396-31
ABUW_RS18960	ABUW_3898	NZ_CP008706.1	3965332	3965783	+	WP_000097932.1		GliB/YraG/YngJ family stress response membrane protein	585.088556	4.149394629	0.347886295	1.92737636	6.626-31	3.661-29
ABUW_RS17500	ABUW_636	NZ_CP008706.1	622327	622557	-	WP_000859008.1		hypothetical protein	5416.80378	4.20956994	0.409093688	0.09038673	5.795-24	1.816-22
ABUW_RS15280	ABUW_3147	NZ_CP008706.1	3173306	3173896	-	WP_000206022.1		hypothetical protein	6879.766036	4.08438872	0.38280476	0.66963968	1416-26	5.525-25
ABUW_RS15250	ABUW_2730	NZ_CP008706.1	2178760	2178175	-	WP_000026486.1		OmpA family protein	759.248105	4.065441683	0.203996147	9.9339416	6.2076-88	4.165-85
ABUW_RS16280	ABUW_3351	NZ_CP008706.1	3387175	3388038	-	WP_000037364.1		hypothetical protein	980.7425242	4.003857996	0.425427886	9.4106706	4.906-21	1.006-9
ABUW_RS18130	ABUW_2452	NZ_CP008706.1	2439044	2440216	+	WP_01053639.1		isovaleryl-CoA dehydrogenase	2343.051086	3.980006833	0.309266681	11.08012418	1.575-28	7.346-27
ABUW_RS04980	ABUW_615	NZ_CP008706.1	626616	627356	+	WP_000866525.1	carO	ornithine uptake point CarO type 3	40059.38539	3.974971822	0.265684524	14.96124712	1326-50	4.086-48
ABUW_RS05995	ABUW_627	NZ_CP008706.1	626720	626975	-	WP_000576648.1		acyl-CoA dehydrogenase	2404.047217	3.968905143	0.334426043	11.86781022	1746-32	1256-30
ABUW_RS17965	ABUW_632	NZ_CP008706.1	629195	629869	+	WP_000739311.1		molecular chaperone	944.5360165	3.893473336	0.435833506	8.933365337	4.101-19	7.826-18
ABUW_RS1860	ABUW_2458	NZ_CP008706.1	2446955	2450347	+	WP_01015762.1		indolepyruvate ferredoxin oxidoreductase family protein	10779.54997	3.872748536	0.302463429	0.28402245	1566-37	1616-35
ABUW_RS17380	no	NZ_CP008706.1	1498801	1499580	+	WP_000498738.1		DUF1295 domain-containing protein	97.9004677	3.8693316	0.308393634	0.52176729	5.686-36	5.086-34
ABUW_RS1760	ABUW_1467	NZ_CP008706.1	1456977	1457951	+	WP_000947654.1		hypothetical protein	1143.003934	3.853622604	0.444583609	6.667936744	4.406-18	7.516-17
ABUW_RS15080	ABUW_3106	NZ_CP008706.1	3269503	3269103	+	WP_0001022216.1	lysM	peptidoglycan-binding protein LysM	1616.12442	3.795257226	0.264571792	14.34490502	1.166-46	2.726-44
ABUW_RS15616	ABUW_3217	NZ_CP008706.1	3296331	3295046	+	WP_000629034.1	add	adenosine deaminase	916.2637994	3.75536916	0.410884296	0.074746345	1.165-19	2.286-18
ABUW_RS17970	ABUW_633	NZ_CP008706.1	6259579	6260338	+	WP_000873962.1		fimbriin/biogenesis outer membrane usher protein	2616.722310	3.743076367	0.350741028	0.67190907	1395-26	5.446-25
ABUW_RS17015	ABUW_1458	NZ_CP008706.1	1457939	1458733	+	WP_000556984.1		PGS-L family deacetylase	1665.510356	3.734004235	0.441979491	8.45320381	2.836-17	4.436-16
ABUW_RS1016	ABUW_325	NZ_CP008706.1	350523	350966	+	WP_01019905.1		hemerythrin domain-containing protein	1429.973452	3.728553171	0.265558201	11.04043692	8.626-45	1.696-42
ABUW_RS1805	ABUW_886	NZ_CP008706.1	8817347	8818177	+	WP_000542602.1		alpha/beta hydrolase	3697.717142	3.683369301	0.277257974	0.284891961	2.835-40	3.966-38
ABUW_RS14240	ABUW_2933	NZ_CP008706.1	2947306	2948451	+	WP_000731756.1		galactose mutarotase	4310.777044	3.68317388	0.273909248	0.44645109	3.236-41	3.346-39
ABUW_RS15335	ABUW_3168	NZ_CP008706.1	3185300	3185527	-	WP_000437051.1		hypothetical protein	2521.1945201	3.6518056	0.344027806	0.63242497	2.026-26	7.836-25
ABUW_RS18175	ABUW_2440	NZ_CP008706.1	2424904	2424941	+	WP_000102046.1		hypothetical protein	33008.50582	3.633610859	0.448548967	0.80019689	5.466-16	7.366-15
ABUW_RS180730	ABUW_1379	NZ_CP008706.1	1392461	1392441	-	WP_000720499.1		hypothetical protein	1322.809218	3.61907881	0.381804467	0.476260491	2.646-21	6.006-20
ABUW_RS18160	ABUW_3122	NZ_CP008706.1	3142445	3143296	+	WP_010064773.1	otsB	trihaloacetyl-phosphatase	1639.033208	3.610775327	0.581340728	6.21110708	5.266-10	3.686-9
ABUW_RS18030	ABUW_0687	NZ_CP008706.1	691498	691692	+	WP_00184681.1		entericidin A/B family lipoprotein	8296.695798	3.574726165	0.31761028	11.25504424	2.195-29	1.161-27
ABUW_RS17460	ABUW_3587	NZ_CP008706.1	3645893	3646249	-	WP_010348511.1		hypothetical protein	928.7160039	3.51074605	0.302091622	1.58916667	6.686-31	2.866-29
ABUW_RS15010	ABUW_2456	NZ_CP008706.1	2444505	2445507	+	WP_010088910.1		hydrosymethylglutaryl-CoA lyase	5990.797706	3.50963561	0.286925559	0.23149491	2.116-34	1.775-32
ABUW_RS18680	ABUW_2437	NZ_CP008706.1	2423677	2427086	-	WP_011416606.1		iron-containing redox enzyme family protein	6730.665542	3.508204892	0.416299943	8.447440363	2.996-17	4.636-16
ABUW_RS10445	ABUW_2149	NZ_CP008706.1	2103817	2104053	+	WP_000917295.1		hypothetical protein	249.4369008	3.502933502	0.335649956	0.43620861	1.696-25	5.936-24
ABUW_RS14885	ABUW_3026	NZ_CP008706.1	3051874	3052251	+	WP_010059437.1		VOC family protein	105.498137	3.465588761	0.36880189	9.396699054	5.636-21	1.256-19
ABUW_RS10170	ABUW_1259	NZ_CP008706.1	274727	274916	+	WP_0111063.1		bifunctional SulP family inorganic anion transporter/carbonic anhydrase	5543.887225	3.441669228	0.28191038	12.216693	2.536-24	2.086-22
ABUW_RS10040	ABUW_2686	NZ_CP008706.1	2675924	2676382	+	WP_010107310.1		hypothetical protein	1393.98074	3.400054986	0.382555224	8.893197862	6.165-19	1.101-17
ABUW_RS10045	ABUW_0070	NZ_CP008706.1	73167	73074	-	WP_000433854.1	fahA	fumarylacetoacetase	12787.00428	3.386101635	0.367107175	9.225419564	2.826-20	5.966-19
ABUW_RS10745	ABUW_2627	NZ_CP008706.1	2623944	2624381	+	WP_000760328.1		DUF1714 domain-containing protein	199.144426	3.352668296	0.350502029	9.44331444	3.161-21	8.086-20
ABUW_RS10080	ABUW_2674	NZ_CP008706.1	2667054	2667324	-	WP_000072985.1		hypothetical protein	324.4146914	3.31418586	0.462920234	7.5030223	8.116-13	8.076-12
ABUW_RS10040	ABUW_0069	NZ_CP008706.1	73148	73180	-	WP_000781235.1	malA	malic/acetoacetate isomerase	4447.88604	3.302583973	0.37939189	8.832046791	1.036-18	1.876-17
ABUW_RS14205	ABUW_3579	NZ_CP008706.1	3637107	3638266	+	WP_000846679.1		hypothetical protein	4553.25095	3.270973926	0.323893166	14.04495514	8.276-45	1676-42
ABUW_RS17370	ABUW_611	NZ_CP008706.1	616874	616975	+	WP_000025860.1		DUF1365 domain-containing protein	33.01958007	3.25761632	0.339518167	9.594925336	8.406-22	2.016-20
ABUW_RS14305	ABUW_1111	NZ_CP008706.1	1109458	1109751	+	WP_011834711.1		aldolhyde dehydrogenase family protein	429.1319369	3.240160214	0.268637068	12.0164002	1.696-33	1.361-31
ABUW_RS17100	ABUW_3515	NZ_CP008706.1	3563387	3564333	+	WP_010107911.1		DnaJ domain-containing protein	9860.619669	3.191991324	0.26981131	11.83041471	2.735-32	1.926-30
ABUW_RS18190	ABUW_2503	NZ_CP008706.1	2499783	2499547	-	WP_011691036.1		c-glycine b	789.4186292	3.19999399	0.2743718457	11.62102025	3.046-31	1.196-29
ABUW_RS100325	ABUW_0066	NZ_CP008706.1	703783	71438	+	WP_000351863.1	hspD	4-hydroxyphenylpyruvate dioxygenase	9314.533216	3.155676109	0.325481082	0.6995412106	3.166-22	8.046-21
ABUW_RS11605	ABUW_1323	NZ_CP008706.1	1343284	1344174	+	WP_000040106.1		trihaloacetyl-phosphate synthase	2544.358405	3.155091272	0.414693146	7.608250211	2.786-14	3.106-13
ABUW_RS10070	ABUW_1767	NZ_CP008706.1	1763246	1763246	+	WP_000185571.1		hypothetical protein	4077.391826	3.104375242	0.356921672	8.781689346	1.616-18	2.876-17
ABUW_RS100335	ABUW_0068	NZ_CP008706.1	72582	73130	-	WP_000101645.1		VOC family protein	2410.96893	3.126892997	0.340576342	8.822088966	1.105-18	2.026-17
ABUW_RS18105	ABUW_2097	NZ_CP008706.1	2079357	2079998	+	WP_000312583.1		CoA transferase subunit B	6393.216324	3.116378901	0.340243458	9.95056426	5.236-20	1.086-18
ABUW_RS17465	ABUW_3588	NZ_CP008706.1	3644663	3644628	-	WP_000738603.1		hypothetical protein	843.7289397	3.11438349	0.300374286	0.36384555	3.456-25	1.176-23
ABUW_RS10715	ABUW_1672	NZ_CP008706.1	1640763	1641233	+	WP_01102885.1		BLUF domain-containing protein	695.9784372	3.102019094	0.191054931	6.29274403	1.116-59	6.406-57
ABUW_RS10305	ABUW_0732	NZ_CP008706.1	738671	738946	+	WP_010095768.1	hchA	protein deglycase HchA	637.2567347	3.103256601	0.249912332	0.51936165	1.656-36	1.546-34
rRNA103	no	no	no	no	no	no	no	no	no	no	no	no	no	no
ABUW_RS11425	ABUW_2349	NZ_CP008706.1	2350333	2350922	+	WP_000084509.1		tautomerase family protein	1324.073997	3.085732225	0.273301488	0.66882637	8.806-37	8.446-35
ABUW_RS18120	ABUW_2450	NZ_CP008706.1	2436477	2438171	+	WP_011819733.1		AMP-binding protein	1167.16743	3.048869748	0.315210586	9.672485251	3.956-22	9.946-21
ABUW_RS18170	ABUW_2439	NZ_CP008706.1	2438766	2438987	+	WP_000108365.1		hypothetical protein	139.181858	3.04182777	0.624724687	8.869090262	1.105-06	5.006-06
ABUW_RS10235	ABUW_2516	NZ_CP008706.1	2507870	2508622	+	WP_010177914.1		hypothetical protein	11.8609751	3.013362368	0.757224763	3.97948207	6.916-05	0.000224227
ABUW_RS00405	ABUW_641	NZ_CP008706.1	645128	644379	+	WP_000179474.1		hypothetical protein	1723.860466	2.999672973	0.326234539	9.22107056	2.896-20	6.066-19
ABUW_RS10760	ABUW_1449	NZ_CP008706.1	1458708	1459307	+	WP_010086127.1		class ISAM-dependent methyltransferase	106.371645	2.986716238	0.43710294	6.854783032	7.146-12	6.316-11
ABUW_RS11616	ABUW_2449	NZ_CP008706.1	2435735	2436406	-	WP_010029902.1		class ISAM-dependent methyltransferase	576.580408	2.96234848	0.29565898	0.02258021	1.176-23	3.096-22
ABUW_RS1750	ABUW_2628	NZ_CP008706.1	2624476	2625789	+	WP_000659371.1		MFS transporter	81.183458	2.957433589	0.291771075	10.5681804	3.096-24	1.006-22
ABUW_RS14940	ABUW_3798	NZ_CP008706.1	3851808	3852050	+	WP_010063828.1		SDR family NAD(P)-dependent oxidoreductase	290.2397891	2.882032964	0.75			

ABLU_RS1800	ABLU_2066	NZ_CP008706.1	2078651	2079355	+	WP_00145567.1				CoA transferase subunit A	2383.51861	2.4	8222708	0.327727942	7.378747432	1.606E-13	1.686E-12
ABLU_RS19290	ABLU_2738	NZ_CP008706.1	2727699	2728505	+	WP_001237338.1				peptidoglycan DD-metalloendopeptidase family protein	5315551463	2.39656669	0.204247289	11.73364977	8.576E-32	5.666E-30	
ABLU_RS07875	ABLU_634	NZ_CP008706.1	633239	633348	+	WP_000055567.1				spore coat protein U domain-containing protein	1453.5572	0.18769403	0.287606891	8.281933649	1.22E-16	1.78E-15	
ABLU_RS14540	ABLU_2372	NZ_CP008706.1	2354857	235868	-	WP_000784879.1				DUF1827 family protein	58.86948507	2.373543996	0.449274566	5.283058907	1.27E-07	6.60E-07	
ABLU_RS18416	ABLU_3782	NZ_CP008706.1	3842838	3843828	-	WP_001972911	mmsB			3-hydroxyisobutyrate dehydrogenase	414.5369476	2.68283585	0.474824825	4.987720646	6.16E-07	2.87E-06	
ABLU_RS15040	ABLU_2354	NZ_CP008706.1	2338683	2337728	-	WP_00053318.1				ArcZ family transcriptional regulator	652.444455	3.367223986	0.235359522	10.05790615	5.48E-24	2.57E-22	
ABLU_RS07179	ABLU_4959	NZ_CP008706.1	48570	486600	+	WP_000340891.1				DMF family transporter	397.9876608	2.364830327	0.225391972	10.492196	9.39E-26	3.47E-24	
ABLU_RS02102	ABLU_061	NZ_CP008706.1	970584	971790	+	WP_000718056.1	wecB			UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	119151954	2.358708409	0.21974584	10.81854	3.02E-27	1.35E-25	
ABLU_RS18080	ABLU_0302	NZ_CP008706.1	325841	326923	+	WP_001246387.1				TPM domain-containing protein	2347.525946	2.352928393	0.15829828	6.4971489	3.63E-54	1.33E-51	
ABLU_RS14500	ABLU_2161	NZ_CP008706.1	214204	214274	+	WP_000193456.1				DUF937 domain-containing protein	594.584944	2.349856548	0.02861844	18.2710084	1.4E-74	1.89E-71	
ABLU_RS02300	ABLU_0468	NZ_CP008706.1	481271	4815	+	WP_000462894.1				DUF2789 domain-containing protein	2297.593528	2.341588567	0.302699321	7.7356915	1.03E-14	1.24E-13	
ABLU_RS18500	ABLU_3395	NZ_CP008706.1	3438237	3439439	+	WP_000236000.1				acetate kinase	893.192592	2.343474746	0.27291897	8.5789191	9.58E-18	1.56E-16	
ABLU_RS02135	no	NZ_CP008706.1	948830	948864	+	WP_085916973.1				hypothetical protein	15.93345802	2.324706434	0.9623641	2.45620485	0.016708425	0.03036918	
ABLU_RS03310	ABLU_0673	NZ_CP008706.1	676016	676357	+	WP_000929502.1				YegP family protein	166.384488	2.314207624	0.20948092	7.71963638	1.18E-14	1.42E-13	
ABLU_RS11405	ABLU_2345	NZ_CP008706.1	2328341	2328676	+	WP_000736693.1				hypothetical protein	40.42819239	2.302817964	0.68122482	3.380507874	0.00072352	0.0092454	
ABLU_RS05485	ABLU_2425	NZ_CP008706.1	241966	241950	-	WP_00125680.1				N-acetyltransferase	284.577192	2.288978411	0.24542007	9.537667072	1.46E-21	3.40E-20	
ABLU_RS14460	ABLU_2916	NZ_CP008706.1	296616	2966326	+	WP_001163531.1				DUF1275 domain-containing protein	47.0054831	2.283331802	0.30697898	7.03264832	2.03E-12	1.95E-11	
ABLU_RS05495	ABLU_0710	NZ_CP008706.1	716255	717043	+	WP_000086443.1				hypothetical protein	621506835	2.285386003	0.184192933	11.7740937	5.31E-32	3.69E-30	
ABLU_RS18045	ABLU_0210	NZ_CP008706.1	250283	250740	+	WP_000830596.1				hypothetical protein	3728.887349	2.277690943	0.44247751	5.14425886	2.69E-07	1.33E-06	
ABLU_RS09100	ABLU_2332	NZ_CP008706.1	2318483	231668	-	WP_000116649.1				amino acid ABC transporter permease	9259.293505	2.264359369	0.21407535	10.7617891	5.22E-27	2.26E-25	
ABLU_RS18745	ABLU_3524	NZ_CP008706.1	3580463	3580960	+	WP_000687235.1				hypothetical protein	3336.22511	2.258007391	0.325999941	6.92640284	4.32E-12	3.95E-11	
ABLU_RS18345	ABLU_2957	NZ_CP008706.1	2969192	2970799	+	WP_000170453.1				citronellal/enoyl-CoA hydratase family protein	160.5196267	2.243020204	0.269681924	8.19326167	8.92E-17	1.33E-15	
ABLU_RS05765	ABLU_181	NZ_CP008706.1	121929	121998	+	WP_001012655.1	baaf			bacAin biosynthesis functional isochromatase/aryl carrier protein	118143734	2.24008418	0.16183541	3.643370201	0.000209091	0.000787914	
ABLU_RS1464	no	no	no	no	no	no	no			hypothetical protein	73.42638533	2.238554241	0.392236579	5.707193	1.16E-08	6.78E-08	
ABLU_RS20090	no	NZ_CP008706.1	250335	250200	-					hypothetical protein	249.0829337	2.235237203	0.199740186	11.9072357	4.53E-29	2.22E-27	
ABLU_RS05485	ABLU_121	NZ_CP008706.1	1143807	114448	-	WP_000570321.1				DUF2238 domain-containing protein	178.3902381	2.223103578	0.269578444	8.246703792	1.63E-16	2.37E-15	
ABLU_RS18010	ABLU_0185	NZ_CP008706.1	206489	207181	+	WP_001015665.1				hypothetical protein	196.420462	2.219365858	0.280138682	7.92179323	2.34E-15	3.00E-14	
ABLU_RS02205	ABLU_060	NZ_CP008706.1	606341	607051	+	WP_001015665.1				hypothetical protein	1633.053233	2.21543085	0.231466026	9.5708193	1.04E-21	2.47E-20	
ABLU_RS18005	ABLU_2594	NZ_CP008706.1	258977	2586240	+	WP_00102394.1				glutathione-dependent formaldehyde dehydrogenase	678.6762962	2.203003839	0.46350006	4.75246192	2.01E-04	8.52E-06	
ABLU_RS19210	ABLU_2701	NZ_CP008706.1	268776	2687731	+	WP_001089621.1				four-helix bundle coagulin-binding protein	7279.886477	2.193630064	0.45810636	4.788219536	1.68E-06	7.22E-06	
ABLU_RS10335	ABLU_2301	NZ_CP008706.1	231463	2314840	-	WP_000347804.1				amino acid ABC transporter permease	1107.851938	2.191853455	0.245914686	8.90981029	5.1E-19	9.58E-18	
ABLU_RS05015	ABLU_062	NZ_CP008706.1	671798	6717203	+	WP_000774219.1				hypothetical protein	573.8837546	2.18775695	0.195249665	11.20541966	3.84E-29	1.93E-27	
ABLU_RS18005	ABLU_2639	NZ_CP008706.1	2637592	2638434	-	WP_001015665.1				universal stress protein	4035.483158	2.18674509	0.267991704	8.169750373	3.36E-16	4.63E-15	
ABLU_RS18425	ABLU_2145	NZ_CP008706.1	210417	210683	-	WP_000183702.1				hypothetical protein	1494.69286	2.17684855	0.287502168	7.5716204	3.69E-14	4.16E-13	
ABLU_RS05480	ABLU_182	NZ_CP008706.1	124268	1242738	+	WP_000914201.1				DUF3016 family protein	17912.05204	2.176157541	0.220869186	9.852686897	6.67E-23	1.08E-21	
ABLU_RS03285	ABLU_0667	NZ_CP008706.1	673231	673480	+	WP_001080594.1				SRPCC family protein	567.1695335	2.175994044	0.275586666	7.866849812	3.64E-15	4.16E-14	
ABLU_RS18040	ABLU_3779	NZ_CP008706.1	3839273	3840046	-	WP_001198691.1				enoyl-CoA hydratase	234.409076	2.16224494	0.329692942	6.558359813	5.44E-11	4.32E-10	
ABLU_RS18070	ABLU_2074	NZ_CP008706.1	2056008	2056409	-	WP_000207886.1				transcriptional repressor	45.75994753	2.16187436	0.1688537011	2.48909266	0.01026072	0.02570203	
ABLU_RS18010	ABLU_3525	NZ_CP008706.1	3589992	3582410	-	WP_000003544.1				polyphosphate-AMP phosphotransferase	2319.475915	2.15654709	0.193811788	11.129081	9.05E-29	4.29E-27	
ABLU_RS18005	ABLU_903	NZ_CP008706.1	903508	903933	-	WP_000706933.1				hypothetical protein	18.6996649	2.14605331	0.149380781	4.49034133	7.1E-06	2.74E-05	
ABLU_RS18490	ABLU_2778	NZ_CP008706.1	2771867	2772506	+	WP_000204068.1				p-hydroxycinnamoyl-CoA hydratase/lyase	2145.60844	2.144957691	0.268676948	7.225073223	5.01E-12	5.07E-12	
ABLU_RS18475	ABLU_3794	NZ_CP008706.1	3857309	3857416	-	WP_001678911				thrombospondin inhibitor 1a	947.513358	2.1481965	0.179316346	2.69155184	0.001710044	0.01930055	
ABLU_RS18475	ABLU_2968	NZ_CP008706.1	287768	2877877	+	WP_000696025.1				MTA and DUF4377 domain-containing protein	8392.94382	2.13182897	0.244927738	8.70299208	3.24E-18	5.61E-17	
ABLU_RS18010	ABLU_2099	NZ_CP008706.1	208150	2082762	+	WP_000095311.1				thiolase family protein	6876.388232	2.13102624	0.345558004	6.10772354	8.80E-10	4.66E-09	
ABLU_RS03090	ABLU_0628	NZ_CP008706.1	629273	629294	-	WP_001197332.1				peroxiredoxin	19.451928	2.0900552	0.369880542	5.75754847	8.53E-09	5.02E-08	
ABLU_RS05480	ABLU_1761	NZ_CP008706.1	175835	1758993	+	WP_000332547.1				SOS response-associated peptidase family protein	561.7380035	2.05816622	0.364420869	5.83352054	5.43E-09	3.37E-08	
ABLU_RS18075	ABLU_936	NZ_CP008706.1	934269	9363030	+	WP_000153428.1				SDR family NAD(P)-dependent oxidoreductase	290.9334479	2.0533896	0.317819015	6.687318639	1.27E-11	1.88E-10	
ABLU_RS18010	ABLU_0204	NZ_CP008706.1	220193	220301	+	WP_00006568.1				NAD-dependent succinate-semialdehyde dehydrogenase	4770.02411	2.01676474	0.310275935	6.789690913	2.02E-11	9.64E-11	
ABLU_RS18020	ABLU_0206	NZ_CP008706.1	23701	232327	-	WP_000046166.1				hydrolase	4210.509722	2.01584264	0.218780489	9.625393348	6.25E-22	1.54E-20	
ABLU_RS18010	ABLU_0402	NZ_CP008706.1	42931	429778	-	WP_000537110.1				DUF853 domain-containing protein	887.729717	2.01542679	0.18777292	10.6723899	1.37E-26	5.44E-25	
ABLU_RS18665	ABLU_2438	NZ_CP008706.1	2428002	2428481	+	WP_000442091.1				CinA family protein	165.3710782	2.00298232	0.178804981	2.16191607	0.000816962	0.01813449	
ABLU_RS18420	ABLU_3783	NZ_CP008706.1	384340	3843537	-	WP_001015665.1				CoA-acylating methylmalonate-semialdehyde dehydrogenase	1549.02384	2.089703291	0.394231435	3.300836291	1.16E-07	6.05E-07	
ABLU_RS05490	ABLU_093	NZ_CP008706.1	176045	176128	-	WP_000100225.1				universal stress protein	977.486021	2.081773856	0.368381927	5.667886609	1.45E-08	8.43E-08	
ABLU_RS18475	ABLU_2968	NZ_CP008706.1	982485	982485	+	WP_000100225.1				ly-like domain repeat protein	22263.86735	2.079178464	0.185425411	11.2159302	3.41E-29	1.74E-27	
ABLU_RS18070	ABLU_0186	NZ_CP008706.1	903708	903200	-	WP_000350280.1				chalcone isomerase family protein	37.63942864	2.070663789	0.487424381	4.247696922	2.16E-05	7.63E-05	
ABLU_RS18070	ABLU_2398	NZ_CP008706.1	3320447	3321067	-	WP_000556679.1				glutathione S-transferase N-terminal domain-containing protein	630.7528837	2.068534592	0.17562049	11.76310817	0.04E-32	4.18E-30	
ABLU_RS02210	ABLU_0466	NZ_CP008706.1	53496	54524	-	WP_000009845.1				NAD(P)-dependent alcohol dehydrogenase	6815103202	2.05590518	0.204756531	10.0409512	1.0E-23	3.01E-22	
ABLU_RS18010	ABLU_0301	NZ_CP008706.1	325229	325819	+	WP_000846931.1				LeuA family protein	2088.037787	2.054226119	0.194488797	10.56434522	4.36E-26	1.64E-24	
ABLU_RS04355	ABLU_0888	NZ_CP008706.1	884968	885664	+	WP_000722324.1				metalloprotease	338.452986	2.051581496	0.176363148	11.63271079	2.81E-31	1.80E-29	
ABLU_RS18130	ABLU_2772	NZ_CP008706.1	2730748	2731937	+	WP_001188805.1				NAD(P)-dependent aldo-keto reductase	1034.932471	2.0486104	0.26424674	7.73801021	9.99E-15	1.21E-13	
ABLU_RS18485	ABLU_2747	NZ_CP008706.1	277717	2771419	-	WP_00041178.1	nhpT			3-(3-hydroxy-phenyl)propanoate transporter MhpT	107.68182	2.040653383</					

ABUW_RS0730	ABUW_2623	NZ_CP008706.1	26 9612	2620562	-	WP_000398495.1	3-hydroxyacyl-CoA dehydrogenase	448.352468	1.8561793 N	0.20099221	9.235080854	2.586-20	5.47E-9
ABUW_RS03470	ABUW_0705	NZ_CP008706.1	7 90624	71695+	+	WP_000011634.1	palmitin-like phospholipase family protein	575.578925	1.855031936	0.186223739	9.96103031	2.25E-23	6.48E-22
ABUW_RS02325	ABUW_0566	NZ_CP008706.1	976659	677399	-	WP_010186266.1	hypothetical protein	389.360919	1.854366959	0.312036416	5.942790175	2.80E-09	1.80E-08
ABUW_RS03930	ABUW_0723	NZ_CP008706.1	9721401	172 8097	-	WP_000701849.1	hypothetical protein	989.8483279	1.855996586	0.434238337	4.26493586	2.00E-05	7.7E-05
ABUW_RS16320	ABUW_2930	NZ_CP008706.1	3008700	30 0085+	+	WP_000182787.1	MFS transporter	67.2518727	1.847673639	0.305544737	6.047092184	147E-09	9.76E-09
ABUW_RS07980	ABUW_6395	NZ_CP008706.1	933575	9334261	+	WP_010719965.1	glutathione S-transferase family protein	468.2076354	1.843748017	0.127 8228	6.780409793	120E-11	1.02E-10
ABUW_RS07320	ABUW_0501	NZ_CP008706.1	9417438	9483244	+	WP_01062699.1	paracatal-inducible protein A	223.192598	1.839418736	0.200998644	9.151089095	5.62E-20	1.1E-19
ABUW_RS0780	ABUW_2835	NZ_CP008706.1	2844057	2845301	-	WP_000077968.1	NADH:flavin oxidoreductase/NADH oxidase family protein	509.2274023	1.838764655	0.1819772	10.10878343	5.05E-24	1.59E-22
ABUW_RS00516	ABUW_0164	NZ_CP008706.1	115619	116089	+	WP_000619878.1	alpha/beta fold hydrolase	528.866829	1.8289071	0.174816235	10.4618361	1.29E-25	4.61E-24
ABUW_RS0610	ABUW_0555	NZ_CP008706.1	936813	9368323	-	WP_00093415.1	hemol uptake protein HemP	362.5923692	1.82626212	0.44217612	4.119684741	3.79E-05	0.0002064
ABUW_RS01780	ABUW_2783	NZ_CP008706.1	2778566	2779182	+	WP_000758290.1	DUF3237 domain-containing protein	23.8619091	1.81585251	0.593252597	3.06008995	0.00220611	0.00530024
ABUW_RS05535	ABUW_1011	NZ_CP008706.1	152314	153134	+	WP_000550750.1	peptidoglycan DD-metalloendopeptidase family protein	1068.61919	1.814919719	0.204163738	8.889810707	6.12E-19	1.10E-17
ABUW_RS16890	ABUW_3473	NZ_CP008706.1	3521217	3521822	-	WP_000053846.1	glutathione S-transferase family protein	525.787908	1.810978307	0.180349778	10.0416779	1.00E-23	3.01E-22
ABUW_RS18130	ABUW_2330	NZ_CP008706.1	2313406	2314149	-	WP_01012006.1	amino acid ABC transporter ATP-binding protein	1680.359521	1.819790193	0.235947615	7.674543315	1.66E-14	1.05E-13
ABUW_RS08585	ABUW_0763	NZ_CP008706.1	9781416	9781847	-	WP_000166020.1	CBS domain-containing protein	1330.439149	1.810522936	0.230804706	7.844393499	4.35E-15	5.43E-14
ABUW_RS12850	ABUW_2716	NZ_CP008706.1	2724274	2724762	+	WP_000941311.1	CuA family protein	155.6848475	1.808254377	0.300271105	6.022072543	1.72E-09	1.10E-08
ABUW_RS15045	ABUW_0190	NZ_CP008706.1	92345	923599	-	WP_000939852.1	pyrroline oxidase-dependent aminotransferase	1728.208527	1.803282628	0.27332448	6.59789192	4.18E-11	3.34E-10
ABUW_RS12720	ABUW_2620	NZ_CP008706.1	261902	2619454	+	WP_000406271.1	GNAT family N-acetyltransferase	105.6371502	1.80215958	0.290806357	6.196588265	5.76E-19	3.98E-09
ABUW_RS18335	ABUW_3663	NZ_CP008706.1	3722859	3723371	-	WP_000021638.1	signal peptide 8	237.5434144	1.801969904	0.316290518	5.71063247	1.1E-08	6.56E-08
ABUW_RS07435	ABUW_0523	NZ_CP008706.1	950451	9509553	-	WP_000166110.1	MFS transporter	920.0376374	1.79916019	0.379677758	4.806694044	1.53E-06	6.69E-06
ABUW_RS05220	ABUW_0663	NZ_CP008706.1	972681	974525	-	WP_000750598.1	hypothetical protein	1709.858461	1.790259626	0.243331414	7.35728938	1.68E-19	1.96E-17
ABUW_RS19670	ABUW_3835	NZ_CP008706.1	3903094	3903789	+	WP_000724221.1	FKBP-type peptidyl-prolyl cis-trans isomerase	2235.055058	1.788166039	0.11471886	12.0178791	1.68E-16	1.54E-14
ABUW_RS1965	ABUW_3217	NZ_CP008706.1	3319966	3320394	-	WP_000145162.1	DedA family protein	93.2177623	1.782836995	0.21478538	8.300550598	1.04E-16	1.02E-15
ABUW_RS1045	ABUW_0274	NZ_CP008706.1	292407	293291	-	WP_010986587.1	hypothetical protein	147.1923873	1.782556707	0.208631932	6.892268793	5.49E-12	4.95E-11
ABUW_RS1090	ABUW_2078	NZ_CP008706.1	2051405	2060097	-	WP_000971581.1	modB	68.9416177	1.77814367	0.263814613	6.74037825	1.57E-11	1.32E-10
ABUW_RS0540	ABUW_0109	NZ_CP008706.1	921071	92238	-	WP_010105141.1	multidrug ABC transporter permease subunit	911711007	1.771238536	0.21315538	8.30161009	9.60E-17	1.42E-15
ABUW_RS07880	ABUW_0672	NZ_CP008706.1	9560275	9561045	+	WP_000179335.1	3-hydroxyacyl-CoA dehydrogenase	810.3932237	1.767467254	0.331916657	5.32638114	1.00E-07	5.28E-07
ABUW_RS07330	ABUW_0503	NZ_CP008706.1	948909	9490616	+	WP_000791569.1	membrane integrity-associated transporter subunit PgC	656.8002325	1.76218801	0.18631858	9.461656484	3.03E-21	6.82E-20
ABUW_RS05520	ABUW_1028	NZ_CP008706.1	1150388	1150819	-	WP_000408888.1	hypothetical protein	1511078986	1.759958984	0.197266868	8.92187189	4.58E-19	8.83E-18
ABUW_RS12725	ABUW_0502	NZ_CP008706.1	9485252	9490199	+	WP_0002017679.1	MCE family protein	1568.249486	1.748394553	0.204732822	8.533984	1.34E-17	2.15E-16
ABUW_RS18335	ABUW_2432	NZ_CP008706.1	2405072	2420906	+	WP_000179391.1	hypothetical protein	217.5339558	1.746102263	0.30269828	5.768457821	8.00E-09	4.83E-08
ABUW_RS19710	ABUW_0401	NZ_CP008706.1	427121	428065	-	WP_000188888.1	flavohemoglobin	987.530162	1.742443908	0.183815728	9.254253261	2.18E-20	4.60E-19
ABUW_RS1940	ABUW_0303	NZ_CP008706.1	326917	327477	+	WP_000258946.1	TPM domain-containing protein	925.810824	1.74183327	0.174628085	9.97089927	2.05E-23	5.93E-22
ABUW_RS09020	ABUW_0186	NZ_CP008706.1	207347	209314	+	WP_010109472.1	betT	7935.009942	1.737385586	0.165469531	10.5009398	8.55E-26	3.16E-24
ABUW_RS1940	ABUW_0333	NZ_CP008706.1	356364	356402	+	WP_010189303.1	hypothetical protein	949.179822	1.736337874	0.24870795	7.066673553	1.99E-12	1.53E-11
ABUW_RS10275	ABUW_0280	NZ_CP008706.1	271694	271784	-	WP_010335486.1	SDR family NAD(P)-dependent oxidoreductase	1478.56875	1.73181082	0.41435291	3.75263516	0.00074966	0.00028042
ABUW_RS19410	ABUW_2374	NZ_CP008706.1	2360880	2361566	-	WP_01043289.1	hydrolase	277.700689	1.72701713	0.17150738	10.06162252	7.53E-24	2.31E-22
ABUW_RS12375	ABUW_0484	NZ_CP008706.1	494759	496164	+	WP_000020862.1	DUF1448 domain-containing protein	270.2034319	1.725938773	0.336490354	4.70936817	2.48E-06	1.04E-05
ABUW_RS15995	ABUW_2799	NZ_CP008706.1	2797240	2798104	+	WP_000972885.1	arginine N-succinyltransferase	767.8974429	1.721514605	0.3010975	4.410447925	1.02E-05	3.82E-05
ABUW_RS1660	ABUW_2606	NZ_CP008706.1	2599973	2600737	-	WP_000459607.1	LamB/YnfC family protein	1423.16541	1.720283479	0.336227357	4.762328888	1.91E-06	8.17E-06
ABUW_RS18330	ABUW_3607	NZ_CP008706.1	3685042	3689199	-	WP_000097519.1	2-methylcitrate synthase	378.1325659	1.717615679	0.274605059	6.249578114	4.12E-10	2.92E-09
ABUW_RS12725	ABUW_0505	NZ_CP008706.1	9504783	9505424	+	WP_000200064.1	hydrolase	833.8059455	1.719353206	0.205197846	8.33719192	7.56E-17	1.1E-16
ABUW_RS09965	ABUW_2052	NZ_CP008706.1	2001365	2011048	+	WP_000731911.1	type I fibrinolytic protein	6554.754857	1.71074423	0.59045565	2.897328917	0.003703549	0.00853112
ABUW_RS12725	ABUW_1173	NZ_CP008706.1	1199398	1200879	+	WP_01019782.1	bauD	55.6408655	1.71064442	0.871661984	1.962941523	0.049652969	0.08287505
ABUW_RS19325	ABUW_2643	NZ_CP008706.1	2641074	2643216	-	WP_000088402.1	type I secretion system permease/ATPase	5868.684779	1.706891542	0.270718849	8.234373925	1.80E-16	2.16E-15
ABUW_RS1775	ABUW_3045	NZ_CP008706.1	3071469	3072122	-	WP_000102241.1	OmpA family protein	37602.819175	1.705793141	0.239239133	7.100075764	1.00E-12	9.84E-12
ABUW_RS19475	ABUW_0175	NZ_CP008706.1	970791	970868	+	WP_000086053.1	gpbD	1006.051678	1.703237528	0.208603409	6.118254804	4.73E-16	6.44E-15
ABUW_RS12550	ABUW_0912	NZ_CP008706.1	930842	9308825	+	WP_000483551.1	hypothetical protein	39.98401575	1.699189928	0.456632094	3.721105573	0.000198329	0.000593661
ABUW_RS10225	ABUW_0683	NZ_CP008706.1	2672874	2674088	+	WP_000464802.1	MFS transporter	64.17278191	1.692888036	0.409568114	4.132180878	3.58E-05	0.00022575
ABUW_RS02070	ABUW_2055	NZ_CP008706.1	205548	205717	+	WP_010990830.1	PQQ-dependent sugar dehydrogenase	379.1106739	1.692234852	0.34226748	4.944182553	7.65E-07	3.03E-06
ABUW_RS10095	ABUW_3310	NZ_CP008706.1	3347544	33478368	+	WP_000230434.1	NAD(P)transhydrogenase subunit alpha	263.9247905	1.691971965	0.30108196	5.61054887	1.92E-08	1.1E-07
ABUW_RS17816	ABUW_3310	NZ_CP008706.1	33719569	33719135	+	WP_001144958.1	hypothetical protein	2023.442237	1.685564845	0.204504393	8.242193829	1.69E-16	2.45E-15
ABUW_RS07785	no	NZ_CP008706.1	949589	9506335	+	WP_000344589.1	class I SAM-dependent methyltransferase	356.6557737	1.685437254	0.17018898	9.907524045	3.86E-23	1.1E-21
ABUW_RS18860	ABUW_2234	NZ_CP008706.1	2221720	2221885	+	WP_000160911.1	malate synthase O	9215.426337	1.683874881	0.177955678	9.462330962	3.01E-21	6.82E-20
ABUW_RS0685	ABUW_0175	NZ_CP008706.1	93311	932520	+	WP_010229651.1	acs	803.180253	1.681705055	0.218192925	7.707775742	1.28E-14	1.03E-13
ABUW_RS19330	ABUW_3888	NZ_CP008706.1	3955453	3956826	+	WP_000550111.1	acetyl-L-alanine-CoA ligase	644.7231233	1.679985194	0.197683642	8.493531739	1.92E-17	3.06E-16
ABUW_RS10110	ABUW_0022	NZ_CP008706.1	25685	27193	+	WP_000122715.1	rydI	554.7221023	1.679885194	0.197683642	8.493531739	1.92E-17	3.06E-16
ABUW_RS16440	ABUW_3383	NZ_CP008706.1	3421482	3422033	-	WP_000669565.1	sodium-dependent transporter	9886.94454	1.678451177	0.162646085	9.97619062	1.94E-23	5.66E-22
ABUW_RS19305	ABUW_2781	NZ_CP008706.1	2776038	2777107	+	WP_010105439.1	phosphatase PAPZ family protein	303.082145	1.678505723	0.277227002	6.04741066	147E-09	9.75E-09
ABUW_RS08085	ABUW_659	NZ_CP008706.1	652339	652770	+	WP_000720299.1	acyl-CoA dehydrogenase family protein	186.856032	1.67721957	0.34519568	4.854165459	1.2E-06	5.36E-06
ABUW_RS04040	ABUW_0648	NZ_CP008706.1	642594	6448229	+	WP_000345328.1	hypothetical protein	280.6947332	1.669387972	0.52119193	3.203010666	0.01059657	0.00398035
ABUW_RS19290	ABUW_3757	NZ_CP008706.1	381340	3813777	-	WP_000483007.1	mechanosensitive ion channel	716.742863	1.668174571	0.226385196	7.40139001	1.31E-12	1.42E-11
ABUW_RS0250	ABUW_0051	NZ_CP008706.1	57168	57370	-	WP_000101016.1	DoxK family protein	809.620673	1.667422146	0.21021042	7.932165588	2.15E-15	2.78E-14
ABUW_RS19165	ABUW_0338	NZ_CP008706.1	356589	361739	-	WP_000161216.1	Hfl family protein	869.365297	1.66441632	0			

ABLUW_RS05845	ABLUW_1817	NZ_CP008706.1	Q230382	Q232757	+	WP_001076822.1	xdhB	xanthine dehydrogenase molybdopterin binding subunit	356.2719751	1.536075931	0.21007227	7.27973192	3.34E-13	3.43E-12
ABLUW_RS0285	ABLUW_3352	NZ_CP008706.1	3383869	3388941	+	WP_00043984.1		TetR/AcrR family transcriptional regulator	492.5632601	1.53394459	0.33254176	4.6912041	3.9E-06	1.58E-05
ABLUW_RS07295	ABLUW_1406	NZ_CP008706.1	482282	1483769	-	WP_001205021.1	proP	glycine betaineL-proline transporter ProP	676.2205604	1.5268185	0.20071927	7.607053084	2.80E-14	3.21E-13
ABLUW_RS0720	ABLUW_0885	NZ_CP008706.1	867406	88148	-	WP_07939453.1		Ig-like domain-containing protein	50908.24393	1.51951849	0.204476246	7.426385811	1.0E-13	1.20E-12
ABLUW_RS0485	ABLUW_3796	NZ_CP008706.1	3853034	3859005	-	WP_000428563.1		DUF003 domain-containing protein	938.690774	1.51705158	0.680599503	2.230710583	0.02570308	0.046705999
ABLUW_RS04225	ABLUW_0822	NZ_CP008706.1	798369	798366	-	WP_000397562.1		NrdH family protein	2194.719324	1.515815582	0.90343748	9.382685556	1.06E-43	1.86E-41
ABLUW_RS06019	ABLUW_931	NZ_CP008706.1	827259	827307	+	WP_000566027.1		3-oxoacid CoA-transferase subunit A	93.05892272	1.515435192	0.339265873	4.466807047	7.94E-06	3.03E-05
ABLUW_RS02255	ABLUW_0052	NZ_CP008706.1	57715	58452	-	WP_000100767.1		dienelactone hydrolase family protein	902.252445	1.51164891	0.257863523	5.861957032	4.57E-09	2.86E-08
ABLUW_RS05445	ABLUW_1103	NZ_CP008706.1	115668	103389	+	WP_000469453.1		alpha-keto acid decarboxylase family protein	4938.377473	1.516447418	0.425871808	3.546720105	0.000390059	0.001005166
ABLUW_RS016	ABLUW_0308	NZ_CP008706.1	331925	331908	-	WP_000090000.1		RdA family protein	674.7818872	1.510248523	0.250254819	6.034847783	1.59E-09	1.05E-08
sRNA44	no	no	no	no	no	no	no	no	4.738178039	1.504838415	1.474266479	1.020737049	0.307379037	0.391784289
ABLUW_RS09990	ABLUW_2057	NZ_CP008706.1	2036942	2038051	-	WP_000842128.1		S-(hydroxymethyl)glutathione dehydrogenase/class II alcohol dehydrog	17.8.705206	1.502205697	0.220346622	6.8201894	9.09E-12	7.89E-11
ABLUW_RS02070	ABLUW_1604	NZ_CP008706.1	904447	904743	-	WP_001277236.1		antibiotic biosynthesis monooxygenase	316.8657159	1.502448948	0.267610444	5.614250644	1.97E-08	1.10E-07
ABLUW_RS0295	ABLUW_2739	NZ_CP008706.1	2728502	2728927	-	WP_001626236.1		GNAT family N-acetyltransferase	2318182866	1.50072552	0.2222926	6.751026745	1.47E-11	1.24E-10
ABLUW_RS0650	ABLUW_2604	NZ_CP008706.1	2597539	2599122	-	WP_001211794.1		S-oxoprolinase/urea amidolyase family protein	1866.678075	1.499219069	0.33510662	4.47379698	7.68E-06	2.95E-05
ABLUW_RS07845	ABLUW_3269	NZ_CP008706.1	3298425	3301932	-	WP_000276867.1		DUF2338 domain-containing protein	2260.401498	1.497742146	0.1995317	10.70737394	9.99E-27	4.11E-25
ABLUW_RS0420	ABLUW_3664	NZ_CP008706.1	3723375	3724271	-	WP_000041516.1		cation transporter	432.966502	1.496882832	0.316921678	4.723196322	3.32E-06	9.72E-06
ABLUW_RS04365	ABLUW_0890	NZ_CP008706.1	886161	886588	-	WP_000966782.1		universal stress protein	938.0748339	1.490726744	0.235196017	6.619962504	3.59E-11	2.90E-10
ABLUW_RS06665	ABLUW_0951	NZ_CP008706.1	955994	951000	+	WP_000070815.1		amino acid permease	5173.800192	1.488236062	0.173240086	8.590740472	8.64E-19	1.42E-18
ABLUW_RS06990	ABLUW_0794	NZ_CP008706.1	978189	9782352	-	WP_012300594.1		DUF2750 domain-containing protein	602.0149776	1.48325191	0.239641989	6.212304348	5.29E-10	3.05E-09
ABLUW_RS01760	ABLUW_0359	NZ_CP008706.1	382230	382661	-	WP_001068069.1		hypothetical protein	9108.50719	1.486030854	0.240669264	6.1745768	6.83E-10	4.56E-09
ABLUW_RS05915	ABLUW_1174	NZ_CP008706.1	1195359	1197206	+	WP_000916246.1	basA	acinetobactin non-ribosomal peptide synthetase subunit BasA	355.4579555	1.485455667	0.427764428	3.47260214	0.000516439	0.001147545
ABLUW_RS05730	ABLUW_1124	NZ_CP008706.1	9200879	9201826	+	WP_001232851.1	bauC	ferric acinetobactin ABC transporter/permease subunit BauC	11718198332	1.4837130227	0.517987241	2.559579576	0.016479886	0.02199516
ABLUW_RS02475	ABLUW_0851	NZ_CP008706.1	831133	832101	+	WP_00117768.1		DUF3298 domain-containing protein	908.029615	1.482974258	0.173626498	8.51671467	1.33E-17	2.10E-16
ABLUW_RS05885	ABLUW_2105	NZ_CP008706.1	2143272	2149474	-	WP_000999401.1		aminopeptidase P family protein	2804.592152	1.478419376	0.171445545	8.623218366	6.51E-18	1.08E-16
ABLUW_RS02610	ABLUW_0300	NZ_CP008706.1	2185823	2186842	-	WP_001103350.1		alpha-ketolactol dehydrogenase subunit beta	780.1459166	1.474117254	0.57086366	2.550095008	0.016769357	0.02107522
ABLUW_RS0440	ABLUW_3179	NZ_CP008706.1	3208785	3207138	+	WP_001047855.1		hypothetical protein	5018516851	1.472689326	0.327183551	4.501049401	6.76E-06	2.62E-05
ABLUW_RS02280	ABLUW_2642	NZ_CP008706.1	2633887	2641077	-	WP_000003555.1		Hyd family type I secretion periplasmic adaptor protein	2921.445758	1.471939997	0.170505377	8.408810061	4.14E-17	6.39E-16
ABLUW_RS0885	ABLUW_3899	NZ_CP008706.1	3960387	3966355	-	WP_000592161.1		DabC family protein	7715166579	1.464547073	0.153648953	9.531973883	1.55E-21	3.98E-20
ABLUW_RS02610	ABLUW_3347	NZ_CP008706.1	3382026	3383437	-	WP_000549965.1		TadD family hydrolase	435.8142991	1.46259819	0.226364337	3.416127091	1.04E-10	7.89E-10
ABLUW_RS01340	ABLUW_0438	NZ_CP008706.1	644205	642330	-	WP_001267639.1		acetyl-CoA C-acetyltransferase	289.0172666	1.4585959376	0.222595541	6.554306394	5.59E-11	4.42E-10
ABLUW_RS01910	ABLUW_2468	NZ_CP008706.1	2432929	2435492	-	WP_001891586.1		hypothetical protein	362.5669837	1.458640184	0.306430445	4.759775692	1.94E-06	8.25E-06
ABLUW_RS0255	ABLUW_3750	NZ_CP008706.1	3806826	3807035	-	WP_000127662.1		OncC family protein	832.0265203	1.4571908002	0.136466095	10.68329834	1.22E-26	4.91E-25
ABLUW_RS02725	ABLUW_1542	NZ_CP008706.1	6294862	6329441	+	WP_000772583.1		transglutaminase family protein	1131.563833	1.457186962	0.231954238	6.290226976	3.17E-10	2.28E-09
ABLUW_RS01305	ABLUW_3152	NZ_CP008706.1	3178003	3179646	+	WP_000047790.1		MFS transporter	530.9016642	1.456554155	0.318240478	4.69419178	2.67E-06	1.9E-05
ABLUW_RS02800	ABLUW_084	NZ_CP008706.1	9078080	9080237	-	WP_000107859.1		iron-containing alcohol dehydrogenase	445.2221518	1.455710898	0.195244421	9.141675987	6.15E-20	1.26E-18
ABLUW_RS01915	no	NZ_CP008706.1	2656702	2657888	-			flavinectin type II domain-containing protein	552.3315222	1.449210537	0.151919748	9.545926036	1.35E-21	3.16E-20
ABLUW_RS01810	ABLUW_3314	NZ_CP008706.1	3341780	3341897	-	WP_001185468.1		Re/Ss-specific NAD(P)+[trans]hydrogenase subunit alpha	145.827742	1.444317827	0.322272623	4.481956436	7.40E-06	2.85E-05
ABLUW_RS03635	ABLUW_2188	NZ_CP008706.1	2172182	2173165	-	WP_000883676.1		SidA/Kcs/PuA family monooxygenase	1174.867092	1.442698752	0.544951822	2.6473877	0.0081163	0.06874589
ABLUW_RS0080	ABLUW_2076	NZ_CP008706.1	2057651	2058421	-	WP_001257948.1		SDR family oxidoreductase	273.1469539	1.442549007	0.68984836	2.09161688	0.036516691	0.063580704
ABLUW_RS01745	ABLUW_1540	NZ_CP008706.1	6282690	627840	+			circularly permuted type 2 ATP-grasp protein	880.105564	1.439724915	0.249953272	5.759976261	8.41E-09	5.05E-08
ABLUW_RS01730	ABLUW_0353	NZ_CP008706.1	375198	376667	+	WP_000707853.1	aadD	succinylglutamate-semialdehyde dehydrogenase	5428.672482	1.431644479	0.24199779	5.944360991	2.78E-09	1.79E-08
ABLUW_RS02725	ABLUW_1402	NZ_CP008706.1	149364	1480383	+	WP_002017500.1	csuE	iron fibrillar tip adhesin CsuE	294.4310251	1.43105079	1.112519792	1.286591474	NA	NA
ABLUW_RS0445	ABLUW_3018	NZ_CP008706.1	3042022	3044007	-	WP_001942919.1	ggt	gamma-glutamyltransferase	449.7010363	1.427366037	0.26646094	5.35319073	8.64E-08	4.59E-07
newcasid9A1	no	no	no	no	no	no	no	no	238.8279859	1.42587174	0.690023721	2.060437665	0.039356719	0.06799665
ABLUW_RS01940	ABLUW_3322	NZ_CP008706.1	3357579	3357882	-	WP_000853610.1		hypothetical protein	526.5199002	1.421410999	0.407556476	3.487649155	0.00487287	0.01047481
ABLUW_RS0685	ABLUW_3874	NZ_CP008706.1	3942424	3942759	+	WP_001214778.1		hypothetical protein	9141.807949	1.420822253	0.302336103	4.699478810	2.81E-06	1.08E-05
ABLUW_RS02330	ABLUW_0365	NZ_CP008706.1	9071663	9071659	-	WP_000007479.1		hypothetical protein	495.8730488	1.417344082	0.217400292	5.222338094	1.77E-07	8.95E-07
ABLUW_RS00860	ABLUW_0174	NZ_CP008706.1	92441	93016	-	WP_000457175.1		DUF805 domain-containing protein	929.161979	1.40955649	0.255007049	5.526240855	3.27E-08	1.83E-07
ABLUW_RS07445	ABLUW_0255	NZ_CP008706.1	9510787	9510985	+	WP_00034780.1		dicarboxylate/amino acid cation symporter	2719.46729	1.40685008	0.267157406	5.7223793	1.35E-07	6.96E-07
ABLUW_RS01775	ABLUW_2834	NZ_CP008706.1	2843490	2843508	-	WP_000744506.1		hypothetical protein	388.7433293	1.408121594	0.300350649	4.688258873	2.76E-06	1.14E-05
ABLUW_RS06020	ABLUW_3214	NZ_CP008706.1	3245260	3244686	-	WP_001018416.1		acyl-CoA dehydrogenase	403.7460432	1.408007211	0.314010765	4.483026838	7.33E-06	2.82E-05
ABLUW_RS04455	ABLUW_1812	NZ_CP008706.1	3209555	3209176	-	WP_000143214.1		hypothetical protein	957.327806	1.4033388023	0.222746925	6.3003699	2.97E-10	2.56E-09
ABLUW_RS02885	ABLUW_914	NZ_CP008706.1	9058083	910682	+	WP_000925702.1	cfpA	ATP-dependent Clp protease ATP-binding subunit CfpA	1541.19663	1.4022195226	0.176238376	7.956809743	1.77E-15	2.29E-14
ABLUW_RS03135	ABLUW_0637	NZ_CP008706.1	638689	641004	-	WP_001274334.1		enoyl-CoA hydratase/isomerase family protein	431.7447847	1.401010393	0.191077734	7.737728796	1.01E-14	1.22E-13
ABLUW_RS02610	ABLUW_0296	NZ_CP008706.1	913234	914746	+	WP_000004363.1		hypothetical protein	65.42528158	1.399030194	0.178960928	0.51050505	5.30E-07	2.51E-06
ABLUW_RS03030	ABLUW_2644	NZ_CP008706.1	2644321	2644678	-	WP_000927323.1		TadC family protein	3198.817316	1.389446905	0.179504039	7.740492171	9.90E-15	12.9E-15
ABLUW_RS05425	ABLUW_1109	NZ_CP008706.1	1126361	1127734	+	WP_000107543.1		diaminobutyrate--2-oxoglutarate transaminase	9708.29737	1.388545465	0.180240037	7.703589873	1.32E-14	1.57E-13
ABLUW_RS01190	ABLUW_2660	NZ_CP008706.1	2656565	2656641	+	WP_00100885.1		right-handed parallel beta-helix repeat-containing protein	934.9875343	1.387811005	0.210215949	6.600947810	4.09E-11	3.27E-10
ABLUW_RS03175	ABLUW_0845	NZ_CP008706.1	651078	651431	+	WP_000457783.1		quaternary ammonium transporter	932.151407	1.38305974	0.335885705	4.180107706	3.82E-05	0.000103069
ABLUW_RS01910	ABLUW_3883	NZ_CP008706.1	3951063	3952395	-	WP_001024448.1		lytic murein transglycosylase	5129.302874	1.380027123	0.141467338	9.754473007	1.77E-22	4.68E-21
ABLUW_RS01145	ABLUW_2333	NZ_CP008706.1	2318780	2316673	-	WP_000830363.1		amino acid ABC transporter substrate-binding protein	5036.266782	1.379919525	0.196121062	8.306774883	9.83E-17	1.45E-16

ABUW_RS0785	ABUW_1474	NZ_CP008706.1	1462522	1462727	-	WP_000429477.1		LysE family translocator	32.9782845	1.307530772	0.495057035	2.64171987	0.00826977	0.01752965
ABUW_RS0735	ABUW_0354	NZ_CP008706.1	376685	3767028	+	WP_000679450.1	asbB	N-succinylserine dihydroase	6654.626774	1.296642293	0.238961731	5.42050404	5.76E-08	3.14E-07
ABUW_RS1065	ABUW_2316	NZ_CP008706.1	230949	2309878	+	WP_00037930.1		DMT family transporter	175.036352	1.29388828	0.33773704	3.838208977	0.00023935	0.000382631
ABUW_RS1015	ABUW_235475	NZ_CP008706.1	2354751	2355311	+	WP_0107021.1		chromate transporter	45.3277905	1.292935553	0.26903788	4.80587306	1.54E-06	6.68E-06
ABUW_RS0280	ABUW_0507	NZ_CP008706.1	62104	62393	-	WP_000349500.1		fomate/nitrite transporter family protein	4611.2045999	1.282227455	0.276696845	4.82769574	1.38E-06	6.06E-06
ABUW_RS0275	no	NZ_CP008706.1	2872923	2873043	-			outer membrane assembly protein BamE	91.843155	1.291877038	0.357624075	5.612388315	0.00030339	0.000870394
ABUW_RS0760	ABUW_801	NZ_CP008706.1	897695	897968	+	WP_00035155.1		hypothetical protein	922.387892	1.29269845	0.460751433	2.803394711	0.005056774	0.011802857
ABUW_RS0160	ABUW_0215	NZ_CP008706.1	238620	240507	+	WP_00068173.1		DMT family transporter	232.5210804	1.29189485	0.92425182	7.077095939	1.45E-12	1.40E-11
ABUW_RS0595	ABUW_018	NZ_CP008706.1	1254849	1256024	+	WP_000254959.1		hyphal-like peptidase domain-containing protein	2375.465078	1.290215479	0.90760301	6.763452881	1.35E-11	1.14E-10
sRNA85	no	no	no	no	no	no	no	no	93.6157108	1.290094273	0.359591513	3.66825743	0.000244209	0.00078714
ABUW_RS0060	ABUW_010	NZ_CP008706.1	125574	125115	-	WP_000995587.1		DUF924 domain-containing protein	1390.804249	1.287830108	0.206005203	6.251444559	4.07E-10	2.89E-09
ABUW_RS1430	ABUW_2952	NZ_CP008706.1	2967003	2967302	-	WP_000847096.1		hypothetical protein	5127333168	1.286983107	0.397967693	3.233888368	0.00022192	0.000388575
ABUW_RS1230	ABUW_2530	NZ_CP008706.1	252848	2528261	-	WP_001056842.1		enoyl-CoA hydratase/isomerase family protein	794.6383576	1.279187061	0.537588194	2.3749492472	0.07336497	0.033072323
ABUW_RS0140	ABUW_0210	NZ_CP008706.1	236055	236477	+	WP_000114353.1		GFA family protein	931271129	1.277918844	0.247549577	5.162274404	2.44E-07	1.22E-06
ABUW_RS0165	ABUW_0360	NZ_CP008706.1	382756	383175	-	WP_000644154.1		hypothetical protein	541.5244468	1.274962102	0.231959746	5.505079188	3.69E-08	2.05E-07
ABUW_RS0380	ABUW_2756	NZ_CP008706.1	2746479	2746706	-	WP_000608974.1		hypothetical protein	837.5659352	1.272040004	0.279778866	4.546590744	5.45E-08	2.15E-05
ABUW_RS1695	ABUW_2404	NZ_CP008706.1	2391629	2392222	-			GNAT family N-acetyltransferase	230.094805	1.2719212	0.204840517	6.209323924	5.32E-10	3.71E-09
ABUW_RS0320	ABUW_0656	NZ_CP008706.1	663238	663669	+	WP_000022555.1	mscL	large-conductance mechanosensitive channel protein MscL	1242.646456	1.27106975	0.92533198	9.564550504	3.29E-12	3.04E-11
ABUW_RS1790	ABUW_2405	NZ_CP008706.1	2392685	2393090	-	WP_000271521.1		FMN-binding negative transcriptional regulator	79.42476577	1.270874554	0.263662546	4.820079969	1.44E-06	6.27E-06
ABUW_RS1915	ABUW_2924	NZ_CP008706.1	2924229	2925553	-	WP_000859908.1		D-serine ammonia-lyase	372.3857111	1.267897379	0.154718046	8.786055007	2.85E-10	5.03E-10
ABUW_RS1055	ABUW_2477	NZ_CP008706.1	2470553	2471170	+	WP_000501111.1		CoA transferase	225.893551	1.267378211	0.216733891	5.84761435	4.96E-09	3.18E-08
ABUW_RS0260	ABUW_0662	NZ_CP008706.1	665299	669405	+	WP_000199613.1		NADH:flavin oxidoreductase/NADH oxidase	3052.869033	1.26520979	0.247364447	5.141760549	3.14E-07	1.53E-06
ABUW_RS0385	ABUW_0627	NZ_CP008706.1	62189	629011	-	WP_08106308.1		MBL fold metallo-hydrolase	210.8798223	1.264549611	0.257837132	4.900600279	9.29E-07	4.22E-06
ABUW_RS1410	ABUW_3781	NZ_CP008706.1	3841007	3842856	-	WP_000069576.1		AMP-binding protein	693.131288	1.263890244	0.39619082	3.19014382	0.00142212	0.000343656
ABUW_RS0255	no	NZ_CP008706.1	2657883	2658188	-			hypothetical protein	8.59415867	1.26244513	0.406072599	2.740438943	0.00615878	0.033262236
ABUW_RS1735	ABUW_2410	NZ_CP008706.1	2393842	2393962	-	WP_000357081.1		LyfR family transcriptional regulator	209.6247986	1.260309369	0.228361336	5.518926245	3.41E-08	1.91E-07
ABUW_RS0095	ABUW_0201	NZ_CP008706.1	224705	229147	+	WP_00010767.1		amino acid permease	1792.061029	1.25633921	0.322444329	3.89959116	9.78E-05	0.000308312
ABUW_RS0160	ABUW_0438	NZ_CP008706.1	450223	451008	+	WP_000049106.1		hypothetical protein	2001.125999	1.255735607	0.254462405	4.934857101	8.02E-07	3.68E-06
ABUW_RS0175	ABUW_969	NZ_CP008706.1	971084	971898	-	WP_02436202.1		alpha/beta fold hydrolase	26.56957756	1.255451505	0.446770722	2.810079628	0.004932924	0.190922459
ABUW_RS0590	ABUW_1142	NZ_CP008706.1	198985	198985	+	WP_000380475.1		carbon starvation protein A	4232.63448	1.253824472	0.323064035	3.81040095	0.00010401	0.000321916
ABUW_RS1630	ABUW_2187	NZ_CP008706.1	2107722	2172161	-	WP_000442353.1		DHA2 family efflux MFS transporter permease subunit	947.7523411	1.250928679	0.465132027	2.71566892	0.006695651	0.014327321
ABUW_RS0195	ABUW_1463	NZ_CP008706.1	186985	1869290	+	WP_00080869.1		YhdD/YjK family protein	918.5373678	1.250105802	0.308927444	4.046697107	5.19E-05	0.00117268
ABUW_RS1410	ABUW_2916	NZ_CP008706.1	292510	2927394	-	WP_000504186.1		TorB-dependent osimophore receptor	886.1762005	1.249275818	0.549058596	2.27530509	0.02287634	0.042280733
ABUW_RS1990	ABUW_2475	NZ_CP008706.1	2467822	247034729	-	WP_00034729.1		hypothetical protein	3881700127	1.248767085	0.248643301	5.022323474	5.1E-07	2.42E-06
ABUW_RS0285	ABUW_0686	NZ_CP008706.1	665299	499120	+	WP_000154085.1		acetyl-CoA carboxylase carboxyltransferase subunit	162.741279	1.24696846	0.392955711	3.173305346	0.00507109	0.003743689
ABUW_RS0430	ABUW_9336	NZ_CP008706.1	9336251	9337186	+	WP_00074595.1		LyfR family transcriptional regulator	72.10919392	1.244039398	0.288824858	4.30724491	1.65E-05	6.02E-05
ABUW_RS1950	ABUW_3485	NZ_CP008706.1	3533892	3534353	+	WP_000845422.1		DMT family transporter	497.964514	1.242067288	0.278285861	4.481327841	8.07E-06	3.08E-05
ABUW_RS1060	ABUW_2800	NZ_CP008706.1	2788101	2793956	-	WP_000558619.1		aspartate aminotransferase family protein	880.954841	1.23016625	0.310210855	4.070585512	4.69E-05	0.00156507
ABUW_RS0980	ABUW_945	NZ_CP008706.1	9442661	9443074	+	WP_000095345.1		YeeY/YeeD family protein	68.82664368	1.228971676	0.337805437	3.638164782	0.000274652	0.000801864
ABUW_RS1685	ABUW_3291	NZ_CP008706.1	3324165	3325793	+	WP_000253062.1		acyl-CoA synthetase	358.5102198	1.227681733	0.319798441	3.83892344	0.00023575	0.00082106
ABUW_RS1675	ABUW_2822	NZ_CP008706.1	2826369	2828339	-	WP_00020586.1		NADPH-dependent 2,4-dienoyl-CoA reductase	335.0566808	1.226621835	0.27341899	4.490786067	7.10E-06	2.74E-05
ABUW_RS0160	ABUW_0731	NZ_CP008706.1	731740	731468	+	WP_000530734.1		zinc-binding dehydrogenase	157.920871	1.219353759	0.1832351	7.244104332	4.35E-13	4.43E-12
ABUW_RS1930	ABUW_2845	NZ_CP008706.1	2859324	2859541	-	WP_000193631.1		BDN domain-containing protein	3342.155228	1.218336687	0.174653387	6.967104663	3.23E-12	3.00E-11
ABUW_RS0590	ABUW_0149	NZ_CP008706.1	217766	218119	+	WP_000580188.1		DUF1034 domain-containing protein	93.2869192	1.214519345	0.266371961	4.561204937	5.09E-06	2.02E-05
ABUW_RS0205	ABUW_0449	NZ_CP008706.1	461097	463320	-	WP_000479308.1		hypothetical protein	9463.97897	1.214293046	0.287193191	5.444625707	5.55E-08	2.17E-05
ABUW_RS1235	ABUW_2537	NZ_CP008706.1	2526793	2530052	-	WP_000470954.1		L-serine ammonia-lyase	1739.075033	1.210710584	0.10718851	7.710373068	1.23E-14	1.46E-10
ABUW_RS1425	ABUW_2951	NZ_CP008706.1	295519	2956986	-	WP_000191753.1		aromatic ring-hydroxylating dioxygenase subunit alpha	78.46639874	1.209949749	0.412562938	2.935825551	0.003333271	0.007744999
ABUW_RS0240	ABUW_0485	NZ_CP008706.1	468316	469595	-	WP_000893466.1		YjK family inner membrane protein	1344.179174	1.206023453	0.114969887	8.493309106	2.01E-17	3.17E-16
ABUW_RS0125	ABUW_0352	NZ_CP008706.1	374167	375198	+	WP_000973732.1	asfA	arginine N-succinyltransferase	7224.677006	1.204741605	0.255037893	4.723774822	2.32E-06	9.71E-06
ABUW_RS0145	ABUW_3784	NZ_CP008706.1	3844523	3844604	+	WP_00048101.1		LyfR family transcriptional regulator	200.997786	1.204022363	0.238688596	5.04432296	4.55E-07	2.81E-06
ABUW_RS0190	ABUW_987	NZ_CP008706.1	988336	989574	+	WP_000862283.1		NADH:flavin oxidoreductase/NADH oxidase family protein	186.0361411	1.201918536	0.278236216	4.304307504	1.68E-05	6.16E-05
ABUW_RS0195	ABUW_844	NZ_CP008706.1	850688	8507475	+	WP_000885644.1		Ippocin family protein	1024.444737	1.205601012	0.276274782	4.583119372	5.44E-08	2.97E-07
ABUW_RS04020	ABUW_0821	NZ_CP008706.1	797022	797876	-	WP_001843842.1		SPFHBand 7/PHB domain protein	2825.87831	1.200319344	0.190506406	10.0810267	6.69E-24	2.07E-22
ABUW_RS1970	ABUW_3489	NZ_CP008706.1	3538557	3539855	+	WP_000956920.1		ABC transporter	876.547017	1.194350211	0.195105005	6.61567875	9.27E-10	6.27E-09
ABUW_RS0325	ABUW_1710	NZ_CP008706.1	171822	171836	+	WP_01817654.1		MxaD/ThiS family protein	238.2220708	1.193727105	0.187786265	6.032488728	1.61E-09	1.06E-08
ABUW_RS0985	ABUW_961	NZ_CP008706.1	954682	955105	-	WP_001019442.1		universal stress protein	810.589663	1.192373357	0.270631674	2.640455464	2.91E-05	7.16E-05
ABUW_RS1135	ABUW_2911	NZ_CP008706.1	2925796	2921448	-	WP_00106195.1		ABC transporter ATP-binding protein	203.5853519	1.19182898	0.20283965	5.872041954	4.30E-09	2.71E-08
ABUW_RS1045	ABUW_2544	NZ_CP008706.1	2544882	2545296	-	WP_000720057.1		DUF333 domain-containing protein	3964.162147	1.190821719	0.310021699	3.166537108	7.29E-05	0.00235616
ABUW_RS0730	ABUW_1530	NZ_CP008706.1	1506658	1501699	+	WP_00083635.1		HAMP domain-containing histidine kinase	566.3884882	1.18593741	0.123403637	9.698256075	7.38E-22	1.80E-20
ABUW_RS01740	ABUW_0355	NZ_CP008706.1	378041	379705	+	WP_00150581.1	asfE	succinylglutamate desuccinylase	5243.551066	1.184453252	0.2036965	5.81479434	1.07E-09	3.73E-08
ABUW_RS1650	ABUW_3019	NZ_CP008706.1	3044311	3046334	-	WP_000857095.1		DHA2 family efflux MFS transporter permease subunit	462.2073541	1.182993784	0.278662374	4.27115869	1.94E-05	6.08E-05
ABUW_RS0540	ABUW_1753	NZ_CP008706.1	1742283	1749526	+	WP_000886601.1		hypothetical protein	493.58747	1.181222311	0.317350628	3.722103662	0.000917544	0.00059752
ABUW_RS0840	ABUW_196	NZ_CP008706.1	1203881	1203880	+	WP_0008								

ABUW_RS00670	ABUW_0135	NZ_CP008706.1	148721	149488	+	WP_001258761.1		transporter	7096.692988	1.10476705	0.13846375	7.99707593	127E-15	1.67E-14
ABUW_RS09310	ABUW_1912	NZ_CP008706.1	1913491	1914069	+	WP_002035810.1		TetR/AcrR family transcriptional regulator	59.5115441	1.101352199	0.64768459	1.700445273	0.089047202	0.13658718
ABUW_RS00690	ABUW_0139	NZ_CP008706.1	153753	154190	+	WP_0000177012.1		DUF2147 domain-containing protein	4566.120137	1.10079113	0.202964327	5.423569489	5.84E-08	3.18E-07
ABUW_RS19900	no	NZ_CP008706.1	2843929	2844051	+			glutathione S-transferase	1413323059	1.100557225	0.243984863	4.510760255	6.46E-06	2.52E-05
ABUW_RS01190	ABUW_0243	NZ_CP008706.1	260358	260753	+	WP_001088855.1		membrane protein	106.903923	1.099522289	0.203538986	5.40199885	6.59E-08	3.55E-07
ABUW_RS08645	ABUW_1775	NZ_CP008706.1	1774456	1774701	-	WP_000949688.1		hypothetical protein	2649.474744	1.095531365	0.26443913	4.142848935	3.43E-05	0.00011792
ABUW_RS16990	ABUW_3493	NZ_CP008706.1	3541870	3542280	-	WP_000084236.1		GFA family protein	889.363156	1.095297291	0.108785427	10.06841931	7.62E-24	2.33E-22
ABUW_RS16870	ABUW_3469	NZ_CP008706.1	3515308	3517464	+	WP_000064284.1	katG	catalase/peroxidase HPI	2277.771277	1.095281989	0.198187058	5.526506123	3.27E-08	1.83E-07
ABUW_RS07315	ABUW_1500	NZ_CP008706.1	1486833	1487450	+	WP_000768113.1		paraquat-inducible protein A	231.098717	1.094750073	0.176350799	6.207797646	5.37E-10	3.74E-09
ABUW_RS13910	ABUW_2862	NZ_CP008706.1	2871643	2871984	-	WP_000768231.1		hypothetical protein	242.0235909	1.094343147	0.133595517	3.280449204	0.00136419	0.002676752
ABUW_RS10365	ABUW_2133	NZ_CP008706.1	2119327	2120466	+	WP_000367591.1		transcriptional regulator	796.4408741	1.094801284	0.22801284	4.798359766	1.60E-06	6.91E-06
ABUW_RS18725	ABUW_3846	NZ_CP008706.1	3914859	3915476	+	WP_000737570.1		thiol disulfide interchange protein DsbA/DsbL	7985.68479	1.092910293	0.240386902	5.464643565	5.46E-06	2.15E-05
ABUW_RS20330	no	NZ_CP008706.1	3870899	3871033	+			hypothetical protein	5.51458729	1.091340475	1.034702535	1.05473838	0.29544994	0.375043033
ABUW_RS14000	no	NZ_CP008706.1	2890034	2892079	-		ureC	urease subunit alpha	409.4467325	1.091943636	0.226789507	4.811261543	1.50E-06	6.52E-06
ABUW_RS15475	ABUW_1366	NZ_CP008706.1	3215372	3216296	+	WP_000470123.1		hypothetical protein	517.6706206	1.090985393	0.246821967	4.420100854	9.86E-06	3.71E-05
ABUW_RS01670	ABUW_0339	NZ_CP008706.1	361832	362507	-	WP_001143885.1		superoxide dismutase family protein	1022.173678	1.090205914	0.243483215	4.477553581	7.55E-06	2.90E-05
sRNA25	no	no	no	no	no	no	no	no	29.4274511	1.08765459	0.46738128	2.327123884	0.19558673	0.037349509
ABUW_RS18250	ABUW_3749	NZ_CP008706.1	3805847	3806515	-	WP_000626445.1		glutathione S-transferase	939.0109193	1.0866196355	0.162342205	2.693862239	2.17E-11	1.80E-10
ABUW_RS05685	ABUW_1500	NZ_CP008706.1	1362207	1363475	-	WP_001052957.1		MgtC/SapB family protein	216.0610863	1.082352117	0.249469379	4.338617109	1.43E-05	5.29E-05
ABUW_RS18295	ABUW_3758	NZ_CP008706.1	381971	3814612	+	WP_000421342.1		DedA family protein	1221.678048	1.081029917	0.136443115	7.922923288	2.32E-15	2.98E-14
ABUW_RS04055	ABUW_0828	NZ_CP008706.1	805153	805827	+	WP_000161505.1		DNA-binding response regulator PmrA	583.5137163	1.075982993	0.173499586	7.82535449	5.06E-06	6.28E-14
ABUW_RS17795	ABUW_3654	NZ_CP008706.1	3714263	3715660	-	WP_000738515.1		ammonium transporter	3737.422396	1.074830725	0.172178416	6.242540373	4.31E-10	3.04E-09
ABUW_RS16885	ABUW_3472	NZ_CP008706.1	3520481	3521158	+	WP_000232919.1		DUF1345 domain-containing protein	394.3406979	1.072000959	0.152138224	7.046230267	1.84E-12	1.75E-11
ABUW_RS04515	ABUW_0920	NZ_CP008706.1	925826	926788	+	WP_000732912.1		MBL fold metallo-hydrolase	2247.770997	1.071095941	0.173756333	6.038574317	1.55E-09	1.03E-08
ABUW_RS07995	ABUW_1638	NZ_CP008706.1	1635801	1636358	+	WP_000932085.1		chorismate mutase	262.2662094	1.069297679	0.23162065	4.615386655	3.92E-06	1.58E-05
ABUW_RS16455	ABUW_3386	NZ_CP008706.1	3425871	3426890	+	WP_000578593.1	magZ	beta-N-acetylhexosaminidase	1549.255862	1.067887296	0.133273389	8.012571109	1.12E-15	1.49E-14
ABUW_RS13035	ABUW_2685	NZ_CP008706.1	2675831	2676531	-	WP_001004676.1		hypothetical protein	78.1812852	1.066355644	0.521431934	6.085505243	0.040849689	0.01794818
ABUW_RS04605	ABUW_0939	NZ_CP008706.1	946349	946924	+	WP_001042786.1		helic-tum-helic transcriptional regulator	38.2051044	1.061999957	0.406479781	2.61267597	0.008938343	0.018419897
ABUW_RS03500	ABUW_0711	NZ_CP008706.1	717122	7171700	-	WP_000037735.1		DJ-1/PIF1 family protein	750.1525846	1.061722705	0.191865368	5.533866024	3.14E-08	1.76E-07
ABUW_RS11470	ABUW_2358	NZ_CP008706.1	2340767	2342074	+	WP_000810595.1		dicarboxylate/amino acid-cation symporter	2310.976507	1.060626494	0.36619438	2.896348367	0.00377533	0.008545897
ABUW_RS05540	ABUW_1132	NZ_CP008706.1	1153246	1154175	+	WP_000886770.1		LysR family transcriptional regulator	3557.898724	1.059191996	0.16572304	6.391338213	1.64E-10	1.23E-09
ABUW_RS02730	ABUW_0555	NZ_CP008706.1	556947	557147	-	WP_000130085.1		TraR/DksA C4-type zinc finger protein	34.01385448	1.058799456	0.456897631	2.31736692	0.020483753	0.03825213
ABUW_RS13450	ABUW_2770	NZ_CP008706.1	2761888	2763558	+	WP_000154593.1		GMC family oxidoreductase	568.2770896	1.058554555	0.209698986	5.047971713	4.47E-07	2.14E-06
ABUW_RS15185	ABUW_3128	NZ_CP008706.1	3149119	3150156	-	WP_000405207.1		cell division protein ZlpA	3904.010834	1.056332191	0.185559897	5.69183092	1.26E-08	7.40E-08
ABUW_RS04465	ABUW_0910	NZ_CP008706.1	903722	905053	-	WP_001986541.1		MFS transporter	3451.342625	1.05619639	0.23617454	4.471762253	7.76E-06	2.97E-05
ABUW_RS18730	ABUW_3847	NZ_CP008706.1	3916566	3916369	+	WP_000080759.1		junctional 3-demethylbiquinone 3-O-methyltransferase/2-octaprenyl-6-hydroxylase	1287.55924	1.053015144	0.20150548	5.229760517	1.70E-07	8.65E-07
ABUW_RS01950	ABUW_0397	NZ_CP008706.1	423531	424796	+	WP_002000599.1		dicarboxylate/amino acid-cation symporter	2045.997729	1.050476657	0.139475446	7.531624295	5.01E-14	5.62E-13
ABUW_RS06975	ABUW_1432	NZ_CP008706.1	1423885	1424109	+	WP_000850407.1		hypothetical protein	38.10184045	1.049238127	0.233510385	4.693252322	7.01E-06	2.71E-05
ABUW_RS04550	ABUW_0927	NZ_CP008706.1	935673	936056	+	WP_001110719.1		SCP2 sterol-binding domain-containing protein	4098.045421	1.048388174	0.172928084	6.062567466	1.34E-09	8.82E-09
ABUW_RS16200	ABUW_3335	NZ_CP008706.1	3368532	3368792	-	WP_000790979.1		hypothetical protein	144.3185675	1.047599046	0.747594347	140.129343	NA	NA
ABUW_RS03590	ABUW_0729	NZ_CP008706.1	735553	736371	+	WP_000426935.1		undecaprenyl-diphosphate phosphatase	3173.796915	1.04750428	0.184893829	5.66543585	1.47E-08	8.53E-08
ABUW_RS04870	ABUW_0993	NZ_CP008706.1	1004810	1006090	-	WP_000858386.1	tolB	Tol-Pal system beta propeller repeat protein TolB	5569.546463	1.046435603	0.203585014	5.140042388	2.75E-07	1.36E-06
ABUW_RS07090	ABUW_1455	NZ_CP008706.1	1446735	1447616	-	WP_000190815.1		ATP-binding protein	531.6085288	1.04117017	0.21015922	4.957274868	7.15E-07	3.32E-06
ABUW_RS18565	ABUW_3814	NZ_CP008706.1	3876585	3878252	-	WP_001857993.1	ldpP	L-lactate permease	5075.973923	1.0395049	0.346597538	2.99919889	0.002707163	0.006326659
ABUW_RS09125	ABUW_1874	NZ_CP008706.1	1874198	1874869	-	WP_000566012.1		3-oxoacyl-CoA-transferase subunit A	65.40665217	1.034433202	0.301819943	3.42731892	0.000609573	0.001657199
ABUW_RS12025	ABUW_2471	NZ_CP008706.1	2464021	2465226	+	WP_000930806.1		3-oxoacyl-CoA thiolase	59.01849803	1.032012039	0.381177254	2.707433425	0.006780567	0.014516889
ABUW_RS02165	ABUW_0439	NZ_CP008706.1	451586	451952	+	WP_000651536.1	rtfA	rhomboresolase	466.7476473	1.031239323	0.264530584	3.898374655	9.88E-05	0.00305776
ABUW_RS18735	ABUW_3848	NZ_CP008706.1	3916366	3917067	+	WP_000973871.1		HAD-1A family hydrolase	1200.667671	1.030383355	0.240169572	4.290232708	1.78E-05	6.47E-05
ABUW_RS15445	ABUW_1380	NZ_CP008706.1	3207160	3208809	-	WP_001985884.1	bfmS	sensor histidine kinase BfmS	9898.990919	1.030093913	0.185940877	5.539900267	3.03E-08	1.17E-07
ABUW_RS12595	ABUW_2592	NZ_CP008706.1	2586352	2587005	-	WP_000217385.1		DUF1989 domain-containing protein	3.460806764	1.029196197	1.106317193	0.930292147	0.352219843	0.438804498
ABUW_RS00190	ABUW_0026	NZ_CP008706.1	29975	31804	+	WP_001113590.1	ldvD	dihydroxy-acid dehydratase	10375.92363	1.028562634	0.17809416	5.717336636	7.68E-09	4.66E-08
ABUW_RS04255	ABUW_0867	NZ_CP008706.1	846075	847349	-	WP_001287579.1	glfA	citrate (5S) synthase	34759.78554	1.028519563	0.228466002	4.501849516	6.74E-06	2.62E-05
ABUW_RS16755	ABUW_3446	NZ_CP008706.1	3490966	3491598	+	WP_000886301.1		LysE family translocator	134.7789979	1.022699227	0.178876079	5.717365521	1.08E-08	6.44E-08
ABUW_RS04110	ABUW_0839	NZ_CP008706.1	818104	818538	+	WP_000371755.1		nuclear transport factor 2 family protein	426.9600946	1.018202535	0.1311217639	7.759646828	8.52E-15	1.05E-13
ABUW_RS20505	ABUW_1495	NZ_CP008706.1	1481619	1481852	-	WP_000437833.1		hypothetical protein	113.0223212	1.01763189	0.378678644	2.687323162	0.007202723	0.015305786
ABUW_RS04210	ABUW_0858	NZ_CP008706.1	838280	839464	-	WP_001118404.1		iron-containing alcohol dehydrogenase	2203.148335	1.017259611	0.157190934	6.471490337	9.70E-11	7.42E-10
ABUW_RS00685	ABUW_0138	NZ_CP008706.1	152692	153603	-	WP_001025107.1		alpha/beta hydrolase	454.225148	1.016837652	0.162173652	6.270054612	3.16E-10	2.58E-09
ABUW_RS07270	ABUW_1491	NZ_CP008706.1	1476869	1479367	+	WP_000603294.1	csuD	Csu fimbrial usher CsuD	970.5711689	1.016460646	1.130137885	0.899412947	NA	NA
ABUW_RS08245	ABUW_1693	NZ_CP008706.1	1690447	1691310	+	WP_000037356.1		iron-containing redox enzyme family protein	1593.608021	1.016154812	0.205811898	4.937296885	7.92E-07	3.64E-06
ABUW_RS10765	ABUW_2214	NZ_CP008706.1	2200933	2201439	-	WP_000108826.1	raaA	ribonuclease E activity regulator RaaA	1700.377994	1.015517467	0.201245059	5.046173413	4.51E-07	2.16E-06
ABUW_RS18545	ABUW_3810	NZ_CP008706.1	3871369	3872583	+	WP_000486251.1		aspartate/tyrosine/aromatic aminotransferase	8779.197376	1.011857965	0.184620554	5.480743836	4.24E-08	2.33E-07
ABUW_RS00980	ABUW_0198	NZ_CP008706.1	222767	223090	-	WP_000082714.1		Azid domain-containing protein	6114.4208597	1.008579636	0.277553944	3.633814826	0.00027	

ABUW_RS08490	ABUW_1743	NZ_CP008706.1	1741697	1742767	+	WP_000868103.1	lysD	UDP-3-O-(3-hydroxymethyl)glucosamine N-acetyltransferase	6862.340316	-1.00348164	0.12718937	-7.892796355	2.955E-16	3.73E-14
ABUW_RS08430	ABUW_0790	NZ_CP008706.1	748784	748951	+	WP_000047869.1		hyphoetetic al protein	67.1210086	-1.0044851	0.384256293	-2.61404645	0.008946183	0.018352389
ABUW_RS08040	ABUW_0661	NZ_CP008706.1	966463	966530	-	WP_000426928.1		endonuclease/exonuclease/phosphatase family protein	495.1799866	-1.004834828	0.247634048	-4.057735084	4.96E-05	0.000957322
ABUW_RS02240	ABUW_0476	NZ_CP008706.1	487891	487966	+			RNAse Ase	2861.241241	-1.007487545	0.286239168	-3.518740458	0.000431969	0.0011747
ABUW_RS00735	ABUW_2004	NZ_CP008706.1	2100651	2100935	-	WP_000050492.1		CUF2523 domain-containing protein	16.51048264	-1.008033831	0.696836566	-1.446529493	0.148028746	0.21216927
ABUW_RS1545	ABUW_2771	NZ_CP008706.1	276338	2764898	-	WP_000733566.1		OpfD family outer membrane porin	96.75848798	-1.008066795	0.360722457	-2.78466048	0.005195425	0.010193934
ABUW_RS02325	ABUW_0653	NZ_CP008706.1	656534	656547	-	WP_000371632.1		methyltransferase	2401281788	-1.008445728	0.251448787	-4.014518172	5.95E-05	0.000955278
ABUW_RS1690	ABUW_3433	NZ_CP008706.1	3478521	3478799	-	WP_000027403.1		hyphoetetic al protein	2365.486317	-1.009626955	0.342272681	-2.949481545	0.003193076	0.007149348
ABUW_RS11105	ABUW_2289	NZ_CP008706.1	2276707	2277792	+	WP_000214682.1	tmaA	RNA [uridine(4)-C5]-methyltransferase TmaA	1911.01959	-1.009998532	0.152638165	-6.816305225	3.68E-11	2.96E-10
ABUW_RS1575	ABUW_3610	NZ_CP008706.1	3668864	3669404	-	WP_000661569.1		acyl-CoA thioesterase	414.9718217	-1.01141618	0.199896926	-5.059636233	4.20E-07	2.03E-06
ABUW_RS1880	ABUW_2839	NZ_CP008706.1	2849146	2850981	-	WP_001191009.1		ABC transporter substrate-binding protein	416.0747568	-1.012422752	0.190545223	-6.725040684	1.76E-11	1.47E-10
ABUW_RS1510	ABUW_2264	NZ_CP008706.1	2248176	2249378	-	WP_000553193.1	nmfG	16S rRNA [guanine(527)-N(7)]-methyltransferase RnmG	1707.58547	-1.013831991	0.156465344	-6.479594573	9.20E-11	7.04E-10
ABUW_RS02435	ABUW_2283	NZ_CP008706.1	2247842	2248724	-	WP_000007121.1		Park family protein	2370.24718	-1.014030912	0.19980917	-6.34201898	2.27E-10	1.67E-09
ABUW_RS06490	ABUW_1330	NZ_CP008706.1	1340816	1341451	-	WP_161263161		hyphoetetic al protein	164.1697805	-1.015274533	0.279293774	-3.635149183	0.00027782	0.000102056
ABUW_RS06765	ABUW_1639	NZ_CP008706.1	1618650	1618767	+	WP_002017886.1		TerfA/RcrI family transcriptional regulator	87.4533435	-1.01536265	0.400095325	-2.538235771	0.01194109	0.023388158
ABUW_RS10380	ABUW_4076	NZ_CP008707.1	46117	45932	+	WP_000933856.1		conjugate release	1866.618744	-1.0160014	0.21045272	-4.759842832	1.94E-06	8.25E-06
ABUW_RS1005	ABUW_1370	NZ_CP008706.1	1386116	1386745	+	WP_000003115.1		hydrolase	6.61571035	-1.01745211	0.130745329	-7.781838524	7.14E-15	8.80E-14
ABUW_RS04510	ABUW_0919	NZ_CP008706.1	925345	925179	-	WP_0003719022.1		diacylglycerol kinase	90.37714678	-1.018310702	0.245419238	-4.149371535	3.33E-05	0.000114004
ABUW_RS02445	ABUW_0534	NZ_CP008706.1	542758	543328	-	WP_000147160.1		LenA family protein	167.510676	-1.01807496	0.1988812	-5.364975187	8.10E-08	4.32E-07
ABUW_RS12140	ABUW_2494	NZ_CP008706.1	2490120	2491626	-	WP_000008183.1		cytosine permease	63.84700107	-1.020875406	0.136554474	-3.224959648	0.001259904	0.003176567
ABUW_RS04335	ABUW_0896	NZ_CP008706.1	893329	893365	-	WP_000179363.1		DOMON-like domain-containing protein	886.3204542	-1.02107776	0.17182568	-5.942510426	2.81E-09	1.80E-08
ABUW_RS18516	ABUW_3186	NZ_CP008706.1	3234918	3235401	-	WP_000219482.1		flavin reductase	1473.464774	-1.022586603	0.137004447	-3.291875319	0.000997654	0.002598621
ABUW_RS1425	ABUW_3380	NZ_CP008706.1	3418022	3420194	-	WP_0001093084.1	dmN	23S rRNA [adenine(2503)-C(2)]-methyltransferase RmN	5309.009945	-1.023228693	0.181021935	-5.653915294	1.57E-08	9.06E-08
ABUW_RS07300	no	NZ_CP008706.1	184180	184282	-			ADP-ribose pyrophosphatase	29.4702167	-1.023635275	0.702493336	-1.460277589	0.144219799	0.20743927
ABUW_RS00590	ABUW_0591	NZ_CP008706.1	581347	590111	+	WP_001033815.1		glycosyltransferase family 2 protein	571.1432936	-1.026098039	0.127050528	-8.480050727	8.55E-16	1.16E-14
ABUW_RS17505	ABUW_1647	NZ_CP008706.1	1633248	1633475	-	WP_000900661.1	gprR	30S ribosomal protein S 8	42249.38501	-1.02600916	0.240791929	-4.260910592	2.04E-05	7.26E-05
ABUW_RS02765	ABUW_0563	NZ_CP008706.1	562998	563189	+	WP_001046004.1		carbamoyl-hydrolyzing class D beta-lactamase OXA-33	23002.84624	-1.026371020	0.169555733	-6.05231954	1.42E-09	9.42E-09
ABUW_RS18085	ABUW_0038	NZ_CP008706.1	46497	46884	-	WP_000555783.1		hyphoetetic al protein	46.0445358	-1.027935605	0.336247332	-3.057081823	0.002235033	0.003633279
ABUW_RS01420	ABUW_1647	NZ_CP008706.1	1071594	1073036	-	WP_000003742.1		deoxyribosylpyrimidine photo-lyase	3.161729836	-1.02855163	0.232350504	-4.426730081	9.57E-06	3.16E-05
ABUW_RS01450	ABUW_0295	NZ_CP008706.1	316037	316066	+	WP_000643712.1	ankK	shikimate kinase AnkK	1659.021892	-1.028906473	0.14852331	-7.629875298	2.35E-14	7.22E-13
ABUW_RS11865	ABUW_2337	NZ_CP008706.1	2320791	2322203	+	WP_000733093.1		LLM class flavin-dependent oxidoreductase	51.9199083	-1.02922644	0.31614271	-3.224714703	0.00100718	0.003176632
ABUW_RS13130	ABUW_2964	NZ_CP008706.1	2977254	2978252	+	WP_000766454.1		GTP-binding protein	430.8643267	-1.029408933	0.10889054	-5.690647078	1.27E-08	7.43E-08
ABUW_RS06880	ABUW_3930	NZ_CP008706.1	3992544	3993479	+	WP_045887726.1		hyphoetetic al protein	985.4247105	-1.029992939	0.256804474	-4.01080605	6.05E-05	0.000980502
ABUW_RS16665	ABUW_1428	NZ_CP008706.1	1474492	1474492	-	WP_000005616.1		TerfA/RcrI family transcriptional regulator	1257.636649	-1.035644337	0.14325811	-8.328636283	8.18E-17	1.23E-15
ABUW_RS05625	ABUW_1629	NZ_CP008706.1	161958	161929	-	WP_000846423.1		hyphoetetic al protein	175.7478276	-1.037710766	0.258227518	-4.018602556	5.55E-05	0.000192551
ABUW_RS17775	ABUW_2633	NZ_CP008706.1	2631183	2631932	+	WP_001050072.1		LspA/RcrC family transcriptional regulator	228.5515362	-1.037856388	0.217212847	-4.77306175	1.77E-06	7.58E-06
ABUW_RS04375	ABUW_0882	NZ_CP008706.1	887420	887896	-	WP_001802084.1	gnaA	transcription elongation factor GnaA	4756.033008	-1.039653783	0.264866049	-3.925059801	8.67E-05	0.000275561
ABUW_RS2130	ABUW_0652	NZ_CP008706.1	657052	658192	-	WP_000004974.1		amino acid permease	4180.142605	-1.03976105	0.223472785	-4.652714303	3.28E-06	1.34E-05
ABUW_RS19710	no	NZ_CP008706.1	1840748	1840973	-			helicase-helix transcriptional regulator	45.49551811	-1.039959662	0.43123978	-2.418501762	0.01688484	0.03062202
ABUW_RS02620	ABUW_0533	NZ_CP008706.1	541450	542383	-	WP_000667229.1	tgt	RNA guanosine(34)-methyltransferase Tgt	5028.588603	-1.040052085	0.244588872	-4.246169985	2.17E-05	7.69E-05
ABUW_RS05105	ABUW_1670	NZ_CP008706.1	1663557	1663557	-	WP_000470704.1	leuE	leucine tRNA synthetase LeuE	373.2957944	-1.040759315	0.163446801	-6.367572235	1.92E-10	1.42E-09
ABUW_RS15950	ABUW_2871	NZ_CP008706.1	2881020	2881892	+	WP_000217929.1	nhf	endonuclease III	491.12237996	-1.041968447	0.221668615	-4.700186814	2.60E-06	1.08E-05
ABUW_RS01490	ABUW_0854	NZ_CP008706.1	831482	831482	+	WP_000588210.1		RNA [cytidine(34)-2'-O]-methyltransferase	948.8238745	-1.042274343	0.150734394	-6.914614819	4.69E-12	4.27E-11
ABUW_RS19630	ABUW_3827	NZ_CP008706.1	3819033	3819436	-	WP_000008925.1		oligosaccharide fipase family protein	2281.262287	-1.043509851	0.208896419	-4.995733567	5.88E-07	2.77E-06
ABUW_RS21030	no	NZ_CP008706.1	331874	331104	-			hyphoetetic al protein	50.287169552	-1.043761065	0.402308723	-2.59442863	0.00474828	0.09348243
ABUW_RS16660	ABUW_4116	NZ_CP008707.1	77868	78528	+	WP_071085161		transacylgylase SLT domain-containing protein	232.098969	-1.046900339	0.239824752	-4.36552102	1.27E-05	4.72E-05
ABUW_RS19135	ABUW_3287	NZ_CP008706.1	3329723	3329723	-	WP_000219215.1	tskK	mino-4-hydroxy-6-hydroxymethylthiolepidine diphosphokinase	749.0834239	-1.047465038	0.161476605	-6.48679192	8.77E-11	6.73E-10
ABUW_RS02440	ABUW_0487	NZ_CP008706.1	501890	501819	+	WP_000187234.1		symmetrical bis(5'-nucleosyl)-tetraphosphatase	3176.031275	-1.048845493	0.172045462	-6.096327585	1.09E-09	7.26E-09
ABUW_RS16005	ABUW_2162	NZ_CP008706.1	214284	2143275	-	WP_000840537.1		hyphoetetic al protein	246.830188	-1.049271574	0.22660396	-4.62873344	3.68E-06	1.49E-05
ABUW_RS19335	no	NZ_CP008706.1	39323	39516	+			hyphoetetic al protein	214.1226008	-1.050216569	0.229190506	-4.582204094	4.60E-06	1.84E-05
ABUW_RS15710	ABUW_2519	NZ_CP008706.1	2565697	2565886	-	WP_00129357.1	gysD	30S ribosomal protein S15	38383.44633	-1.051941623	0.191652105	-5.475513605	4.35E-08	2.40E-07
ABUW_RS16000	ABUW_2262	NZ_CP008706.1	2247708	2247945	-	WP_000222429.1		PadB/RegB/SpoB family partition protein	2035.02331	-1.05198664	0.14607785	-7.089055498	1.25E-12	1.23E-11
ABUW_RS19150	ABUW_3100	NZ_CP008706.1	3199894	3141064	-	WP_000101442.1	bbaA	adenosylmethionine-8-amino-7-oxononanoate transaminase	3760.01081	-1.054003607	0.162947245	-6.4681373	9.91E-11	7.54E-10
ABUW_RS19210	ABUW_0391	NZ_CP008706.1	415084	419179	-	WP_000472273.1	comF	ComF family protein	554.7378396	-1.054002806	0.1581602	-8.227046354	1.92E-16	2.76E-15
ABUW_RS19335	ABUW_4111	NZ_CP008707.1	70277	72286	+	WP_000212594.1	traN	conjugate transfer protein TraN	547.51621	-1.054905196	0.154034643	-6.848493161	7.46E-12	6.58E-11
ABUW_RS19515	ABUW_2253	NZ_CP008706.1	2236369	2240247	+	WP_000375831.1		TerfA/RcrI family transcriptional regulator	1762.725105	-1.057288948	0.11020771	-9.507662841	1.95E-21	4.46E-20
ABUW_RS00005	ABUW_0001	NZ_CP008706.1	95	1692	+	WP_000948768.1	dnaA	chromosomal replication initiator protein DnaA	7678.194564	-1.058447466	0.237738295	-4.452163863	8.50E-06	3.23E-05
ABUW_RS01425	ABUW_0885	NZ_CP008706.1	844176	844108	-	WP_000916555.1		rhodanese-related sulfurtransferase	4834.55596	-1.058777515	0.22011682	-4.810022764	15.1E-06	6.55E-06
ABUW_RS02685	ABUW_0554	NZ_CP008706.1	58197	59435	+	WP_000100218.1		YcgN family cysteine cluster protein	505.2437464	-1.058910292	0.20716004	-5.11815856	3.16E-07	1.55E-06
no	no	no	no	no	no	no	no	no	420.2230604	-1.060734623	0.21770456	-4.893354210	9.91E-07	4.47E-06
ABUW_RS08195	ABUW_1414	NZ_CP008706.1	1405921	1406844	+	WP_000316496.1		hyphoetetic al protein	72.0904668	-1.06345274	0.308354445	-3.447791479	0.0059519	0.01545928
ABUW_RS19340	ABUW_2921	NZ_CP008706.1	2930821	2931828	+	WP_000769047.1		formyl						

ABLW_RS6315	ABLW_3358	NZ_CP008706.1	3396481	339686	+	WP_001054464.1		DUF4 D4 domain-containing protein	121607615	-1.0396142	0.239287688	-4.637139624	3.53E-06	144E-05
ABLW_RS6320	ABLW_3354	NZ_CP008706.1	3350220	335811	+	WP_001076479.1		segregation/condensation protein A	2010.654444	-1.039870399	0.162888555	-6.81679454	9.5E-12	8.23E-11
ABLW_RS6320	ABLW_4035	NZ_CP008707.1	20560	2114	+	WP_000778008.1		hypothetical protein	55.5361077	-1.110024089	0.354185593	-3.134611142	0.001720821	0.004240481
ABLW_RS6325	ABLW_4878	NZ_CP008706.1	877606	878520	+	WP_000423293.1		LyfH family transcriptional regulator	240.8648879	-1.03988008	0.256883656	-4.324839594	1.53E-05	5.59E-05
ABLW_RS6325	ABLW_544	NZ_CP008706.1	933044	933114	-	WP_001042478.1	air	alanine racemase	576.361621	-1.11981593	0.197578121	-7.533731615	4.93E-14	5.55E-13
ABLW_RS6325	ABLW_5861	NZ_CP008706.1	840917	841024	-	WP_000887999.1		DUF493 domain-containing protein	25.8.053308	-1.112422589	0.246612731	-4.516343005	6.46E-06	2.52E-05
ABLW_RS1725	ABLW_3540	NZ_CP008706.1	36994	370994	+	WP_00160337.1		PAS domain-containing sensor histidine kinase	917.563069	-1.10276186	0.20307738	-6.48149005	4.22E-08	2.33E-07
ABLW_RS2690	ABLW_2519	NZ_CP008706.1	260546	2606323	-	WP_094273310.1		RHS domain-containing protein	209.859819	-1.112941807	0.305575059	-3.64212534	0.000270399	0.000709584
ABLW_RS2690	ABLW_9739	NZ_CP008706.1	1736031	1737227	+	WP_000194463.1		1-deoxy-D-xylulose-5-phosphate reductoisomerase	5527.045313	-1.113370005	0.165570333	-6.724453506	1.76E-11	1.48E-10
ABLW_RS8460	ABLW_1737	NZ_CP008706.1	1734454	1735206	+	WP_000102222.1	upp5	di-trans-poly-(cis-decaprenyl)carotenase	3300.332732	-1.110521485	0.177277552	-6.281232307	3.36E-10	2.40E-09
ABLW_RS11070	ABLW_2338	NZ_CP008706.1	232228	2323048	+	WP_000078420.1		methionine transfer	77.42487562	-1.110395606	0.264154074	-4.2197069389	2.47E-05	8.65E-05
ABLW_RS11070	ABLW_2292	NZ_CP008706.1	2279239	2279829	+	WP_001181797.1		lecithin retinol acyltransferase family protein	438.235189	-1.114194221	0.307402724	-3.624542446	0.000289473	0.000842694
ABLW_RS05835	ABLW_195	NZ_CP008706.1	928070	928618	-	WP_001187843.1	foIE	GTP cyclohydrolase [FoIE]	809.4445	-1.114362768	0.207704924	-5.365124472	8.09E-08	4.32E-07
ABLW_RS1635	ABLW_3221	NZ_CP008706.1	3250919	3250993	-			IRNA- Pro	854.140052	-1.118375853	0.333949259	-3.36089758	0.000779178	0.002056587
ABLW_RS14910	ABLW_3072	NZ_CP008706.1	3094000	300356	-	WP_000146428.1		oxaloductase	290.917417	-1.115843328	0.191694829	-5.82093598	5.85E-09	3.61E-08
ABLW_RS14910	ABLW_2359	NZ_CP008706.1	2342758	2343825	+	WP_000956445.1		type IIsparaginase	7550.164452	-1.110714743	0.269052704	-4.162160846	3.29E-05	0.000108614
ABLW_RS1925	ABLW_339	NZ_CP008706.1	335288	3354043	+	WP_000482796.1		ImmA/Ec family metallo- endopeptidase	3275.88993	-1.118256628	0.114189646	-9.79332771	1.20E-22	3.30E-21
ABLW_RS1925	ABLW_4021	NZ_CP008707.1	93658	1195	+	WP_000146727.1		hypothetical protein	138.934517	-1.115822216	0.418654104	-2.674089273	0.007453049	0.01678945
ABLW_RS1935	ABLW_3261	NZ_CP008706.1	3291265	3292686	+	WP_000103065.1	gigB	anti- anti- sigma factor GgB	4356.001168	-1.120883016	0.16565871	-8.86052565	7.99E-19	1.45E-17
ABLW_RS201790	ABLW_195	NZ_CP008706.1	971787	9718521	+	WP_001022905.1	bacH	acetylcholinesterase-like thioesterase BacH	163.439164	-1.07130836	0.297307465	-3.770972646	0.00016208	0.000493347
ABLW_RS87850	ABLW_1607	NZ_CP008706.1	160122	1603074	+	WP_000102900.1	mutL	DNA mismatch repair endonuclease MutL	1932.023051	-1.123585329	0.117558683	-9.557157943	1.21E-21	2.84E-20
ABLW_RS9176	no	NZ_CP008706.1	851927	852056	+			hypothetical protein	59.199285	-1.02141485	0.170708996	-6.585114437	4.54E-11	3.62E-10
sRNA20	no	no	no	no	no	no	no	no	53.3703263	-1.025444894	0.308523096	-3.7441953074	0.000180427	0.000543305
ABLW_RS05660	ABLW_156	NZ_CP008706.1	184180	185088	-	WP_000089887.1	ydgG	aromatic amino acid DMF transporter YdgG	77.33532657	-1.07008096	0.384298004	-2.932636458	0.003360972	0.007702705
ABLW_RS00925	ABLW_9187	NZ_CP008706.1	209373	210254	-	WP_0007733010.1	omp33-36	porin Omp33-36	43762.53578	-1.02222319	0.332087754	-3.397362005	0.00680389	0.00182877
ABLW_RS19145	ABLW_2414	NZ_CP008706.1	2400358	2400867	+	WP_000992233.1		rhodanese-like domain- containing protein	29.33491776	-1.028393376	0.374564266	-3.01549452	0.002590632	0.006107465
ABLW_RS19145	ABLW_3016	NZ_CP008706.1	3039175	3039942	-	WP_000578618.1		hypothetical protein	1078.934985	-1.09692299	0.235738852	-4.792104545	1.65E-06	7.10E-06
ABLW_RS19145	no	NZ_CP008706.1	11184	11994	+	WP_001958891.1		SAM- dependent DNA methyltransferase	527.296373	-1.100319375	0.416306378	-2.714749135	0.006632599	0.014244532
ABLW_RS081910	ABLW_1686	NZ_CP008706.1	1682008	1682511	+	WP_000338807.1		low molecular-weight phosphotyrosine protein phosphatase	6000.224796	-1.111994446	0.179457547	-6.303437598	2.91E-10	2.14E-09
ABLW_RS02505	ABLW_5071	NZ_CP008706.1	570741	570758	+	WP_000987745.1		GPW3025 family protein	40.40051453	-1.03026336	0.336011569	-2.86104185	0.004221816	0.00940343
sRNA30	no	no	no	no	no	no	no	no	119.3376122	-1.035017959	0.191645419	-0.95212451	0.341466539	0.427595427
ABLW_RS18205	ABLW_3740	NZ_CP008706.1	3796249	3797088	-	WP_000490209.1		zinc ABC transporter substrate-binding protein	769.9475184	-1.040797308	0.15462708	-7.334402092	2.23E-13	2.31E-12
ABLW_RS00860	ABLW_0012	NZ_CP008706.1	19398	14843	-	WP_000368393.1		alpha/beta fold hydrolase	168.810367	-1.110418354	0.235689667	-4.810130345	1.49E-06	6.50E-06
ABLW_RS14835	ABLW_3057	NZ_CP008706.1	308339	3083974	-	WP_000260163.1	rml	ribosomal protein S16- alanine N- acetyltransferase	344.2318445	-1.01520339	0.171229904	-6.829173767	3.36E-11	2.73E-10
ABLW_RS18335	ABLW_3766	NZ_CP008706.1	3819776	3818743	-	WP_001026049.1		4'- phosphatase/ thienyl transferase superfamily protein	568.5876529	-1.03535546	0.306030289	-3.70994463	0.000207305	0.000616889
ABLW_RS02425	ABLW_0494	NZ_CP008706.1	505559	505587	-	WP_000804895.1	gpm	S05 ribosomal protein L13	44506.47449	-1.139138121	0.217185718	-5.244194806	1.55E-07	7.97E-07
ABLW_RS18785	ABLW_3452	NZ_CP008706.1	3498629	3499993	+	WP_000128071.1		hypothetical protein	751.45891	-1.093919731	0.27951209	-6.190488185	5.34E-19	9.97E-18
ABLW_RS11010	ABLW_2488	NZ_CP008706.1	248443	2485228	+	WP_001103492.1	poBcr	kuR family transcriptional regulator PoBcr	224.0887496	-1.143083036	0.196782121	-5.810707319	6.15E-09	3.77E-08
ABLW_RS06600	ABLW_145	NZ_CP008706.1	1400841	1410077	+	WP_000107096.1		hypothetical protein	72.7703038	-1.144621255	0.335724386	-3.409407501	0.00065041	0.001753441
ABLW_RS01390	ABLW_0231	NZ_CP008706.1	250130	250219	-			IRNA- Ser	922.9454877	-1.14534156	0.282512508	-4.054124186	5.03E-05	0.000167781
ABLW_RS19140	ABLW_3118	NZ_CP008706.1	318079	318828	-	WP_0001005882.1	bioC	malonyl-ACP-D- methyltransferase BioC	1733.301845	-1.148298406	0.160603972	-7.14875501	8.69E-13	8.60E-12
ABLW_RS081910	ABLW_1687	NZ_CP008706.1	1682031	1683565	+	WP_001166920.1	murB	UDP- N- acetylmuramate dehydrogenase	1205.344704	-1.148553071	0.119442063	-9.618984885	8.85E-22	1.68E-20
ABLW_RS01170	ABLW_0632	NZ_CP008706.1	635133	635774	-	WP_001019520.1		hemolysin II family protein	966.91482932	-1.149223321	0.182067603	-6.130392697	2.75E-10	2.00E-09
ABLW_RS08290	ABLW_894	NZ_CP008706.1	891695	892761	+	WP_001051728.1		MFS transporter	384.8763576	-1.150197329	0.19163575	-5.999187603	1.97E-09	1.29E-08
ABLW_RS10540	no	NZ_CP008706.1	2873969	2874660	-			hypothetical protein	914.438783	-1.15118911	0.217623161	-7.487486492	3.08E-05	0.000195418
ABLW_RS102635	ABLW_2601	NZ_CP008706.1	2693279	2694187	-	WP_000465923.1		wf1 repeat family protein	292.153688	-1.151070232	0.293591869	-3.92482140	8.75E-05	0.00027794
sRNA48	no	no	no	no	no	no	no	no	60.425978	-1.15576574	0.383073797	-3.017038781	0.00252183	0.006038041
ABLW_RS20500	no	NZ_CP008706.1	564581	564676	-			GpE family phage tail protein	1656.075731	-1.156841227	0.260074082	-4.444121926	8.66E-06	3.29E-05
ABLW_RS14845	ABLW_3059	NZ_CP008706.1	308095	308076	-	WP_000992299.1		metal- dependent hydrolase	394.9154091	-1.158063625	0.218618534	-5.297188888	1.18E-07	6.15E-07
ABLW_RS14050	ABLW_2893	NZ_CP008706.1	290103	290176	-	WP_000492619.1		hypothetical protein	623.8783973	-1.158459962	0.198587316	-6.414957542	1.41E-10	1.06E-09
ABLW_RS19005	ABLW_4105	NZ_CP008707.1	6419	66905	+	WP_000104740.1	traC	type IV secretion system protein TraC	812.6160825	-1.169544694	0.149654353	-7.748165502	9.32E-15	1.14E-13
ABLW_RS19005	ABLW_3144	NZ_CP008706.1	319318	3170882	+	WP_0000605098.1		DUF2062 domain- containing protein	499.3722901	-1.163207269	0.234842406	-4.95319397	7.30E-07	3.38E-06
ABLW_RS00800	ABLW_0161	NZ_CP008706.1	179492	179587	+	WP_0001052249.1		YkgJ family cysteine cluster protein	418.253966	-1.163943161	0.237356448	-4.903177558	9.40E-07	4.27E-06
ABLW_RS08170	ABLW_092	NZ_CP008706.1	1788865	1787285	+	WP_000591945.1		cyl operon YkgJ family protein	324.3220714	-1.164312313	0.426438568	-2.7301963	0.006327352	0.019647164
ABLW_RS11775	ABLW_2420	NZ_CP008706.1	2407492	2408358	-	WP_0002029987.1		cysteine ABC transporter substrate-binding protein	349.4307749	-1.165417275	0.19162872	-7.20893584	5.64E-13	5.68E-12
sRNA99	no	no	no	no	no	no	no	no	20022.1852	-1.165470542	0.33714706	-3.546857507	0.000546534	0.001468676
ABLW_RS06035	ABLW_4235	NZ_CP008706.1	4278330	4279082	+	WP_001982119.1	gpiB	30S ribosomal protein S2	62338.18678	-1.166481308	0.218993257	-5.303331904	1.14E-07	5.97E-07
ABLW_RS19045	ABLW_4110	NZ_CP008707.1	73100	73459	+	WP_0001044930.1		hypothetical protein	47.65014111	-1.168187584	0.431931664	-2.70795185	0.008709984	0.014500599
ABLW_RS19075	ABLW_606	NZ_CP008706.1	600625	601029	+	WP_031844287.1	taeE	ne(37'-NE)- theonylcarbamoyltransferase complex ATPase subu	735.9505476	-1.168633951	0.150623909	-7.758616711	5.85E-15	1.05E-13
ABLW_RS07145	ABLW_628	NZ_CP008706.1	623520	624677	-	WP_001027866.1		hypothetical protein	686.089281	-1.169920546	0.156716072	-7.46522633	8.32E-14	9.15E-13
ABLW_RS17525	ABLW_3600	NZ_CP008706.1	3660780	3660855	-			IRNA- Gly	3504.760168	-1.169937106	0.263343369	-4.12043533	3.64E-05	0.000240484
ABLW_RS16520	ABLW_3197	NZ_CP008706.1	3225587	3226330	-	WP_000735356.1		methionine synthase	7548.28161	-1.170599397	0.336042108	-3.003192226	0.00021836	0.000254516
ABLW_RS19550	ABLW_2383	NZ_CP008706.1	2370150	2371334	-	WP_000472481.1		hypothetical protein	175.8016632	-1.173354191	0.196074487	-5.985246788	2.16E-09	1.41E-08
ABLW_RS20185	no	NZ_CP008706.1	940876	941003	+			sulfate exporter TauH/ Sae family protein	35.62498375	-1.174238963	0.498552467			

ABUW_RS03960	ABUW_0809	NZ_CP008706.1	788167	788556	+	WP_000433920.1			hypothetical protein	6153287307	-1234474854	0.396011746	-3.117268282	0.000825354	0.004478898
ABUW_RS1975	no	NZ_CP008706.1	3321274	3321825	-	WP_02937364.1	inC		translation initiation factor IF-3	192553424	-1235727855	0.98745879	-5.547045498	5.87E-11	4.62E-10
ABUW_RS19065	ABUW_4008	NZ_CP008707.1	5454	6050	+	WP_000059525.1			hypothetical protein	1042363952	-1236923769	0.27195599	-4.548249772	5.4E-06	2.16E-05
ABUW_RS0010	ABUW_976	NZ_CP008706.1	960195	96105	+	WP_00004519.1	adcC		lisdmg efflux RND-transporter outer membrane channel subunit A	934430653	-1237947827	0.17648954	-7.014267957	2.3E-12	2.19E-11
ABUW_RS1505	ABUW_3801	NZ_CP008706.1	386249	3862550	-	WP_000336104.1			DUF4844 domain-containing protein	1372667144	-1238050191	0.47976212	-2.580555072	0.009864305	0.02010698
ABUW_RS02280	ABUW_0444	NZ_CP008706.1	475056	475957	-	WP_000219141.1	mslB		VA (N6-isopentenyl)adenosine(37) C-2'-methylthiotransferase M	9419385056	-1238153416	0.148226753	-5.325866608	6.66E-17	1.02E-15
ABUW_RS1875	ABUW_2610	NZ_CP008706.1	2603566	2603883	-	WP_001038420.1			hypothetical protein	6261028053	-1239102541	0.223421405	-5.546190627	2.82E-08	1.05E-07
ABUW_RS07280	ABUW_1489	NZ_CP008706.1	1475527	1476045	+	WP_000876475.1	csuB		Csu fibrinolytic biogenesis protein CsuB	1241077787	-12395983703	1.337523895	-0.926774996	0.35044337	0.44051149
ABUW_RS02335	ABUW_0475	NZ_CP008706.1	487759	487835	+				RNA-1e	1654816179	-1240340089	0.343570187	-3.619160024	0.000306019	0.000885741
ABUW_RS01530	ABUW_0311	NZ_CP008706.1	334494	335123	-	WP_000106937.1	gmkI		guanylate kinase	2869207225	-1242411978	0.158998053	-7.810985375	5.54E-15	6.65E-14
ABUW_RS19440	ABUW_4092	NZ_CP008707.1	56584	57222	+	WP_001993862.1			recombinase family protein	1737259632	-1242732161	0.21616761	-5.775402739	7.68E-09	4.66E-08
ABUW_RS12220	ABUW_2511	NZ_CP008706.1	2505791	2506261	-	WP_000008105.1			hypothetical protein	43217391408	-124455111	0.94593602	-1.13658212	0.188280757	0.259877757
ABUW_RS10980	ABUW_2035	NZ_CP008706.1	2243192	2244202	-	WP_000050479.1			tetraacyldisaccharide 4'-kinase	9731520933	-1246782825	0.143981459	-6.81932903	4.75E-18	8.03E-17
ABUW_RS01795	ABUW_1887	NZ_CP008706.1	1216532	1219287	+	WP_001093105.1	baalI		scitobactacin biosynthesis phosphopantetheinyl transferase Baa	2316884162	-1247494927	0.46500781	-2.682293196	0.00730974	0.019492341
ABUW_RS08600	ABUW_1766	NZ_CP008706.1	1764140	1765072	+	WP_001043692.1			IS5-like element EBa33 family transposase	4651070373	-1247923228	0.217484948	-5.071797517	9.58E-09	5.73E-08
ABUW_RS00980	ABUW_0016	NZ_CP008706.1	9828	9904	+				RNA-1e	16562146857	-1248252527	0.342711981	-3.642278638	0.000270235	0.000790594
ABUW_RS13570	ABUW_3597	NZ_CP008706.1	3595202	3597297	-				RNA-1p	49310007699	-1249333346	0.27078195	-6.426067252	3.76E-06	1.53E-05
ABUW_RS01700	ABUW_1457	NZ_CP008706.1	1442920	1450003	+	WP_000192080.1			protein kinase	14910091713	-125103547	0.297935616	-4.16901016	2.68E-05	9.33E-05
ABUW_RS15615	ABUW_2183	NZ_CP008706.1	218236	2184184	+	WP_000412283.1			DUF2797 domain-containing protein	98921445785	-12519063	0.233951677	-3.16104262	8.74E-08	4.63E-07
ABUW_RS15815	ABUW_3257	NZ_CP008706.1	3257636	3257912	-				RNA-1e	16586133776	-1252727292	0.339182322	-3.693265765	0.000272092	0.00055781
ABUW_RS07490	ABUW_634	NZ_CP008706.1	6320409	1521251	-	WP_001003277.1			zinc-ribon and DUF3426 domain-containing protein	1191550553	-1254102631	0.193957393	-9.680129643	3.66E-22	9.28E-21
ABUW_RS02335	ABUW_0475	NZ_CP008706.1	487759	594188	+	WP_000598623.1	wecB		UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	10701862239	-1262108092	0.195040897	-6.787538373	1.14E-11	9.74E-11
ABUW_RS02250	ABUW_0660	NZ_CP008706.1	663586	665562	+	WP_001080163.1			DNA-3-methyladenine glycosylase	48210071698	-1266304023	0.1834423	-6.904141536	5.05E-12	4.58E-11
ABUW_RS00880	ABUW_2035	NZ_CP008706.1	220169	2201688	-	WP_000048401.1			DNA replication protein	9851403322	-1266647941	0.241968219	-5.234769987	1.65E-07	8.44E-07
ABUW_RS15445	ABUW_2996	NZ_CP008706.1	3105293	310162	-	WP_000505370.1			hypothetical protein	68419806279	-1268584294	0.1966403	-7.477830735	7.56E-14	8.40E-13
ABUW_RS14030	ABUW_4087	NZ_CP008706.1	409537	54286	+	WP_000412263.1	APH(3')		Vitfamily aminoglycoside O-phosphotransferase	189719928	-1269284003	0.16851086	-6.007417078	1.17E-15	1.54E-14
ABUW_RS01250	ABUW_0539	NZ_CP008706.1	547175	547471	-	WP_000218943.1			hypothetical protein	1081484916	-1269480254	0.2460891	-5.158605521	2.49E-07	1.24E-06
ABUW_RS19055	ABUW_4006	NZ_CP008706.1	404753	41753	+	WP_000222737.1			hypothetical protein	2261161406	-1271153841	0.184916264	-6.874105105	6.24E-12	5.57E-11
ABUW_RS17000	ABUW_2616	NZ_CP008706.1	2607400	2606088	-	WP_000873472.1			hypothetical protein	77718742824	-1274204618	0.316769197	-4.035240909	5.45E-05	0.000190581
ABUW_RS00930	ABUW_2045	NZ_CP008706.1	2025164	2026361	-	WP_000084016.1			DNA replication protein	98713305872	-1274689775	0.253472243	-5.028916275	4.93E-07	2.34E-06
ABUW_RS01200	ABUW_2328	NZ_CP008706.1	231923	2311693	-	WP_000414050.1			LysKamC family transcriptional regulator	116118308	-1275944297	0.250901733	-4.742316751	2.16E-06	8.93E-06
ABUW_RS19330	ABUW_3431	NZ_CP008706.1	3530664	3530739	+				RNA-1ys	5061165311	-12776354166	0.443925085	-2.876633979	0.003981946	0.000961064
ABUW_RS12995	ABUW_2676	NZ_CP008706.1	2668657	2668848	-	WP_001045792.1			hypothetical protein	18718995879	-1279884816	0.32218569	-3.972471219	7.1E-05	0.00023056
ABUW_RS19650	ABUW_0197	NZ_CP008706.1	151872	153620	+	WP_001034707.1			LysM peptidoglycan-binding domain-containing protein	1545191672	-1283605247	0.272361919	-4.710873002	2.44E-06	1.02E-05
ABUW_RS01790	ABUW_1655	NZ_CP008706.1	165928	165919	+	WP_001521030.1	ton		ion transporter	9861426562	-1285842711	0.116102011	-8.797373743	140E-18	2.5E-17
ABUW_RS01620	ABUW_1749	NZ_CP008706.1	174193	1747583	-	WP_000040963.1			RNA-binding protein	16771596827	-1286620251	0.229192167	-5.618802062	1.96E-08	1.19E-07
ABUW_RS01780	ABUW_0390	NZ_CP008706.1	390608	390925	-	WP_000098635.1			hypothetical protein	74174004152	-1291162065	0.322428373	-4.004306068	6.22E-05	0.000203246
ABUW_RS01435	ABUW_0754	NZ_CP008706.1	751411	751587	+	WP_001001967.1			hypothetical protein	9103819125	-1292459437	0.514082237	-2.514188686	0.01930658	0.023765662
ABUW_RS17520	ABUW_3599	NZ_CP008706.1	3606092	3606706	-				RNA-1hr	29451731604	-1297619959	0.304272741	-4.26460561	2.00E-05	7.7E-05
ABUW_RS01795	ABUW_0160	NZ_CP008706.1	176803	179400	+	WP_0001050537.1			MBL fold metallo-hydrolase	28211584124	-1298788224	0.204501915	-6.351001895	2.14E-10	1.58E-09
ABUW_RS04740	ABUW_0126	NZ_CP008706.1	1338831	1339385	+	WP_000208716.1	lyszyme		lyszyme	3121601936	-1301994331	0.177365146	-7.34075638	2.12E-10	2.2E-12
ABUW_RS01825	ABUW_0372	NZ_CP008706.1	396481	396735	-	WP_000103717.1	PpgC		DNA domain-containing protein	13848191057	-1302363998	0.59937838	-2.20125846	0.027716794	0.04089586
ABUW_RS00950	ABUW_0377	NZ_CP008706.1	147703	141915	+	WP_001198074.1	GNA1		family N-acetyltransferase	6177447367	-1303427705	0.175143505	-1.17451437	0.082816222	0.18333292
ABUW_RS02080	no	NZ_CP008706.1	2891956	2892194	-				hypothetical protein	5514343002	-1305719524	0.259907374	-5.02338943	5.06E-07	2.40E-06
ABUW_RS00960	ABUW_8301	NZ_CP008706.1	8343037	8343431	+	WP_001024039.1			DUF4845 domain-containing protein	14402144316	-1306148309	0.166976101	-8.322827695	8.59E-17	1.29E-15
ABUW_RS19630	ABUW_3220	NZ_CP008706.1	3250784	3250860	-				RNA-Arg	10558179714	-1309511669	0.308601723	-4.22693475	2.37E-05	8.31E-05
ABUW_RS19205	ABUW_0382	NZ_CP008706.1	401920	404875	+	WP_000471101.1			hypothetical protein	1221110632	-1309992553	0.42685556	-2.657916751	0.007942671	0.01642344
ABUW_RS01790	ABUW_0365	NZ_CP008706.1	389667	387299	-	WP_000339167.1			hypothetical protein	1107189028	-131005511	0.26357046	-4.970406088	6.68E-07	3.12E-06
ABUW_RS02030	ABUW_0535	NZ_CP008706.1	543416	544443	-	WP_001110110.1			hypothetical protein	75616805979	-1310743386	0.260056899	-6.299941915	2.98E-10	2.16E-09
ABUW_RS01940	ABUW_2042	NZ_CP008706.1	2023029	2024046	-	WP_000084016.1			DNA replication protein	9871545107	-1314552567	0.238091902	-5.521189105	3.37E-08	1.88E-07
ABUW_RS19450	ABUW_4094	NZ_CP008707.1	57721	58056	-	WP_001074611.1			hypothetical protein	6991799104	-1316020819	0.32065101	-4.104782974	4.05E-05	0.000197712
ABUW_RS01705	ABUW_0346	NZ_CP008706.1	367358	368635	+	WP_000360761.1			hypothetical protein	4246164162	-1317474916	0.12316243	-10.6936181	1.02E-26	4.7E-25
ABUW_RS19405	ABUW_4082	NZ_CP008706.1	51428	51880	-	WP_000776261.1			hypothetical protein	32610126942	-1321895268	0.397993698	-3.320849464	0.000897293	0.002347528
ABUW_RS01430	ABUW_0087	NZ_CP008706.1	96296	96285	+	WP_001066271.1	ATP-1		ATP-binding protein	3331400039	-132331035	0.19202025	-6.884484422	5.78E-12	5.9E-11
ABUW_RS01935	ABUW_016	NZ_CP008706.1	152902	152977	-				RNA-Aan	11418801338	-1324416434	0.423386293	-3.063014609	0.00219195	0.000272729
ABUW_RS01990	ABUW_1640	NZ_CP008706.1	1652839	1654422	-	WP_001019396.1	ABC-F		family ATP-binding cassette domain-containing protein	7491267832	-1326054208	0.281973994	-4.70609163	2.53E-06	1.05E-05
ABUW_RS19060	ABUW_2895	NZ_CP008706.1	2902539	2904182	-	WP_000194951.1	cysN		sulfate adenylyltransferase subunit CysN	7728131994	-1328251965	0.17254556	-7.703770856	1.32E-14	1.57E-13
sRNA164	no	no	no	no	no	no	no	no	no	42715802554	-1329490839	0.478274705	-2.791437012	0.005247457	0.019465285
ABUW_RS12255	ABUW_2521	NZ_CP008706.1	251109	251890	-	WP_000073989.1			ATP-dependent helicase	935111872	-1335989313	0.223166911	-5.98674675	2.14E-09	140E-08
ABUW_RS19950	ABUW_2252	NZ_CP008706.1	2239075	2239629	-	WP_000841073.1			type II secretion system protein	4231684463	-1336163835	0.205320721	-6.507345358	7.65E-11	5.93E-10
ABUW_RS01740	ABUW_1645	NZ_CP008706.1	1631147	1632592	-	WP_000075891.1	dnaB		replicative DNA helicase	83371621725	-13381363575	0.104447684	-10.25977126	1.07E-24	3.96E-23
ABUW_RS19830	ABUW_3280	NZ_CP008706.1	3291094	3292062	+	WP_000273589.1	glaA		RabU family protein phosphatase GlaA	16921807685	-1339682507	0.12			

ABUW_RS00600	ABUW_1540	NZ_CP008706.1	128281	128268	+	WP_00018659.1		Aa2 domain-containing protein	68.80787692	-1.424768772	0.439539339	-3.24	650063	0.0018886	0.00304309		
ABUW_RS1085	ABUW_2696	NZ_CP008706.1	268243	268276	-	WP_000636785.1		transposase	9.46	0.96965	-1.426225568	0.57294141	-2.48907306	0.02807583	0.025270203		
ABUW_RS1370	ABUW_2754	NZ_CP008706.1	274372	274425	-	WP_00107774.2		adenosine deaminase	3552.053443	-1.428214402	0.96638224	-7.27507779	3.466	13	3.546	12	
ABUW_RS0095	ABUW_3718	NZ_CP008706.1	377743	377694	-	WP_00092542.1		hypothetical protein	89.0048823	-1.436338456	0.29083821	-4.936605376	7.876	07	3.626	06	
ABUW_RS0660	ABUW_3427	NZ_CP008706.1	347262	347325	-	WP_00107506.1	purU	formyltetrahydrofolate deformylase	3650.483239	-1.436607359	0.94585664	-9.852013567	6.726	23	1.886	21	
ABUW_RS08430	ABUW_9731	NZ_CP008706.1	972625	972647	-	WP_000543879.1	adeN	multisig efflux transcriptional repressor AdeN	9.46	0.50487	-1.437903684	0.23540028	-6.98335876	1.05	09	6.776	09
ABUW_RS01545	ABUW_0314	NZ_CP008706.1	336833	337393	+	WP_002194578.1	pRv	type IV plus modification protein PIV	87.2603096	-1.423214832	0.316579022	-4.646884471	3.375	06	1.386	05	
ABUW_RS09040	ABUW_9557	NZ_CP008706.1	953946	955055	+	WP_001028599.1		amidase	4.8	393.9482	-1.443940852	0.639801327	-2.256389272	0.020466263	0.041033772		
ABUW_RS09700	ABUW_9955	NZ_CP008706.1	996037	996243	+	WP_032017216.1		hypothetical protein	559.664388	-1.44425456	0.279382747	-5.95447919	2.355	07	1.9E-06		
ABUW_RS0225	ABUW_1540	NZ_CP008707.1	23711	23893	+	WP_000373885.1		hypothetical protein	92.3356475	-1.451242521	0.441956721	-3.286572211	0.0010148	0.002629565			
ABUW_RS05070	ABUW_1333	NZ_CP008706.1	104407	104529	+	WP_00188558.1	ena	GTPase Ena	734.1334813	-1.45120969	0.964482383	-8.823418477	1.1E-18	2.01E-17			
ABUW_RS14945	ABUW_3079	NZ_CP008706.1	319786	319790	-	WP_000830726.1		hypothetical protein	273.938851	-1.452100839	0.302788839	-4.795853259	1.62E-06	6.99E-06			
ABUW_RS18545	ABUW_3263	NZ_CP008706.1	3293552	3293929	+	WP_000266123.1		DUF4951 domain-containing protein	3915292085	-1.453589395	0.202348652	-7.931588241	6.79E-13	6.79E-12			
ABUW_RS18995	ABUW_3293	NZ_CP008706.1	3326394	3326663	-	WP_000567533.1		HPH family phosphoesterase	1027.674933	-1.456028414	0.81994289	-8.00040715	1.24E-15	1.63E-14			
ABUW_RS07555	ABUW_1548	NZ_CP008706.1	153487	1533870	-	WP_001021679.1	rpsP	30S ribosomal protein S6	43.8103465	-1.456834386	0.247250073	-5.898254621	3.67E-09	2.34E-08			
ABUW_RS19425	ABUW_4089	NZ_CP008707.1	54566	55391	+	WP_001898464.1		IS30-like element ISAbeta U5 family transposase	4088.571038	-1.45918855	0.900231612	-9.90638464	8.52E-20	1.73E-18			
ABUW_RS1915	ABUW_4026	NZ_CP008707.1	56164	57597	+	WP_000241977.1		hypothetical protein	12.8908658	-1.466007296	0.36333351	-4.034860058	5.46E-05	0.000807026			
ABUW_RS00755	ABUW_0162	NZ_CP008706.1	61724	618626	+	WP_000240700.1		UDP-3-O-acetyl-N-acetylglucosamine deacetylase	2634.371151	-1.4705202636	0.12209919	-9.00559403	3.32E-33	2.57E-31			
sRNA72	no	no	no	no	no	no	no	no	227.966532	-1.469595932	0.32205046	-4.54909052	5.39E-06	2.94E-05			
ABUW_RS10625	ABUW_2599	NZ_CP008706.1	259143	259254	+	WP_000770261.1		hypothetical protein	970.3792277	-1.470691082	0.216250019	-6.832052144	8.37E-12	7.28E-11			
ABUW_RS10960	ABUW_2254	NZ_CP008706.1	2240285	2241058	-	WP_000497300.1		TatD family hydrolase	3090.423944	-1.474080811	0.12680151	-11.46240896	2.04E-30	1.17E-28			
ABUW_RS0505	ABUW_2273	NZ_CP008706.1	2258931	2258984	+	WP_000818866.1	maf	septum formation protein Maf	768.491604	-1.476310247	0.137386333	-10.74570672	6.21E-27	2.63E-25			
ABUW_RS00820	ABUW_1212	NZ_CP008706.1	1252061	1252054	-	WP_000464149.1		DUF2726 domain-containing protein	300.722539	-1.4801359706	0.307140761	-4.819080864	1.44E-06	6.27E-06			
ABUW_RS19100	ABUW_1025	NZ_CP008706.1	246467	246991	-	WP_000670913.1		hypothetical protein	129.846697	-1.486101638	0.39219286	-7.78992233	0.000100694	0.000458917			
ABUW_RS05565	ABUW_1037	NZ_CP008706.1	106019	101104	+	WP_001020845.1	rplM	50S ribosomal protein L31	6336.271843	-1.488064104	0.278395853	-5.345059563	9.04E-08	4.79E-07			
ABUW_RS18985	ABUW_3880	NZ_CP008706.1	394856	394473	+	WP_00071235.1		matrin family metalloprotein	5144406483	-1.48985773	0.455002324	-3.274395972	0.001058882	0.002727771			
ABUW_RS00690	ABUW_9962	NZ_CP008706.1	994167	995317	+	WP_032017212.1		zonular occludens toxin	3614.947018	-1.490159975	0.262190142	-5.688642459	1.28E-08	7.50E-08			
ABUW_RS02585	ABUW_0547	NZ_CP008706.1	552023	552941	+	WP_002013430.1		topotin domain-containing protein	605.3055747	-1.492803783	0.234382122	-6.369102608	1.90E-10	1.44E-09			
ABUW_RS18550	ABUW_3264	NZ_CP008706.1	3294899	3294526	+	WP_000371931.1		MarR family transcriptional regulator	556.329164	-1.494082834	0.305073265	-4.897455006	9.71E-07	4.39E-06			
ABUW_RS19065	ABUW_2255	NZ_CP008706.1	2241976	2241114	+	WP_00183027.1		PilZ domain-containing protein	353.9904428	-1.496494216	0.98011788	-8.31332327	9.31E-17	1.38E-15			
ABUW_RS19175	ABUW_2599	NZ_CP008706.1	2595973	2596983	+	WP_000890089.1		LysR family transcriptional regulator	9156.623434	-1.497114451	0.201655763	-7.424109558	1.94E-13	1.22E-12			
ABUW_RS18995	ABUW_2261	NZ_CP008706.1	2246373	2247008	-	WP_000254044.1		MetA/TotG/EstB protein channel family protein	1024.525071	-1.498177902	0.115452865	-8.5834268	9.21E-19	1.51E-18			
ABUW_RS10815	ABUW_2842	NZ_CP008706.1	285598	2857601	+	WP_001028931.1		hypothetical protein	974.662033	-1.503222743	0.200189907	-7.508899619	5.87E-14	6.57E-13			
ABUW_RS10990	ABUW_2260	NZ_CP008706.1	2241029	2244357	-	WP_000606664.1		heptolym transporter EabD	188.363632	-1.502182483	0.145473235	-10.38195607	3.00E-25	1.02E-23			
ABUW_RS00830	ABUW_0167	NZ_CP008706.1	90519	91714	+	WP_086642004.1	prfB	peptide chain release factor 2	8124.107348	-1.516434589	0.140049186	-10.82787149	2.54E-27	1.9E-25			
ABUW_RS18365	ABUW_3164	NZ_CP008706.1	318061	318966	-	WP_00107343.1	upp	uracil phosphoribosyltransferase	5288.398026	-1.516973894	0.199526078	-7.602885324	2.90E-14	3.31E-13			
ABUW_RS02060	no	NZ_CP008706.1	267185	267130	-			hypothetical protein	479.173092	-1.523291459	0.222648674	-6.841882165	7.83E-12	6.88E-11			
ABUW_RS19175	ABUW_3531	NZ_CP008706.1	3058852	3058899	+	WP_000355491.1		type IV plus twitching motility protein PflT	604.5924693	-1.524071673	0.253833991	-6.004229861	1.92E-09	1.26E-08			
ABUW_RS19175	ABUW_2019	NZ_CP008706.1	2004581	2005723	-	WP_000186400.1		hypothetical protein	255.810815	-1.525107486	0.221806761	-6.875838599	6.16E-12	5.52E-11			
ABUW_RS08730	ABUW_1793	NZ_CP008706.1	1877286	1877387	-	WP_000210726.1	cydX	cytochrome bd-1 oxidase subunit CydX	394.533744	-1.52656066	0.459670795	-3.38919177	0.00000369	0.00226197			
ABUW_RS19360	ABUW_4072	NZ_CP008706.1	42340	42534	+	WP_000560244.1		hypothetical protein	267.469145	-1.526032499	0.384322546	-3.970770721	7.17E-05	0.0002019			
ABUW_RS19040	ABUW_9332	NZ_CP008706.1	9309795	931415	+	WP_00107389.1		TetR/ArbR family transcriptional regulator	336.319610	-1.526907912	0.290873193	-5.249364455	1.53E-07	7.84E-07			
ABUW_RS19250	ABUW_408	NZ_CP008707.1	671832	68470	+	WP_000672680.1	traW	type-F conjugative transfer system protein TraW	73.26654751	-1.527841982	0.335971811	-4.547528432	5.43E-06	2.9E-05			
ABUW_RS18760	ABUW_3246	NZ_CP008706.1	3275271	3277076	+	WP_002017987.1		chromatin-binding protein	30180.38661	-1.531046468	0.217669369	-7.033819391	2.01E-12	1.90E-11			
ABUW_RS19145	ABUW_4386	NZ_CP008707.1	52381	53406	+	WP_00188464.1		IS30-like element ISAbeta U5 family transposase	3980.718091	-1.533995919	0.169847244	-6.833728946	5.76E-22	1.43E-20			
ABUW_RS10565	ABUW_1332	NZ_CP008706.1	1343403	1344095	+	WP_000180899.1	nci	ribonuclease II	2896.835898	-1.541391994	0.888671407	-8.17043632	3.03E-16	4.22E-15			
ABUW_RS00465	ABUW_1945	NZ_CP008706.1	194476	194670	+	WP_000101027.1		methylene tetrahydrofolate reductase C-terminal domain-containing protein	249.894874	-1.541391994	0.261962527	-5.90405513	3.55E-09	2.26E-08			
ABUW_RS19175	ABUW_1945	NZ_CP008706.1	194476	194670	+	WP_000101027.1		PIT/PIA family type 4 plus ATPase	995.758021	-1.5450872	0.176654201	-8.746393752	2.20E-18	3.86E-17			
ABUW_RS06365	ABUW_1905	NZ_CP008706.1	191895	191938	+	WP_000204017.1		hypothetical protein	79.4819486	-1.545555098	0.31719708	-4.873084536	1.10E-06	4.91E-06			
ABUW_RS19360	ABUW_1724	NZ_CP008706.1	1721879	1721932	-	WP_00101937.1		hypothetical protein	477.558418	-1.548610653	0.250369299	-6.177337487	6.52E-10	4.49E-09			
ABUW_RS19070	ABUW_2256	NZ_CP008706.1	2241429	2242409	-	WP_001075416.1		DNA polymerase II subunit delta'	603.0453584	-1.555233598	0.14859521	-1.15166693	1.05E-30	6.23E-29			
ABUW_RS19360	ABUW_3571	NZ_CP008706.1	3628500	3629159	-	WP_000916692.1		hypothetical protein	2130.826286	-1.555358928	0.268424023	-5.866492791	4.45E-09	2.79E-08			
ABUW_RS19195	ABUW_2323	NZ_CP008706.1	2307578	2307564	+		RNAI-1e	34.87147999	-1.554567599	0.605481881	-2.567485186	0.00243917	0.020792312				
ABUW_RS19685	no	NZ_CP008706.1	674650	674740	-	WP_085940648.1		B4 family transposase ISAbeta 1	463.718697	-1.558027536	0.251777324	-6.98189883	6.09E-10	4.20E-09			
ABUW_RS02655	ABUW_0540	NZ_CP008706.1	54748	54769	-	WP_000424605.1		hypothetical protein	96.977951	-1.558621853	0.293230585	-6.51614584	7.26E-11	5.66E-10			
ABUW_RS02655	ABUW_0540	NZ_CP008706.1	54748	54769	-	WP_000424605.1		hypothetical protein	96.977951	-1.558621853	0.293230585	-6.51614584	7.26E-11	5.66E-10			
ABUW_RS02655	ABUW_0540	NZ_CP008706.1	54748	54769	-	WP_000424605.1		hypothetical protein	96.977951	-1.558621853	0.293230585	-6.51614584	7.26E-11	5.66E-10			
ABUW_RS19040	ABUW_9332	NZ_CP008706.1	9309795	931415	+	WP_00107389.1		TetR/ArbR family transcriptional regulator	336.319610	-1.526907912	0.290873193	-5.249364455	1.53E-07	7.84E-07			
ABUW_RS19250	ABUW_408	NZ_CP008707.1	671832	68470	+	WP_000672680.1	traW	type-F conjugative transfer system protein TraW	73.26654751	-1.527841982	0.335971811	-4.547528432	5.43E-06	2.9E-05			
ABUW_RS18760	ABUW_3246	NZ_CP008706.1	3275271	3277076	+	WP_002017987.1		chromatin-binding protein	30180.38661	-1.531046468	0.217669369	-7.033819391	2.01E-12	1.90E-11			
ABUW_RS19145	ABUW_4386	NZ_CP008707.1	52381	53406	+	WP_00188464.1		IS30-like element ISAbeta U5 family transposase	3980.718091	-1.533995919	0.169847244	-6.833728946	5.76E-22	1.43E-20			
ABUW_RS10565	ABUW_1332	NZ_CP008706.1	1343403	1344095	+	WP_000180899.1	nci	ribonuclease II	2896.835898	-1.541391994	0.888671407	-8.17043632	3.03E-16	4.22E-15			
ABUW_RS00465	ABUW_1945	NZ_CP008706.1															

ABUW_RS14605	ABUW_3009	NZ_CP008706.1	3036911	3037789	-	WP_00064707.1		hypothetical protein	27.55395468	-1.686408472	0.57980503	-2.90830314	0.00363341	0.008266958
ABUW_RS14606	ABUW_4096	NZ_CP008706.1	58930	59196	+	WP_00077867.1		hypothetical protein	84.05733059	-1.691960468	0.475603766	-3.556196421	0.000376263	0.00707633
ABUW_RS15080	ABUW_935	NZ_CP008706.1	943558	146071	+	WP_00089593.1	recO	DNA repair protein RecO	884.4678057	-1.6919365	0.17623661	-8.600343327	7.976122	1.952120
ABUW_RS14445	ABUW_2975	NZ_CP008706.1	2991309	2992187	+	WP_000696108.1		homocysteine S-methyltransferase family protein	592.732493	-1.695501216	0.283466325	-5.98191422	2.216109	1.446108
ABUW_RS07555	ABUW_1448	NZ_CP008706.1	1430388	1441038	+	WP_000801894.1		hypothetical protein	853.2455004	-1.701951888	0.276029888	-6.899262004	3.596111	2.906101
ABUW_RS07795	ABUW_596	NZ_CP008706.1	592937	594106	+	WP_002013631.1		MF5 transporter	495.3069794	-1.7091184	0.213292197	-8.01303762	1.126115	1.496101
ABUW_RS02340	ABUW_0679	NZ_CP008706.1	683804	684166	+	WP_000191861		response regulator	9023.2299273	-1.711001055	0.196897478	-8.65913048	3.586119	6.175117
ABUW_RS1216	ABUW_2306	NZ_CP008706.1	2290958	2292046	+	WP_000204465.1	queG	RNA epoxycyclohex[34] reductase QueG	388.219102	-1.724092303	0.216223384	-8.0171087	1.194115	1.515116
ABUW_RS04790	ABUW_0977	NZ_CP008706.1	983636	990019	-	WP_001985534.1		lysophospholipid acyltransferase family protein	2154.018004	-1.736160472	0.177319063	-9.7191101	1.235122	3.356121
ABUW_RS02930	ABUW_0596	NZ_CP008706.1	594190	594963	-	WP_001985908.1		hypothetical protein	1105.355826	-1.736165036	0.216072309	-6.65009644	2.936111	2.396101
ABUW_RS12620	ABUW_2598	NZ_CP008706.1	2591406	2591927	+	WP_000024256.1		hypothetical protein	914.058063	-1.73616934	0.216667792	-7.903810561	2.716115	3.446114
ABUW_RS14065	ABUW_2896	NZ_CP008706.1	2904193	2905091	-	WP_000140408.1	cysD	sulfate adenylyltransferase subunit CysD	7926.503791	-1.742848894	0.218209597	-8.98926607	2.646115	3.696115
ABUW_RS04505	ABUW_1905	NZ_CP008706.1	1022791	1023885	+	WP_00057073.1		acyl-CoA desaturase	9930.02931	-1.749344826	0.217000085	-6.450384511	1.105110	8.475101
ABUW_RS03865	ABUW_0788	NZ_CP008706.1	769640	769858	+	WP_00077769.1		hypothetical protein	986.357941	-1.775224775	0.27323938	-6.496958008	8.206111	6.316110
ABUW_RS04435	ABUW_0904	NZ_CP008706.1	899218	900981	+	WP_000290935.1		alkaline phosphatase D family protein	197.067541	-1.785221012	0.241181629	-7.42529146	1.346113	1.426112
ABUW_RS04720	ABUW_0682	NZ_CP008706.1	972845	973223	-	WP_000457363.1		GtaA family protein	24.46107772	-1.791974992	0.577263638	-3.80408292	0.00190889	0.004666329
ABUW_RS07105	ABUW_1958	NZ_CP008706.1	1450199	1450833	+			RNA-Leu	315.7478288	-1.79391916	0.476853216	-3.76194467	0.00018554	0.000509867
ABUW_RS01540	ABUW_0315	NZ_CP008706.1	333366	336639	+	WP_000101600.1		GlpH/Fnt family pseudopilin	911.056043	-1.806585609	0.22770593	-7.530549002	2.165115	2.815116
ABUW_RS01780	ABUW_2421	NZ_CP008706.1	2406441	2409301	-	WP_000476792.1		transporter substrate-binding domain-containing protein	276.397073	-1.814250019	0.216800446	-8.372929194	5.632117	8.646116
ABUW_RS00960	ABUW_4007	NZ_CP008707.1	41890	5282	+	WP_000790917.1		hypothetical protein	422.042738	-1.81916536	0.362968872	-5.01671803	5.395107	2.555106
ABUW_RS1060	ABUW_2274	NZ_CP008706.1	225916	2260178	+	WP_000153516.1		cupin domain-containing protein	1620.873493	-1.832070844	0.195718302	-10.42688699	1.875125	6.516124
ABUW_RS1620	ABUW_3218	NZ_CP008706.1	325094	3250670	-			RNA-Pro	1082.580712	-1.833180262	0.356992765	-6.429327164	3.676106	1.496105
ABUW_RS03070	ABUW_9224	NZ_CP008706.1	922491	923222	+	WP_000883491.1	GntR family transcriptional regulator	1072.836297	-1.839987964	0.20216443	-9.1009187	9.035120	1.625118	
ABUW_RS14660	ABUW_2939	NZ_CP008706.1	3021420	3020927	-	WP_000780944.1	DUF4391 domain-containing protein	570.009173	-1.842477969	0.233106918	-7.903321674	2.726115	3.446114	
ABUW_RS03020	ABUW_0643	NZ_CP008706.1	613659	6136040	-	WP_00066105.1		hypothetical protein	58.62407643	-1.842680044	0.424730885	-4.339259399	1.446105	5.296105
ABUW_RS01795	ABUW_1774	NZ_CP008706.1	1760231	1760746	+	WP_000729387.1	DUF2280 domain-containing protein	58.6483286	-1.843648853	0.826871279	-2.232368287	0.025590632	0.046566402	
ABUW_RS18210	ABUW_2162	NZ_CP008706.1	2086533	2086584	-	WP_000668585.1		hypothetical protein	30.02057414	-1.851097416	0.854827253	-2.165463736	0.0303529	0.0539689
ABUW_RS03360	ABUW_0683	NZ_CP008706.1	619152	620016	+	WP_000687891.1		hypothetical protein	751.036037	-1.856876449	0.16010104	-9.76629869	1.575122	4.196121
ABUW_RS18230	ABUW_4039	NZ_CP008707.1	23906	23962	+	WP_000710365.1		hypothetical protein	497.882776	-1.85861910	0.297566997	-6.246259146	4.206110	2.985109
ABUW_RS15105	ABUW_2707	NZ_CP008706.1	2688875	2691046	-	WP_000377525.1		coppin-translocating P-type ATPase	1657.206891	-1.861019191	0.237510056	-7.835401637	4.675115	5.816116
ABUW_RS01745	ABUW_0686	NZ_CP008706.1	6173140	6173778	-	WP_000590066.1	TeuR/AcR family transcriptional regulator	44.50382304	-1.878673042	1.22729396	-1.536371431	0.04445639	0.8292125	
ABUW_RS03345	ABUW_0980	NZ_CP008706.1	842277	849473	+	WP_000729762.1		putative-binding chemotaxis protein CheW	2168.743622	-1.880603036	0.261736088	-7.18102389	8.716116	6.756101
ABUW_RS20285	ABUW_2897	NZ_CP008706.1	2905084	2905216	-	WP_002010185.1		hypothetical protein	1976.95203	-1.887263412	0.229645298	-8.221747195	2.016116	2.886116
ABUW_RS01585	ABUW_0222	NZ_CP008706.1	24494	244845	+	WP_000726401.1	TeuR/AcR family transcriptional regulator	10.8170043	-1.889904041	0.776281429	-2.436406663	0.04333997	0.02819443	
ABUW_RS17385	ABUW_2635	NZ_CP008706.1	2634617	2635147	+	WP_085120603.1	GNAT family N-acetyltransferase	865.193934	-1.889334347	0.20550225	-9.15040084	3.876120	8.056119	
ABUW_RS19995	ABUW_3674	NZ_CP008706.1	3730894	3732342	-	WP_00518003.1		hypothetical protein	31.7560919	-1.89255884	0.1866973	-1.135321006	7.156130	3.956128
ABUW_RS04425	ABUW_0902	NZ_CP008706.1	898516	898686	-	WP_000180261.1		hypothetical protein	453.7988756	-1.920540583	0.274516164	-9.696093164	2.636112	2.456111
ABUW_RS01755	ABUW_0765	NZ_CP008706.1	765258	766134	+			RNA-Arg	3.723196614	-1.926296374	1.338324007	-1.439334842	0.60005676	0.21540212
ABUW_RS18195	ABUW_4034	NZ_CP008707.1	20322	20540	+	WP_00043201.1		hypothetical protein	20.9817377	-1.927471447	0.646647768	-2.985326885	0.002832728	0.00616435
ABUW_RS03965	ABUW_0810	NZ_CP008706.1	786559	789101	+	WP_000109703.1		hypothetical protein	738.126905	-1.954846322	0.47241144	-7.02994107	1.006112	9.846112
ABUW_RS15175	ABUW_3125	NZ_CP008706.1	3146270	3146734	-	WP_00014863.1	bfr	bacterioferritin	1289.81949	-1.956795834	0.403685637	-4.847325877	1.255106	5.535106
ABUW_RS17910	ABUW_3453	NZ_CP008706.1	3500553	3501316	+	WP_000967566.1		hypothetical protein	4224.585304	-1.972219138	0.212500498	-9.287503353	1.585120	3.406119
ABUW_RS03975	ABUW_0812	NZ_CP008706.1	789693	790196	+	WP_000172901.1		hypothetical protein	1646.005819	-1.975867246	0.278714498	-7.063781413	1.626112	1.556111
ABUW_RS06176	ABUW_0776	NZ_CP008706.1	9190336	9190981	-	WP_000189388.1		sulfatransferase Tusk family protein	451.570286	-1.983724247	0.006908089	-6.817669439	9.256112	8.026111
ABUW_RS03070	ABUW_0906	NZ_CP008706.1	918400	919916	+	WP_00077769.1		hypothetical protein	802.3074534	-1.916382368	0.301961927	-6.690650794	2.236111	1.846110
ABUW_RS01240	ABUW_0253	NZ_CP008706.1	266667	268742	+			RNA-Phe	53.84837325	-2.016668317	0.560306341	-3.599256641	0.000319128	0.000919062
ABUW_RS02700	ABUW_0550	NZ_CP008706.1	551375	553520	-	WP_000556351.1			296.442053	-2.022420979	0.330794853	-8.762851006	1.190118	3.366117
ABUW_RS01655	ABUW_0444	NZ_CP008706.1	516272	516635	-	WP_001096325.1	YfhJ family 4Fe-4S cluster ferredoxin	132.2757823	-2.023012605	0.394277765	-5.0093252	2.886107	1.425106	
ABUW_RS01665	ABUW_0318	NZ_CP008706.1	341387	341569	+	WP_000146489.1	prelin-type II terminal cleavage/methyltransferase domain-containing protein	325.648921	-2.040058651	0.166189897	-1.00603491	5.535120	6.056137	
ABUW_RS11616	ABUW_2387	NZ_CP008706.1	2376040	2376040	+	WP_000474201.1		hypothetical protein	610.4540051	-2.043625662	0.353334878	-5.738320922	7.306110	4.465108
ABUW_RS01670	ABUW_0319	NZ_CP008706.1	341566	341991	+	WP_000783361.1	prelin-type II terminal cleavage/methyltransferase domain-containing protein	305.5426716	-2.048244651	0.19231476	-1.18864632	1.196132	1.002130	
ABUW_RS18180	ABUW_2472	NZ_CP008706.1	3504451	3504672	+	WP_000284370.1	inA	translation initiation factor F-1	5707.830075	-2.058982483	0.226314219	-9.097892695	9.216120	1.856118
ABUW_RS17020	ABUW_3499	NZ_CP008706.1	3547232	3547232	-	WP_000887662.1	DUF4062 domain-containing protein	336.7441462	-2.073264996	0.21184628	-9.786646216	1.286122	3.476121	
ABUW_RS17975	no	NZ_CP008706.1	966536	966533	+			GNAT family N-acetyltransferase	28.0202194	-2.079535079	0.718964536	-2.659193876	0.007834043	0.009387636
ABUW_RS01800	ABUW_0662	NZ_CP008706.1	615514	6155641	+	WP_000774578.1		hypothetical protein	12.03631639	-2.087764409	0.24524795	-2.46118346	0.007786652	0.00360058
ABUW_RS02320	no	NZ_CP008706.1	3371498	3371820	+	WP_000184446.1		hypothetical protein	92.3160254	-2.096317943	0.705493192	-2.917467188	0.002963306	0.006890463
ABUW_RS01425	ABUW_0290	NZ_CP008706.1	309823	310881	+	WP_002190661.1		plus assembly protein PBM	448.1295578	-2.099062175	0.224062944	-9.36818084	7.386121	1.625119
ABUW_RS19216	ABUW_4038	NZ_CP008707.1	22368	22895	-	WP_000312250.1	type II toxin-antitoxin system RelE/PaeE family toxin	610.432189	-2.100722922	0.303435043	-6.923188808	4.426112	4.046111	
ABUW_RS19230	ABUW_4041	NZ_CP008707.1	25960	24658	+	WP_000873188.1		hypothetical protein	378.4862268	-2.105789831	0.327226358	-6.435266841	1.235110	9.325101
ABUW_RS17275	ABUW_3550	NZ_CP008706.1	3607699	3608335	+	WP_000278216.1	type II secretion system F family protein	1040.985169	-2.10248949	0.210971746	-10.15342081	3.205124	1.035122	
ABUW_RS11616	ABUW_0316	NZ_CP008706.1	333932	339210	+	WP_00019374.1		hypothetical protein	436.927162	-2.1170991	0.242651882	-8.948636859	3.606119	6.875118
ABUW_RS18175	ABUW_2422	NZ_CP008706.1	2409332	2410063	-	WP_001010393.1	amino acid ABC transporter ATP-binding protein	83.9656982	-2.162840301	0.371849244	-5.870229224	4.356109	2.735108	
ABUW_RS01670	ABUW_2276	NZ_CP008706.1	2261957	2261865	+	WP_000851464.1	helic-tum-helix transcriptional regulator	492.0673339	-2.19196169	0.3363568	-6.538283661	6.225111	4.886110	
ABUW_RS04420	ABUW_0901	NZ_CP00870												

ABUW_RS03355	ABUW_0682	NZ_CP008706.1	687035	691555	+	WP_000658892.1		Hpt domain-containing protein	6681.129179	-2.776668267	0.203779582	-13.62682286	2.77E-42	3.99E-40
ABUW_RS01435	ABUW_0292	NZ_CP008706.1	31519	312259	+	WP_000076101.1		type 4a plus biogenesis protein PLO	1434.943211	-2.800639599	0.270915543	-10.33768521	4.76E-25	1.60E-23
sRNA7	no	no	no	no	no	no	no	no	1268.471058	-2.88116217	0.415583376	-6.932703238	4.13E-12	3.79E-11
ABUW_RS09450	ABUW_1942	NZ_CP008706.1	1941385	1942269	+	WP_001007514.1		ribose-phosphate pyrophosphokinase	1577.014582	-2.958020648	0.638457225	-4.63307569	3.60E-06	1.47E-05
ABUW_RS19495	ABUW_4103	NZ_CP008707.1	63264	63524	+	WP_000876194.1		hypothetical protein	26.90464355	-3.011441861	0.857806995	-3.510628474	0.000447049	0.001249281
ABUW_RS1585	ABUW_2381	NZ_CP008706.1	2367863	2368657	-	WP_000114471.1		ATP-binding cassette domain-containing protein	719.963052	-3.087527617	0.453741516	-6.804598811	1.01E-11	8.72E-11
ABUW_RS05000	ABUW_1019	NZ_CP008706.1	1030394	1031227	-	WP_000083117.1	cysT	sulfate ABC transporter permease subunit CysT	116.0387869	-3.087918763	0.438045079	-7.049317326	1.80E-12	1.71E-11
ABUW_RS14420	ABUW_2970	NZ_CP008706.1	2984536	2985159	+	WP_000166965.1	betI	transcriptional regulator BetI	4254.12659	-3.168078762	0.375622964	-8.487443716	2.11E-17	3.32E-16
ABUW_RS16080	ABUW_3310	NZ_CP008706.1	3344551	3344952	+	WP_001047580.1	rsfS	ribosome silencing factor	10929.26628	-3.277828487	0.242266493	-5.329846611	1.04E-41	1.45E-39
ABUW_RS15690	ABUW_2382	NZ_CP008706.1	2368667	2369707	-	WP_000651495.1	tauA	taurine ABC transporter substrate-binding protein	782.0023615	-3.326803266	0.541732256	-6.11047034	8.20E-10	5.58E-09
ABUW_RS05005	ABUW_1020	NZ_CP008706.1	1031308	1031916	-	WP_000149921.1		alpha/beta hydrolase	280.8572397	-3.372580059	0.54102429	-6.233696919	4.56E-10	3.21E-09
ABUW_RS05010	ABUW_1021	NZ_CP008706.1	1031947	1032954	-	WP_001216001.1		sulfate ABC transporter substrate-binding protein	524.9851564	-3.382883506	0.58556233	-5.777213724	7.59E-09	4.63E-08
ABUW_RS08030	ABUW_1645	NZ_CP008706.1	1640257	1640811	+	WP_00133116.1		TetR/AcrI family transcriptional regulator	113.2415457	-3.411391653	1.051249331	-3.245083305	0.001174163	0.002962788
sRNA56	no	no	no	no	no	no	no	no	13.12046502	-3.506290946	1.408774015	-2.488895244	0.01281072	0.025270629
sRNA57	no	no	no	no	no	no	no	no	16.02129697	-3.596357615	1.112177036	-2.233619738	0.00122321	0.003089542
ABUW_RS12115	ABUW_2489	NZ_CP008706.1	2485285	2485581	-	WP_001062883.1		NAD(P)H-dependent oxidoreductase	443.6515256	-3.626463031	0.405328818	-8.946965707	3.65E-19	6.94E-16
ABUW_RS20210	no	NZ_CP008706.1	2411445	2411558	+	WP_002017921.1		hypothetical protein	7.891497102	-3.64434503	0.902996819	-4.035833743	5.44E-05	0.000160422
ABUW_RS08010	ABUW_1641	NZ_CP008706.1	1637480	1637816	+	WP_0010243508.1		hypothetical protein	261.4524357	-3.669831186	0.326131162	-1.125262352	2.25E-29	1.18E-27
ABUW_RS1280	ABUW_2319	NZ_CP008706.1	2304179	2304616	-	WP_001161759.1		PACE efflux transporter	486.7408237	-4.520461432	0.542224696	-8.336878535	7.63E-17	1.18E-15

Table S17. RNA-seq data: Absolute and relative expression (Col/MEP > 2-fold up)

locus_tag	old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	-log10
ABUW_RS07255	ABUW_1488	NZ_CP008706.1	1474973	1475521	+	WP_000577009.1	csuA	Csu fimbrial biogenesis protein CsuA	288.6416321	5.8011913	1.275685781	4.547492401	5.43E-06	2.20E-05	4.65577319
ABUW_RS07275	ABUW_1492	NZ_CP008706.1	1479364	1480383	+	WP_002017500.1	csuE	Csu fimbrial tip adhesin CsuE	294.4313251	5.56707664	1.08628993	5.02586728	NA	NA	#VALUE!
ABUW_RS07270	ABUW_1491	NZ_CP008706.1	1478699	1479367	+	WP_000603294.1	csuD	Csu fimbrial usher CsuD	970.5711689	5.54398119	1.028646788	4.91026004	NA	NA	#VALUE!
ABUW_RS07260	ABUW_1489	NZ_CP008706.1	1475527	1476045	+	WP_000876475.1	csuB	Csu fimbrial biogenesis protein CsuB	124.0737787	4.94519459	1.306885417	3.793919688	0.000154378	0.000471023	3.326791953
ABUW_RS07265	ABUW_1490	NZ_CP008706.1	1476039	1476872	+	WP_001886519.1	csuC	Csu fimbrial biogenesis chaperone CsuC	340.6660512	4.67444495	1.123172632	4.16122234	3.18E-05	0.000110997	3.954688759
ABUW_RS07250	ABUW_1487	NZ_CP008706.1	1474362	1474898	+	WP_000790104.1	csuAB	Csu fimbrial major subunit CsuAB	1918.820395	4.543705543	1.248088359	3.640531946	NA	NA	#VALUE!
ABUW_RS00335	ABUW_0068	NZ_CP008706.1	72582	73130	-	WP_000141645.1		VOC family protein	2410.96693	4.09491267	0.353748256	11.57578051	5.47E-31	6.88E-29	28.1624156
ABUW_RS00340	ABUW_0069	NZ_CP008706.1	73148	73780	-	WP_000781235.1	maiA	maleylacetate isomerase	4447.188604	3.965621677	0.373842519	10.60773315	2.74E-26	2.09E-24	23.67985371
ABUW_RS10090	ABUW_2697	NZ_CP008706.1	2682890	2682966	-			tRNA-Met	1582.975218	3.874501463	0.401107748	9.657866001	4.55E-22	1.99E-20	19.70146901
ABUW_RS1225	ABUW_2513	NZ_CP008706.1	2506933	-	WP_000072126.1			cold-shock protein	808.9924084	3.856104203	0.750083195	5.10902008	2.73E-07	1.40E-06	5.853871964
ABUW_RS00345	ABUW_0070	NZ_CP008706.1	73767	75074	-	WP_000435854.1	fahA	fumarylacetoacetase	12787.00428	3.813773533	0.36715688	10.38447877	1.91E-23	22.7189663	
ABUW_RS07135	ABUW_1464	NZ_CP008706.1	1453227	1454795	+	WP_000181272.1		CoA-acylating methylmalonate-semialdehyde dehydrogenase	524.0297573	3.704209434	0.275315745	13.45440661	2.90E-41	1.67E-38	37.77728353
ABUW_RS10085	ABUW_2696	NZ_CP008706.1	2682483	2682716	+	WP_000636765.1		transposase	1646.096965	3.69340621	0.570016215	6.479475692	9.20E-11	8.85E-10	9.066512712
ABUW_RS20160	no	NZ_CP008706.1	197527	167821	+			hypothetical protein	15.5197219	3.49162364	13.14483706	2.65827004	0.00791033	0.01493917	1.782676195
sRNA44	no	no	no	no	no	no	no	no	4.738178039	3.477104649	1.345458952	2.584326073	0.00975695	0.019853915	1.702163842
ABUW_RS12520	ABUW_2577	NZ_CP008706.1	2570866	2571342	-	WP_001047031.1	tsaE	type VI secretion system baseplate subunit TsaE	1299.496828	3.474918795	0.290171146	11.97541121	4.78E-33	7.41E-31	30.13018179
ABUW_RS19295	ABUW_4055	NZ_CP008707.1	32005	33741	-	WP_000480966.1	APH(8)-	family aminoglycoside O-phosphotransferase	480.2357999	3.370843966	0.434823342	7.752444827	9.91E-15	1.46E-13	12.83564714
ABUW_RS00325	ABUW_0066	NZ_CP008706.1	70383	71438	+	WP_000353163.1	hppD	4-hydroxyphenylpyruvate dioxygenase	93.16153215	3.35014011	0.325488895	9.2264035	7.61E-25	4.71E-23	22.32697909
ABUW_RS07245	ABUW_1486	NZ_CP008706.1	1473140	1473778	-	WP_0005990096.1		TetR/AcrI family transcriptional regulator	44.50382304	3.330204056	1.159167038	2.872953315	0.004066542	0.009142912	2.03891546
ABUW_RS18335	ABUW_3766	NZ_CP008706.1	3819776	3818743	+	WP_001286049.1		4'-phosphopantetheinyl transferase superfamily protein	568.5876529	3.18423005	0.29343096	11.30940241	1.18E-29	1.23E-27	26.91009489
ABUW_RS0740	ABUW_1465	NZ_CP008706.1	1454899	1456296	+	WP_001058165.1		amino acid permease	11.5931751	3.257958912	0.268997698	12.1147508	9.18E-34	1.61E-31	30.79317412
ABUW_RS12515	ABUW_2576	NZ_CP008706.1	2569038	2570849	-	WP_000568824.1	tsaF	type VI secretion system baseplate subunit TsaF	948.544954	3.237017187	0.253824671	12.75296517	3.00E-37	8.00E-35	34.09366496
ABUW_RS13120	ABUW_2703	NZ_CP008706.1	2687015	2687371	+	WP_001088692.1		four-helix bundle copper-binding protein	7279.866477	3.215399861	0.457521102	7.027898178	2.10E-12	2.52E-11	10.59859946
ABUW_RS10055	ABUW_2690	NZ_CP008706.1	2678666	2677881	-	WP_000072673.1		cold-shock protein	45815.85517	3.074180625	0.438025087	7.018275248	2.25E-12	2.69E-11	10.57024772
ABUW_RS12330	ABUW_2514	NZ_CP008706.1	2507184	2507484	-	WP_000338517.1		hypothetical protein	200.4946675	3.065282676	0.715162674	4.539863446	5.03E-06	2.27E-05	4.643974143
ABUW_RS15175	ABUW_1325	NZ_CP008706.1	1346270	1346734	-	WP_001214863.1	bfr	bacterioferritin	12989.31849	3.04189823	0.40281897	7.551526766	4.50E-16	6.57E-15	12.12434361
ABUW_RS19300	ABUW_4056	NZ_CP008707.1	33741	34544	-	WP_025464697.1	aph(3')-Ib	aminoglycoside O-phosphotransferase APH(3')-Ib	857.9827749	2.99716429	0.44012432	6.809842145	9.77E-12	1.07E-10	9.970616222
ABUW_RS01750	ABUW_0357	NZ_CP008706.1	380432	380740	+	WP_004571408.1		hypothetical protein	96.23606246	2.952070889	0.40105243	7.35530837	1.90E-13	2.59E-12	11.58670021
ABUW_RS20020	ABUW_4046	NZ_CP008707.1	26577	27569	+	WP_001381192.1		Tnfr family NTP-binding protein	580.781501	2.801270144	0.242635872	11.54516074	9.25E-29	28.03385827	
sRNA5	no	no	no	no	no	no	no	no	3.947129552	2.757266202	1.483247444	1.858215543	0.063138412	0.30031454	0.987030171
ABUW_RS15170	ABUW_1324	NZ_CP008706.1	3144782	3145975	-	WP_001992111.1		MFS transporter	835.9180838	2.639545963	0.284014658	9.293969243	1.49E-20	5.27E-19	18.27818938
ABUW_RS09985	ABUW_2056	NZ_CP008706.1	2035907	2036884	+	WP_000719470.1		DUF4882 family protein	429.0684263	2.624256719	0.300920493	8.720764398	2.70E-16	7.14E-17	16.14630179
ABUW_RS19305	ABUW_4057	NZ_CP008707.1	34574	35365	+	WP_001261470.1		ANT(3')-I family aminoglycoside nucleotidyltransferase AadA2	653.4054952	2.624234272	0.422473822	6.21159318	5.25E-10	4.14E-09	8.35556111
ABUW_RS06150	ABUW_0258	NZ_CP008706.1	1294750	1295040	-	WP_000453627.1		hypothetical protein	24.15352877	2.610491703	0.560156467	4.660456515	3.36E-06	1.34E-05	4.872895202
ABUW_RS20425	ABUW_0650	NZ_CP008706.1	655407	655565	-	WP_000692859.1		hypothetical protein	6450.455749	2.597702984	0.318185219	8.199426136	2.42E-16	4.77E-15	11.32181612
ABUW_RS03205	ABUW_0651	NZ_CP008706.1	655569	656774	-	WP_000512708.1		RicB family protein	16281.97678	2.578217003	0.343524079	7.505200249	6.15E-14	9.02E-13	12.04479346
ABUW_RS06480	ABUW_1324	NZ_CP008706.1	1338270	1338626	+	WP_000138204.1		hypothetical protein	24.05395814	2.57729907	0.552602601	4.66392859	3.10E-06	1.32E-05	4.879426069
ABUW_RS08510	ABUW_1747	NZ_CP008706.1	1745412	1745894	-	WP_000476758.1		regulatory protein RecX	1036.097036	2.563049811	0.292043395	8.776283922	1.69E-18	4.48E-17	16.34871292
ABUW_RS01660	ABUW_0337	NZ_CP008706.1	358122	359551	+	WP_000790118.1		MFS transporter	4481.333756	2.556436625	0.1996849	6.087210555	1.15E-09	8.89E-09	8.046240308
ABUW_RS13710	ABUW_2821	NZ_CP008706.1	2826194	2826283	-			tRNA-Ser	99.40023687	2.542124244	0.445349158	5.708160238	1.14E-08	7.81E-08	1.71861543
ABUW_RS00785	ABUW_0158	NZ_CP008706.1	175584	176159	+	WP_001584194.1		TMEM55/GDI family protein	1185.273301	2.525192726	0.25019877	10.05302441	5.93E-24	3.32E-22	21.47886192
ABUW_RS12510	ABUW_2575	NZ_CP008706.1	2568076	2569074	-	WP_001190395.1	tsaG	type VI secretion system baseplate subunit TsaG	368.6562697	2.51969474	0.262446495	8.600777147	7.93E-22	3.20E-20	19.45489050
ABUW_RS20235	ABUW_2515	NZ_CP008706.1	2507870	2508022	+	WP_001279164.1		hypothetical protein	11.0629751	2.509784006	0.764619062	3.282397488	0.000202824	0.002677349	2.482793605
sRNA73	no	no	no	no	no	no	no	no	40.42812639	2.490462068	0.683254717	3.644997988	0.000267394	0.000784083	3.105637962
ABUW_RS120105	no	NZ_CP008706.1	1408830	1409884	-	WP_085918973.1		hypothetical protein	15.93348052	2.457083392	0.196779146	2.538041428	0.01136657	0.002378668	1.650185767
ABUW_RS06025	ABUW_0233	NZ_CP008706.1	1275970	1277088	-	WP_000976525.1		OrpW family protein	350.0831077	2.465536007	0.26320503	9.33316512	1.03E-20	3.80E-19	12.4825164
ABUW_RS06465	ABUW_025	NZ_CP008706.1	1336623	1338481	+	WP_001083663.1		hypothetical protein	19.42723645	2.444193561	0.583966098	4.186777663	2.83E-05	0.000100439	3.99808782
ABUW_RS10050	ABUW_2689	NZ_CP008706.1	2678239	2678463	+	WP_000530500.1		hypothetical protein	226.7599471	2.431962919	0.426426747	5.702404104	1.18E-08	7.84E-08	7.105689397
ABUW_RS02785	ABUW_0567	NZ_CP008706.1	565618	566793	-	WP_000963361.1		phage tail sheath protein	92.3917995	2.408926589	0.30123585	8.002451925	1.22E-15	2.18E-14	16.854351
ABUW_RS09970	ABUW_2053	NZ_CP008706.1	2013437	2023271	+	WP_00074086.1		molecular chaperone	1028.755828	2.40603887	0.60639242	3.967788514	7.25E-05	0.000238008	3.623408445
ABUW_RS02780	ABUW_0566	NZ_CP008706.1	565087	566005	-	WP_00107672.1		phage major tail tube protein	1067.591896	2.395479906	0.30479035	10.2720331	1.56E-15	2.75E-14	15.9666731
ABUW_RS02265	ABUW_2687	NZ_CP008706.1	2676668	2676987	+	WP_001882898.1		hypothetical protein	86.073126	2.388423749	0.38019115	6.63121109	3.33E-11	3.36E-10	9.473660723
ABUW_RS09715	ABUW_1999	NZ_CP008706.1	1998188	1998406	-	WP_002074156.1		hypothetical protein	120.2460439	2.376006998	0.324583596	7.320178004	2.48E-13	3.34E-12	11.6725535
ABUW_RS04435	ABUW_0904	NZ_CP008706.1	889218	900981	+	WP_000390145.1		alkaline phosphatase D family protein	1177.087541	2.374949088	0.22978396	10.32955642	5.9E-25	2.22E-24	22.8455222

ABUW_S00965	ABUW_2002	NZ_CP008706.1	203085	203488	+	WP_000739.9.1	type I fibrinolytic protein	6554.745857	2.360892927	1.59043983	3.995700977	6.375e-05	0.0002151	3.67672289
ABUW_S00966	ABUW_2010	NZ_CP008706.1	204654	204942	+	WP_000740.96.1	hypothetical protein	10.7492727	2.342976355	0.33346245	0.02570634	2.10e-02	1.03534582	1.03534582
ABUW_S00968	ABUW_2021	NZ_CP008706.1	201411	201559	+	WP_000740.96.1	hypothetical protein	50.68445	2.336781259	0.37848783	6.17999233	5.64e-06	5.505e-09	8.25963731
ABUW_S003685	ABUW_0749	NZ_CP008706.1	744422	744868	+	WP_000604.956.1	hypothetical protein	219.703758	2.193960656	0.265923993	8.7473978	9.17e-06	8.245558e-06	1.03534582
ABUW_S003675	ABUW_0382	NZ_CP008706.1	409290	409475	+	WP_000471.161.1	hypothetical protein	92.10632	2.30773805	0.433028366	5.523309346	8.86e-08	5.475e-07	4.26204782
ABUW_RS10420	ABUW_2414	NZ_CP008706.1	212945	210288	+	WP_00037442.1	hypothetical protein	922.864811	2.284387184	0.2134.677	6.704858	9.73e-27	8.005e-25	24.09697601
ABUW_RS10635	ABUW_2811	NZ_CP008706.1	28.0801	28.1241	+	WP_000773509.1	hypothetical protein	438.0404251	2.27768	0.3266624	6.994002743	2.67e-12	3.14e-11	0.30570335
ABUW_RS10636	ABUW_2536	NZ_CP008706.1	255981	255941	+	WP_01013008.1	TetR/ACR family transcriptional regulator	21.7683288	2.277594.09	0.92803155	2.454.82682	0.014.074.01	0.027582696	15.09435351
ABUW_RS10335	ABUW_2331	NZ_CP008706.1	23.9.863	23.9044	+	WP_000347804.1	amino acid ABC transporter permease	107.85308	2.270890385	0.246106989	9.227.14735	2.78e-20	9.56e-19	0.8594211
ABUW_RS08855	ABUW_2332	NZ_CP008706.1	20.976	20.7836	+	WP_000740.96.1	hypothetical protein	107.093058	2.263962241	0.363064671	6.23599647	4.50e-10	3.85e-09	1.05413927
ABUW_RS10350	ABUW_2079	NZ_CP008706.1	20.1675	257.345	-	WP_00.066523.1	type I/secretion system contractile sheath large subunit	4496.179095	2.25690873	0.26422532	8.53200961	1.44e-17	3.28e-16	1.4867824
ABUW_RS10525	ABUW_121	NZ_CP008706.1	125261	125263	+		IRNA_Asn	43.4583954	2.25684093	0.44055103	4.54508.92	5.02e-28	0.96e-27	6.53077984
ABUW_RS10630	ABUW_2806	NZ_CP008706.1	28.0642	28.0543	+	WP_000428942.1	APC family transcriptional regulator	250.3002455	2.25557106	0.27490613	8.204877528	2.38e-16	4.58e-15	0.33919452
ABUW_RS10505	ABUW_2574	NZ_CP008706.1	256667	256.6709	+	WP_000509.82.1	hypothetical protein	359.85124	2.246958897	0.222956308	0.70.80234	6.95e-24	3.76e-22	21.4248192
ABUW_RS10630	ABUW_2806	NZ_CP008706.1	28.0642	28.0543	+	WP_000428942.1	APC family transcriptional regulator	250.3002455	2.25557106	0.27490613	8.204877528	2.38e-16	4.58e-15	0.33919452
ABUW_RS10630	ABUW_2806	NZ_CP008706.1	28.0642	28.0543	+	WP_000428942.1	APC family transcriptional regulator	250.3002455	2.25557106	0.27490613	8.204877528	2.38e-16	4.58e-15	0.33919452
ABUW_RS10630	ABUW_2806	NZ_CP008706.1	28.0642	28.0543	+	WP_000428942.1	APC family transcriptional regulator	250.3002455	2.25557106	0.27490613	8.204877528	2.38e-16	4.58e-15	0.33919452
ABUW_RS10630	ABUW_2806	NZ_CP008706.1	28.0642	28.0543	+	WP_000428942.1	APC family transcriptional regulator	250.3002455	2.25557106	0.27490613	8.204877528	2.38e-16	4.58e-15	0.33919452
ABUW_RS10630	ABUW_2806	NZ_CP008706.1	28.0642	28.0543	+	WP_000428942.1	APC family transcriptional regulator	250.3002455	2.25557106	0.27490613	8.204877528	2.38e-16	4.58e-15	0.33919452
ABUW_RS10630	ABUW_2806	NZ_CP008706.1	28.0642	28.0543	+	WP_000428942.1	APC family transcriptional regulator	250.3002455	2.25557106	0.27490613	8.204877528	2.38e-16	4.58e-15	0.33

ABLUW_RS19025	ABLUW_3095	NZ_CP008706.1	312189	3121863	+			IRNA: Gln	198.173635	1764370221	0.321045885	5.492273371	3.975E-08	2.38E-07	6.623423043
ABLUW_RS06340	ABLUW_1000	NZ_CP008706.1	130819	1310481	+	WP_000692540.1		stress-responsive nuclear envelope protein	20.43787207	1762853336	0.428019517	4.138041498	3.506E-05	0.00022396	3.91508747
ABLUW_RS19765	ABLUW_1610	NZ_CP008706.1	8060447	8060647	+	WP_000462396.1		hypothetical protein	4.998927239	1754923725	1.117066481	1.570789734	0.183756229	0.173401408	0.70094738
ABLUW_RS02030	no	NZ_CP008707.1	31709	32644	+		wtII	class II integron integrase IntII	41861039602	175381671	0.28193197	0.230401753	4.656E-01	3.95E-09	4.603402904
ABLUW_RS13460	ABLUW_2772	NZ_CP008706.1	2764390	2766276	-	WP_001935611		MRP transporter	243.5147894	1751387905	0.291765017	0.00271794	1.946E-09	1.475E-08	7.832682665
ABLUW_RS01595	ABLUW_0324	NZ_CP008706.1	346371	347312	-	WP_085191555.1		acetylpropionyl(methylcrotonyl)-CoA carboxylase subunit alpha	406.5285196	1744007348	0.263833103	6.903254578	3.846E-11	8.33E-01	9.416301226
ABLUW_RS19520	ABLUW_3218	NZ_CP008706.1	3250594	3250670	-			IRNA: Pro	6082.580710	17439971696	0.39319103	4.434073956	9.255E-06	3.57E-05	4.447331794
ABLUW_RS07365	ABLUW_1450	NZ_CP008706.1	144282	1443589	+	WP_085920632.1		M6S family metalloprotease	799.2567573	1740453828	0.255079358	6.823292893	8.90E-12	9.74E-11	0.1144104
ABLUW_RS16915	ABLUW_3277	NZ_CP008706.1	330245	331613	+	WP_001054522.1	rho	transcription termination factor Rho	2.08510344	1740437566	0.175068537	9.940487439	2.77E-23	1.33E-21	20.87614836
ABLUW_RS08090	ABLUW_1660	NZ_CP008706.1	1652839	1654422	-	WP_000193596.1		ABC F family ATP-binding cassette domain-containing protein	749.2675832	1739374724	0.269388364	6.480812719	9.0E-11	8.53E-10	0.069050969
ABLUW_RS18145	ABLUW_2455	NZ_CP008706.1	2442667	2444658	+	WP_00044820.1		acetylpropionyl(methylcrotonyl)-CoA carboxylase subunit alpha	3837.508829	1735889364	0.29478012	5.888700098	3.89E-09	2.83E-08	7.548213564
ABLUW_RS19030	ABLUW_3096	NZ_CP008706.1	312195	3122029	+			IRNA: Gln	175.4921436	1732319021	0.26031273	6.054761957	2.84E-11	2.89E-10	9.539102167
ABLUW_RS03310	ABLUW_0673	NZ_CP008706.1	676016	676357	+	WP_000291502.1		YagP family protein	1166.384488	171815882	0.303119953	5.068180558	1.445E-08	9.43E-08	7.025483037
ABLUW_RS03040	ABLUW_0691	NZ_CP008706.1	698433	698508	+			IRNA: Val	1056.04106	170990117	0.303859457	5.62727455	1.833E-08	1.16E-07	6.935542011
ABLUW_RS18140	ABLUW_2454	NZ_CP008706.1	2441852	2442655	+	WP_000121729.1		enoyl-CoA hydratase/isomerase family protein	1274.636723	1696702884	0.329855710	5.143727914	2.698E-07	1.38E-06	8.601020914
ABLUW_RS02390	ABLUW_0487	NZ_CP008706.1	499193	500320	+	WP_000687306.1		acyl-CoA dehydrogenase family protein	363.2200255	1692253745	0.289469865	5.84604462	0.030E-09	3.58E-08	7.446189373
ABLUW_RS01760	ABLUW_2009	NZ_CP008706.1	2003522	2004464	+	WP_005142463.1		replication initiation factor domain-containing protein	378.6741463	1687474644	0.235933971	7.15171886	8.57E-10	1.08E-11	0.065667624
ABLUW_RS19405	ABLUW_4017	NZ_CP008707.1	8455	8869	+	WP_001670890.1		hypothetical protein	276.4059579	168696081	0.262842564	6.14194117	1.33E-10	1.26E-09	8.896261455
ABLUW_RS19045	ABLUW_2688	NZ_CP008706.1	2677144	2677159	-	WP_000932376.1		NAD(P)+ binding domain-containing protein	1219.487287	1684142314	0.193527524	10.9695442	3.35E-38	4.79E-26	26.19662440
ABLUW_RS19055	ABLUW_4040	NZ_CP008707.1	29599	29346	-	WP_000679427.1		quaternary ammonium compound efflux SMR transporter GacDac2	2271.26195	167834127	0.251093996	6.696368303	2.29E-11	2.37E-10	9.623251654
ABLUW_RS02775	ABLUW_0565	NZ_CP008706.1	564679	565020	-	WP_001671615.1		phage tail assembly protein	5204.559227	1671688533	0.301984648	5.552215579	2.82E-08	1.74E-07	0.759450732
ABLUW_RS07100	ABLUW_1461	NZ_CP008706.1	145589	145662	+			IRNA: Trp	600.6303261	1671490042	0.366617246	4.568524974	4.91E-06	2.01E-05	6.945892459
ABLUW_RS14020	ABLUW_2886	NZ_CP008706.1	2893565	2893881	+	WP_000683811.1		hypothetical protein	132.3608328	1672860637	0.369480776	4.527598574	5.97E-06	2.40E-05	4.61878758
ABLUW_RS04580	ABLUW_0933	NZ_CP008706.1	934756	944061	-	WP_000371300.1		hypothetical protein	147.747576	166983757	0.35816451	4.682338522	3.19E-06	1.33E-05	4.874164359
ABLUW_RS02015	ABLUW_0573	NZ_CP008706.1	571460	571909	-	WP_001058841.1		phage vision morphogenesis protein	93.373641	1662855144	0.349124448	4.762810316	1.91E-06	8.53E-06	5.069050955
ABLUW_RS01405	ABLUW_0692	NZ_CP008706.1	698653	698609	+			IRNA: Asp	1455.582607	165837343	0.266433896	6.22607473	4.78E-10	4.06E-09	8.314673966
ABLUW_RS13070	ABLUW_2693	NZ_CP008706.1	2680667	2681056	-	WP_000427182.1		hypothetical protein	175.128006	1654334507	0.29291957	5.647743047	1.633E-08	1.05E-07	6.97819071
ABLUW_RS20460	ABLUW_1424	NZ_CP008706.1	1414827	1414997	+	WP_000072947.1		hypothetical protein	101438001	1650416217	0.68318107	2.42127246	0.0146628	0.02919335	1524101929
srNA50	no	no	no	no	no	no	no	no	157.516753	1653602075	0.203634919	8.1024494	4.65E-16	8.87E-16	14.05207638
ABLUW_RS19240	no	NZ_CP008707.1	25247	25726	+			hypothetical protein	363.2716329	1650834769	0.252744008	6.531628827	6.51E-11	6.30E-10	9.20059451
ABLUW_RS01500	ABLUW_2573	NZ_CP008706.1	256292	256636	-	WP_000556196.1	tsaM	type VIa secretion system membrane subunit TsaM	1822.36996	1645001466	0.31614395	0.17967165	3.99E-34	9.04E-32	31.06471493
ABLUW_RS07180	ABLUW_1459	NZ_CP008706.1	1450338	1450411	+			IRNA: Trp	6075.719996	1643616295	0.312770562	5.25502236	1.48E-07	7.98E-07	8.99779789
ABLUW_RS08945	ABLUW_1838	NZ_CP008706.1	1833801	1834528	+	WP_000939185.1	pcaH	protocatechuate 3,4-dioxygenase subunit beta	17.7083444	163822059	0.217788614	6.029761763	1.64E-09	1.25E-08	7.930389887
ABLUW_RS01715	ABLUW_1460	NZ_CP008706.1	1450439	1450523	+			IRNA: Leu	793.7242603	1637464807	0.41779487	3.919302805	8.88E-05	0.00287876	3.54183938
ABLUW_RS01605	ABLUW_0306	NZ_CP008706.1	33012	330676	-	WP_000678123.1	bfr	bacterioferritin	5792.398281	1637359961	0.429256238	3.814468584	0.000136477	0.00041931	3.758169358
ABLUW_RS07295	ABLUW_1496	NZ_CP008706.1	1482282	1483769	-	WP_001050512.1	proP	glycine betaine1L-proline transporter ProP	676.2205604	1633609402	0.201026164	8.163352545	4.42E-16	8.41E-11	14.01700231
ABLUW_RS09880	ABLUW_2055	NZ_CP008706.1	2034784	2033794	+	WP_000682735.1		type I fibrinolytic protein	524.478197	1630522755	0.327475903	4.979061924	6.39E-07	3.09E-06	5.10441621
ABLUW_RS16100	ABLUW_3092	NZ_CP008706.1	310759	312162	+	WP_000621866.1	hpfE	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	7003.354107	1627188021	0.251082496	6.48347253	8.97E-11	8.42E-10	9.07476809
ABLUW_RS12030	ABLUW_2530	NZ_CP008706.1	252148	2522621	-	WP_001169642.1		enoyl-CoA hydratase/isomerase family protein	794.633876	1617619743	0.53639199	3.0196655	0.00253064	0.005973282	2.232786982
ABLUW_RS05540	ABLUW_1192	NZ_CP008706.1	1193246	1194175	+	WP_000688770.1		LyxR family transcriptional regulator	3557.898724	161969512	0.165637991	9.752066724	1.64E-22	7.41E-21	20.108197
ABLUW_RS1485	ABLUW_2570	NZ_CP008706.1	2560765	2561028	-	WP_000198112.1		PAAR domain-containing protein	100.558059	1616045042	0.205109999	7.87580831	3.39E-15	5.68E-14	13.24565166
ABLUW_RS01935	ABLUW_1216	NZ_CP008706.1	1252902	1252977	-			IRNA: Asn	114.8801338	161004326	0.415232071	3.885197253	0.000102257	0.000325687	3.847189576
srNA76	no	no	no	no	no	no	no	no	2019.93002	1592021451	0.298408667	5.330315772	9.55E-08	5.13E-07	6.719004749
ABLUW_RS19590	ABLUW_3100	NZ_CP008706.1	3124146	3124526	+	WP_000932661.1		aspartate 1-decarboxylase	3019.399188	1589432388	0.172728828	9.20136191	3.52E-30	1.16E-19	9.70217991
srNA32	no	no	no	no	no	no	no	no	48.9865243	158876671	0.416357441	3.336319025	0.00082071	0.002103621	2.647311872
ABLUW_RS12495	ABLUW_2572	NZ_CP008706.1	2561816	2562774	-	WP_000557241.1	tagF	type VIa secretion system-associated protein TagF	365.591647	1588898239	0.184350882	6.017374995	6.85E-18	1.66E-16	5.77889191
ABLUW_RS19115	ABLUW_2449	NZ_CP008706.1	2437335	2439440	-	WP_001029992.1		class I SAM-dependent methyltransferase	578.580408	1587753696	0.30576257	5.92766707	2.07E-07	1.08E-06	5.966570245
ABLUW_RS03515	ABLUW_0580	NZ_CP008706.1	587349	5873952	-	WP_001191042.1	tsaB	type VIa secretion system cuticle sheath small subunit	1065.932678	158751814	0.286927323	5.532818203	3.16E-08	1.93E-07	3.54183938
ABLUW_RS19225	ABLUW_3340	NZ_CP008706.1	3347403	3347365	+	WP_000538009.1		pyocyan actin/beta-PN family protein	286.2391919	1583838194	0.200446931	7.900662631	2.77E-15	4.76E-14	13.32233035
ABLUW_RS19040	ABLUW_4003	NZ_CP008707.1	4174	2556	+	WP_000258411.1		zeta toxin family protein	588.298929	1578952697	0.260337605	6.065019596	1.32E-09	1.02E-08	7.91939828
ABLUW_RS19495	ABLUW_4193	NZ_CP008707.1	63264	63324	+	WP_000678141.1		hypothetical protein	26.90464355	1573560761	0.486149868	3.267812194	0.00208861	0.00307481	2.51218716
ABLUW_RS19175	ABLUW_2400	NZ_CP008706.1	2387462	2387462	-	WP_000448952.1		malonate decarboxylase subunit delta	85.82535069	1573543639	0.51017775	3.072191654	0.002105146	0.005095991	2.292464654
ABLUW_RS19335	ABLUW_2229	NZ_CP008706.1	2218907	2218623	+	WP_000552882.1		energy transducer TonB	67.88272103	156484607	0.270640191	5.78201958	7.38E-09	5.09E-08	7.39232822
ABLUW_RS12540	no	NZ_CP008706.1	2973969	2974660	-			hypothetical protein	914.438783	1557871836	0.26815502	5.80367447	6.27E-09	4.38E-08	3.758825889
ABLUW_RS07125	ABLUW_1462	NZ_CP008706.1	1450719	1451636	-	WP_000602869.1		LyxR family transcriptional regulator	356.4512962	1552599928	0.281106134	5.24461188	3.30E-08	2.91E-07	6.696803943
ABLUW_RS01805	ABLUW_3311	NZ_CP008706.1	3345224	3346025	+	WP_000697823.1		SDS family NAD(P)+ dependent oxidoreductase	276.0356469	1554319566	0.221069767	7.008283344	2.41E-12	2.87E-11	10.5421181
ABLUW_RS19390	ABLUW_2193	NZ_CP008706.1	219823	219842	-	WP_001035051.1		alpha-lactoside dehydrogenase subunit beta	780.1659186	1548800342	0.579187326	2.627737982	0.007523499	0.019787592	180.8841496
ABLUW_RS20440	ABLUW_0779	NZ_CP008706.1	764737	764889	+	WP_001051449.1		hypothetical protein	3.737227768	154771837	1.082896958	1.45610212	0.14355716	0.208608596	6.078890911
ABLUW_RS19175	ABLUW_2678	NZ_CP008706.1	2669697	2670326	-	WP_000241196.1		hypothetical protein	772.238274	1543980734	0.399967908	3.860261647	0.000110266	0	

ABUW_RS09575	ABUW_969	NZ_CP008706.1	97 084	97 998	-	WP_024436202.1				alpha/beta fold hydrolase	26.55957756	14300 0003	0.448987504	3.184972947	0.00447675	0.003607 02	2.44284577
ABUW_RS02690	ABUW_0548	NZ_CP008706.1	553035	553226	-	WP_000434811.1				hydrolytic protein	83.58032267	14279 1892	0.316964 08	4.51922 821	6.2 E-06	2.48E-05	4.60548319
ABUW_RS17255	ABUW_3546	NZ_CP008706.1	3604299	3604383	-					IRNA-Lou	930.899283	14227 9319	0.340936795	4.17297088	3.0 E-05	0.00005886	3.97518165
ABUW_RS1910	ABUW_2386	NZ_CP008706.1	2374626	2375921	-	WP_00032377.1				monooxygenase	608.3180311	1420006 149	0.189425 91	7.493396677	6.56E-14	9.54E-13	9.02045 93
ABUW_RS05605	ABUW_1145	NZ_CP008706.1	1709003	1709299	-	WP_000695009.1				LysR family transcriptional regulator	589.909449	1419594062	0.175999355	8.084898248	6.40E-16	1.19E-14	13.02453034
ABUW_RS0150	ABUW_2943	NZ_CP008706.1	29434	294628	-	WP_001813126.1				amino acid permease	3242.94365	1419475081	0.232547324	6.164028738	8.17E-09	8.087777943	
ABUW_RS02219	ABUW_0450	NZ_CP008706.1	464142	464188	+					IRNA-Avg	2063.981214	1419010749	0.468993528	3.020526856	0.002477903	0.005865729	2.23 8778006
ABUW_RS02485	ABUW_4910	NZ_CP008707.1	62770	6410	+	WP_000691626.1				hydrolytic protein	69.58426426	1418805444	0.430046221	3.23126282	0.001231163	0.003125592	2.505067713
ABUW_RS02400	ABUW_0489	NZ_CP008706.1	501183	503123	+	WP_000672540.1				acetyl(propionyl)methyl-oxonyl-CoA carboxylase subunit alpha	428.74025338	1416973379	0.216528982	6.574398827	4.89E-11	4.79E-10	9.316664487
sRNA5	no	no	no	no	no	no	no	no	no	no	4161584247	1416578395	0.430646089	3.269425888	0.00100392	0.002614393	2.582629 028
ABUW_RS02035	ABUW_0535	NZ_CP008706.1	2813299	281348	-					hydrolytic protein	324.7326784	1414968092	0.36283523	3.899753869	9.63E-05	0.000309127	3.509836301
ABUW_RS19085	ABUW_4013	NZ_CP008707.1	7231	7557	+	WP_000078385.1				H-N histone family protein	2241937613	1414375456	0.251056 145	5.633701801	1.76E-08	1.0E-07	6.950781977
ABUW_RS00985	ABUW_0999	NZ_CP008706.1	223087	223782	-	WP_000431598.1				AcrC family ABC transporter permease	919.87937	1413160538	0.19782158	7.166726211	7.68E-13	1.007446448	
ABUW_RS01760	ABUW_0664	NZ_CP008706.1	670429	671023	-	WP_000734697.1				self-repeat family protein	431.9565547	1412750544	0.16302045	8.618510099	6.78E-18	1.66E-16	15.779913
ABUW_RS15320	ABUW_3122	NZ_CP008706.1	314245	3143296	+	WP_000647733.1			otaB	939.033208	1411696431	0.596396083	2.366709763	0.019747001	0.034172243	14.663265514	
ABUW_RS12755	ABUW_2629	NZ_CP008706.1	2626050	2626604	-	WP_00321204.1				TeiR/AcrR family transcriptional regulator	27.46681933	1410929733	0.509587045	2.768770807	0.00562682	0.012200339	19.16328192
ABUW_RS1690	ABUW_2403	NZ_CP008706.1	2390433	2391620	-	WP_000941072.1				MFS transporter	122.9665987	1413836810	0.29183346	4.841864289	1.29E-06	5.95E-06	9.225643034
ABUW_RS1790	ABUW_0365	NZ_CP008706.1	386667	387299	-	WP_000339187.1				hydrolytic protein	167.083028	1414005189	0.25951942	5.433340303	5.53E-08	3.23E-07	6.49242193
ABUW_RS1590	ABUW_2674	NZ_CP008706.1	2667054	2667332	-	WP_000772985.1				hydrolytic protein	324.1169494	1408771733	0.485316041	2.902798418	0.003698446	0.00839103	2.076682759
ABUW_RS1940	ABUW_4100	NZ_CP008707.1	65449	61071	+	WP_000776095.1				type-F conjugative transfer system acetate transfer	312.9025756	1407597725	0.12020307	6.627664769	3.4 E-11	3.43E-10	9.46417058
ABUW_RS17010	ABUW_1518	NZ_CP008706.1	1503894	1504400	-	WP_000694317.1				GNA1 family N-acetyltransferase	25.36516504	1406529434	0.644413607	2.182650116	0.02906158	0.052016495	12.8588916
ABUW_RS1070	ABUW_2201	NZ_CP008706.1	2187451	2187624	-	WP_010241480.1				Rrf2 family transcriptional regulator	5389.859218	1403578192	0.181770123	7.724720549	1.16E-13	1.73E-12	7.00470028
ABUW_RS07800	ABUW_1997	NZ_CP008706.1	1994365	1994793	+	WP_001028233.1				membrane protein	618.4302409	1403368757	0.216335854	6.519716096	7.17E-11	6.88E-10	9.12411662
ABUW_RS0508	ABUW_2058	NZ_CP008706.1	2038281	2041952	-	WP_000632243.1				hydrolytic protein	2580.471181	1402633207	0.291692489	4.812551501	1.51E-06	6.85E-06	5.964309429
ABUW_RS01940	ABUW_0233	NZ_CP008706.1	252271	252174	-	WP_00051861.1				hydrolytic protein	1582.899022	1392418375	0.345882354	0.025930666	5.68E-05	0.000190064	3.71280155
ABUW_RS18045	ABUW_3283	NZ_CP008706.1	3317725	3317933	+	WP_00063959.1				hydrolytic protein	1000.834856	1392368548	0.196080084	7.343329209	2.08E-13	2.83E-12	11.54821056
ABUW_RS19185	ABUW_2428	NZ_CP008706.1	2418710	2418326	+	WP_000116421.1				hydrolytic protein	2211249893	13190978711	0.21039114	6.545319544	7.29E-11	6.98E-10	9.19644071
ABUW_RS00895	ABUW_1786	NZ_CP008706.1	1782797	1783030	-	WP_000610034.1				hydrolytic protein	2409.906415	1389860546	0.296724894	4.684003841	2.8 E-06	1.22E-05	4.915640169
ABUW_RS02905	ABUW_9609	NZ_CP008706.1	919252	919932	-	WP_000276394.1				hydrolytic protein	96.21082281	1389529325	0.238072802	5.365573187	5.33E-09	3.77E-08	7.42360855
ABUW_RS01795	ABUW_3620	NZ_CP008706.1	3617831	3617952	-	WP_001075439.1			eat	85.25755336	13836136	0.375116862	3.703809777	0.000212386	0.000335055	3.704705072	
ABUW_RS01390	ABUW_0078	NZ_CP008706.1	85518	86330	+	WP_000019467.1				amino acid permease	2574.016251	1389040819	0.358598261	3.90300318	9.50E-05	0.000305736	3.54653421
ABUW_RS01795	ABUW_0355	NZ_CP008706.1	3607776	361211	+	WP_001009481.1				serine acyl-oxo peptidase	272.4169303	1373331381	0.210440765	6.304448076	6.56E-11	6.33E-10	9.18953629
ABUW_RS12295	ABUW_2529	NZ_CP008706.1	2521857	2521848	-	WP_0003386291.1				2-[(1L)-erythro-12-hydroxyphenylacetyl-CoA isomerase	1400.827279	1366492769	0.425572274	3.257349011	0.001022208	0.002818687	2.540353183
ABUW_RS11675	ABUW_2418	NZ_CP008706.1	2405579	2406217	-	WP_000207773.1				LysR family translocator	92.8183645	1371847167	0.164480065	0.50177345	9.02E-24	4.60E-22	21.33742747
ABUW_RS03685	ABUW_0810	NZ_CP008706.1	781559	781911	+	WP_010101970.1				hydrolytic protein	738.528905	1371649794	0.260853463	4.51781384	2.5 E-07	1.30E-06	5.886056648
ABUW_RS1525	ABUW_2578	NZ_CP008706.1	2571242	2571625	-	WP_000653195.1				type VI secretion system lysis protein	7035.970453	1367702648	0.243360751	5.61943036	1.97E-08	1.24E-07	6.960578316
ABUW_RS16635	ABUW_3221	NZ_CP008706.1	3250917	3250993	-					IRNA-Pro	954.100052	1366590148	0.331003293	4.0833007	3.65E-05	0.00012697	3.96229888
ABUW_RS02205	ABUW_0449	NZ_CP008706.1	461697	463520	-	WP_0004179308.1				hydrolytic protein	15463.187897	1366453354	0.261704972	5.118377947	3.16E-07	1.60E-06	9.759800017
ABUW_RS03830	ABUW_0576	NZ_CP008706.1	572367	573526	-	WP_000127411.1				phage holo factor protein	82.89085996	1360763886	0.591745628	2.277595796	0.022750671	0.042221005	13.97483407
ABUW_RS1620	ABUW_3335	NZ_CP008706.1	3365532	3365792	-	WP_000790979.1				hydrolytic protein	14.3186575	1353549074	0.174726653	1.81033679	NA	NA	91.841UE1
ABUW_RS05930	ABUW_1214	NZ_CP008706.1	1252818	1252893	-					IRNA-An	78.0741006	1351284384	0.434545281	2.046653397	0.002134814	0.005120047	2.586687088
ABUW_RS19065	ABUW_4008	NZ_CP008707.1	45454	6050	+	WP_000056825.1				hydrolytic protein	1002.963952	1350505809	0.267507063	4.854486546	4.45E-07	2.20E-06	5.61757379
ABUW_RS02385	ABUW_0486	NZ_CP008706.1	54970	49910	+	WP_000140685.1				acetyl-CoA carboxylase carboxyltransferase subunit	162.7416279	1347888453	0.38379104	3.427674524	0.000608775	0.00162279	9.7177959
ABUW_RS18230	ABUW_3339	NZ_CP008706.1	3373094	3374074	+	WP_000710381.1				hydrolytic protein	5716.02048	1348766919	0.195339048	6.95056257	5.02E-12	5.62E-11	10.2503368
ABUW_RS19595	ABUW_2769	NZ_CP008706.1	2797440	2798104	-	WP_000722685.1			astA	787.8974429	1344318338	0.38310108	3.149119859	0.006265465	0.001996741	2.713744446	
ABUW_RS06930	ABUW_1422	NZ_CP008706.1	1410219	1410840	+	WP_000510282.1				hydrolytic protein	18.38272232	133822449	0.498671757	2.68357787	0.007283901	0.01536436	18.0472071
ABUW_RS19810	ABUW_2611	NZ_CP008706.1	2604136	2604852	-	WP_010165491.1				hydrolytic protein	488.561447	1331888925	0.321397896	4.1172184	3.83E-05	0.000192377	3.877000802
ABUW_RS1740	ABUW_2626	NZ_CP008706.1	2621822	2621453	+	WP_001033905.1				exo-alpha-sialidase	5911551667	1329406799	0.28103456	4.730430262	2.24E-06	9.90E-06	5.004368405
ABUW_RS01500	ABUW_1953	NZ_CP008706.1	1954656	1955084	+	WP_000077758.1				TolC family protein	44.09186663	1328705665	0.330992312	0.419168657	5.84E-05	0.000194794	3.710424442
ABUW_RS017520	ABUW_1541	NZ_CP008706.1	1520459	1520459	-	WP_000243522.1				alpha-E domain-containing protein	258.0434316	1327598866	0.28510436	4.656552719	3.22E-06	1.36E-05	4.86641902
ABUW_RS03950	ABUW_0807	NZ_CP008706.1	784297	784659	+	WP_000835166.1				hydrolytic protein	42.63824352	1321719178	0.356091452	3.72075616	0.000193732	0.000582063	3.235003007
ABUW_RS02445	ABUW_2588	NZ_CP008706.1	2581405	2581630	-	WP_001000265.1				hydrolytic protein	14.01882389	1322878763	0.637535356	2.074085757	0.037987855	0.066142207	1.97950119
ABUW_RS19515	ABUW_3194	NZ_CP008706.1	3221258	3221809	-	WP_001042572.1				GDHXXLY family transcriptional regulator	40.66063937	1322785045	0.36485019	6.288242226	0.002883357	0.00033724	3.789777691
ABUW_RS19055	ABUW_3101	NZ_CP008706.1	3102141	3102141	-	WP_00071616.1				TDGXXLY domain-containing protein	47.44265995	1317782577	0.15849309	8.13448192	9.22E-17	1.90E-16	9.1724664
ABUW_RS01710	ABUW_9608	NZ_CP008706.1	9697406	9698188	-	WP_005142463.1				replication initiation factor domain-containing protein	454.4096042	131641499	0.21007073	6.23331879	4.57E-10	3.90E-09	4.818935303
sRNA30	no	no	no	no	no	no	no	no	no	no	119376152	1315019883	0.934418346	1.408050279	0.188981029	0.22033874	4.066010001
ABUW_RS19065	ABUW_2692	NZ_CP008706.1	2680084	2680629	-	WP_010196811.1				N-acetylmannosidase	97.5						

ABUW_RS17335	ABUW_3562	NZ_CP008706.1	368004	3620 933	-	WP_000925020.1		FUSC family protein	755.4744807	1266497723	0.224589049	5.639379319	1.7 E-08	1.096E-07	6.962573502
ABUW_RS05600	ABUW_1144	NZ_CP008706.1	1869458	1869534	+			rRNA-Val	135.2602102	1218724 865	0.644244062	1.958456801	0.050176435	0.084467452	107733006
ABUW_RS0 905	ABUW_2093	NZ_CP008706.1	20749 9	2076340	+	WP_000263726.1		GstF family permease	788.2064039	1218180029	0.26978946	4.6748 0562	2.946E-06	1.26E-05	4.896264352
ABUW_RS02345	ABUW_0599	NZ_CP008706.1	597328	598092	-	WP_00118964.1		OLDF84 family protein	225.7289896	120086624	0.97312717	7.28338 855	3.33E-10	4.40E-12	1135654732
ABUW_RS23020	ABUW_3187	NZ_CP008706.1	31604 95	316 568	-	WP_000707883.1		hypothetical protein	206.8995859	1259574676	0.28879907	4.36109557	1.296E-05	4.93E-05	4.30895809
ABUW_RS05470	ABUW_0631	NZ_CP008706.1	608039	608226	-	WP_002015237.1		ammonium transporter	169.018825	125559925	0.24708175	5.093698436	3.5 E-07	1.77E-06	5.752020734
ABUW_RS17340	ABUW_3543	NZ_CP008706.1	3603274	3603798	-	WP_000777730.1	rimP	ribosome maturation factor RimP	10056.9393	1256630 994	0.214 03778	5.14860353	2.68E-07	1.38E-06	5.8601029 4
ABUW_RS08910	ABUW_931	NZ_CP008706.1	927256	927927	+	WP_000568027.1		3'-oxoacyl-CoA-transferase subunit A	93.05852272	1255090012	0.346448246	3.622734496	0.000291605	0.000846808	3.07 0292878
ABUW_RS06385	ABUW_0509	NZ_CP008706.1	192 057	1922174	+	WP_000094258.1		hypothetical protein	15.2926261	125485 116	0.44040442	2.8493 5444	0.004381042	0.00976351	2.0 0394025
ABUW_RS0535	ABUW_3168	NZ_CP008706.1	3165300	3165527	-	WP_000543705.1		hypothetical protein	252.1945201	1254427 026	0.35117117	3.562522038	0.000567309	0.00042909	2.98 975365
ABUW_RS1925	ABUW_2323	NZ_CP008706.1	2307578	2307654	+			rRNA-Is	34. 61747999	1250 918 13	0.507022233	2.465732728	0.010673332	0.02683383	157 0137336
ABUW_RS05610	ABUW_1146	NZ_CP008706.1	1170995	1172293	-	WP_000704 56.1		aminopeptidase P family protein	572.7794548	1248423967	0.14 959 907	8.817053737	1.8E-18	3.36E-17	5.6003 0292
ABUW_RS06445	ABUW_1521	NZ_CP008706.1	1333899	1334405	+	WP_000308382.1			49.72942953	12483177 9	0.349636342	3.570337076	0.000356529	0.00101682	2.99356705
ABUW_RS14330	ABUW_2948	NZ_CP008706.1	2962890	2964 911	-	WP_004041872.1		FAD-dependent oxidoreductase	98.40976079	1247357715	0.332273321	3.754004142	0.000174032	0.000527596	3.277698506
ABUW_RS19355	ABUW_2 031	NZ_CP008706.1	218956	21078 9	-	WP_001077517.1		thiamine pyrophosphate-dependent dehydrogenase E1 component subunit	638.3666658	1243447363	0.60626784	2.050986929	0.04026822	0.069720953	1.56636685
ABUW_RS19200	ABUW_3739	NZ_CP008706.1	3795681	3796079	-	WP_000084237.1		ATP synthase subunit I	7626. 02559	1242847787	0.322052447	3.859147 81	0.00010783	0.00035872	3.445254095
ABUW_RS04425	ABUW_0902	NZ_CP008706.1	898516	898860	-	WP_032068 06.1		DUF1833 family protein	453.7988756	1242389473	0.25 918 173	4.933774753	8.07E-07	3.85E-06	5.4153927
ABUW_RS19505	ABUW_2810	NZ_CP008706.1	2809373	2810509	-	WP_003068963.1		ATP-binding protein	4 09.430355	1238901407	0.1645658	7.6235 5672	5.33E-14	7.96E-13	10.0906905
ABUW_RS19555	ABUW_2649	NZ_CP008706.1	2647360	2644337	-	WP_00103556.1		KpsFGluQ family sugar-phosphate isomerase	4038.74366	1235535064	0.06902609	0.039422467	1.58E-19	4.88E-18	9.711690 9
ABUW_RS05645	ABUW_1775	NZ_CP008706.1	1774456	1774701	-	WP_000594968.1		hypothetical protein	2649.474744	1227446887	0.26459269	4.678906672	2.9 E-06	1.25E-05	4.90308997
ABUW_RS09785	ABUW_2010	NZ_CP008706.1	2007127	2007411	-	WP_000500492.1		DUF2523 domain-containing protein	19.52870962	1237397643	0.816627983	2.027716045	0.042788252	0.073516509	1.0362 031
ABUW_RS04815	ABUW_0210	NZ_CP008706.1	237 320	237 395	-			rRNA-Thr	3702.39219	1235526079	0.22286572	5.656577848	2.76E-08	1.70E-07	6.79958 079
ABUW_RS18180	ABUW_2298	NZ_CP008706.1	2285450	2286335	+	WP_000192618.1			1300.918795	12348737 9	0.338462289	3.648482441	0.0001063794	0.000774604	3.110892232
ABUW_RS02760	ABUW_0440	NZ_CP008706.1	452 340	454 335	+	WP_001588905.1		TRAP transporter large permease subunit	225.7903063	1234248024	0.2922 9224	4.223705776	2.406E-05	8.72E-05	4.05948359
ABUW_RS19520	ABUW_2405	NZ_CP008706.1	240032	2405350	+	WP_0010 6326.1	hscB	Fe-S protein assembly co-chaperone HscB	1082.852946	1233857532	0.220762663	5.589007996	2.28E-08	1.42E-07	6.8477 1556
ABUW_RS05070	ABUW_0077	NZ_CP008706.1	62 890	63827	-	WP_000202842.1	hutU	uracilate hydratase	3694.336268	1233180244	0.9790455	6.23186935	4.63E-10	3.94E-09	8.404507878
ABUW_RS02385	ABUW_0260	NZ_CP008706.1	82960	277874	+	WP_00193548.1		SDR family NAD(P)-dependent oxidoreductase	7983.6429	123222799	0.448005764	2.75047352	0.000595092	0.0120783	185224544
ABUW_RS05655	ABUW_0318	NZ_CP008706.1	343058	343569	+	WP_00193548.1		prepilin-type N-terminal cleavage/methylation domain-containing protein	1479.56875	123083 875	0.461820258	2.665175 99	0.007694823	0.016069739	175362098
ABUW_RS05665	ABUW_1067	NZ_CP008706.1	1024504	1025 036	+	WP_000253006.1		TerR/ACf family transcriptional regulator	325.648821	1230759092	0.131 6375	9.344080684	9.27E-21	3.46E-19	8.46029 39
ABUW_RS19340	ABUW_4068	NZ_CP008707.1	40701	40895	+	WP_000707874.1		hypothetical protein	410.833924	1230110484	0.176523602	7.004207017	2.49E-12	2.93E-11	10.53332328
ABUW_RS19375	ABUW_2673	NZ_CP008707.1	2661326	2666794	-	WP_00108417 1		hypothetical protein	53.114616	1229176102	0.62576373	1.95619666	0.045398428	0.08374558	107947307
ABUW_RS17225	ABUW_3549	NZ_CP008707.1	3598641	3599042	-	WP_000897046.1		ribosome-binding factor A	487.200979	1229697407	0.401594627	3.06 919214	0.002198699	0.005257304	2.27239899
ABUW_RS190225	ABUW_064	NZ_CP008707.1	674526	670776	-	WP_000305256.1		glycosyltransferase family 2 protein	14401.454 4	1225264593	0.19957805	6.84522407	7.53E-10	6.03E-09	8.21039525
ABUW_RS19 200	ABUW_2505	NZ_CP008707.1	2500923	250 339	-	WP_000600070.1		MFS transporter	5291.489325	12234 5044	0.262748232	4.05620527	3.22E-08	1.36E-05	4.866461932
ABUW_RS20500	no	NZ_CP008706.1	564581	564676	-			hypothetical protein	77.95704362	1222862 13	0.289895946	4.2866369	2.46E-05	5.05 687034	
ABUW_RS195875	ABUW_3269	NZ_CP008706.1	3298425	330 332	-	WP_000267686.1		Opt family phage tail protein	1656.075731	1221623548	0.2584 74524	4.725508459	2.30E-06	1.08E-05	4.995678626
ABUW_RS195045	ABUW_3099	NZ_CP008706.1	3124343	31240 4	+	WP_000500559.1	ph	DUF2339 domain-containing protein	2260.401498	1221052451	0.140308227	8.702643263	3.24E-18	7.0E-17	6.08510 98
ABUW_RS19660	ABUW_4186	NZ_CP008707.1	77866	78528	-	WP_01708581.1		aminoacyl-tRNA hydrolase	5600.845586	1220458853	0.175262044	6.963623302	3.32E-12	3.86E-11	0.414127
ABUW_RS19700	ABUW_2658	NZ_CP008706.1	2654223	2654396	-	WP_000230993.1		transglycosylase SLT domain-containing protein	232.098699	122029596	0.21687876	5.606240242	2.07E-08	1.30E-07	6.880506648
ABUW_RS19290	ABUW_2460	NZ_CP008706.1	2451468	2454300	-	WP_001019211.1		DUF4862 family protein	375.148 68	1207793228	0.23574041	5.03389727	3.00E-07	1.53E-06	5.815369508
ABUW_RS19 910	ABUW_4106	NZ_CP008706.1	66902	67297	+	WP_0007178 92.1		acyl-CoA dehydrogenase C-terminal domain-containing protein	794.320181	1205595454	0.26548443	4.4737 6259	7.69E-06	3.01E-05	4.521435054
ABUW_RS19 910	ABUW_4106	NZ_CP008706.1	66902	67297	+	WP_0007178 92.1		hypothetical protein	61.03658 4	1203962945	0.25948707	4.640303043	3.48E-06	1.46E-05	4.83567474
ABUW_RS19070	ABUW_4009	NZ_CP008707.1	6056	6247	+	WP_000182323.1		hypothetical protein	240.185 93	1202432637	0.29858077	3.02706213	5.65E-05	0.00019321	3.72291201
ABUW_RS19190	ABUW_0343	NZ_CP008706.1	260358	260753	+	WP_00198885.1		membrane protein	906.903923	120218665	0.20363904	5.90319606	3.37E-09	2.4 E-08	7.58339359
ABUW_RS19230	ABUW_2341	NZ_CP008706.1	3371440	3373497	-	WP_000534868.1		lysine-type ribonucleoside synthase	1168.99801	1200683627	0.19497767	6.86055065	7.36E-10	6.02E-09	8.20420369
ABUW_RS14890	ABUW_3068	NZ_CP008706.1	3095531	3096991	+	WP_001986486.1		hypothetical protein	242.7292224	1198462572	0.307442837	3.89839319	9.69E-05	0.000316668	3.507703478
ABUW_RS19000	ABUW_0265	NZ_CP008706.1	283097	283495	-	WP_001101808.1		hypothetical protein	776.4736635	1197275799	0.19122422	6.778603627	1.84E-11	1.93E-10	9.71442691
ABUW_RS02700	ABUW_0550	NZ_CP008706.1	550203	550392	-	WP_000506351.1		hypothetical protein	296.4426053	1196662 05	0.19498557	6.18671683	8.42E-10	6.80E-09	8.16749 887
ABUW_RS19075	ABUW_0544	NZ_CP008706.1	69272	69964	+	WP_000557460.1		M21 family metalloproteinase	3836.934725	1193765991	0.208746955	5.71869831	1.08E-08	7.20E-08	7.142627004
ABUW_RS19285	no	NZ_CP008706.1	2635604	2654 48	-			hypothetical protein	34.27594609	1190529052	0.428059375	2.78242 98	0.00545432	0.01793934	192834 507
ABUW_RS19330	ABUW_3167	NZ_CP008706.1	3183396	3185072	-	WP_001001666.1		mechanosensitive ion channel	4 4 9.22788	1189454297	0.302628898	3.9304 5333	8.48E-05	0.000275977	3.50927 711
ABUW_RS19235	ABUW_3168	NZ_CP008706.1	316 829	316340	-	WP_001038910.1		hypothetical protein	1054.91331	118913546	0.188317522	6.31665796	2.69E-10	6.82 602099	
ABUW_RS190430	ABUW_0887	NZ_CP008706.1	883247	884971	+	WP_000221993.1		CapA family protein	821.54802 6	1187010052	0.16821586	4.054987715	1.73E-12	2.1E-11	0.2157 0564
ABUW_RS190360	ABUW_0741	NZ_CP008706.1	743345	743345	+	WP_00105665.1		hypothetical protein	63.8785693	1186034724	0.331997933	3.5724 6991	0.000353703	0.00009097	9.896007085
ABUW_RS19 935	ABUW_2087	NZ_CP008706.1	20677 79	2068955	-	WP_001025581.1		hypothetical protein	53.9691056	1186577862	0.333550767	3.554039618	0.000378066	0.00106882	2.97 154745
ABUW_RS19005	ABUW_0368	NZ_CP008706.1	39799	391843	+	WP_001982092.1		tetracycline resistance MFS efflux pump	311.2459599	1184873712	0.207134899	5.720297275	1.06E-08	7.19E-08	7.1469 047
ABUW_RS19140	ABUW_2373	NZ_CP008706.1	2356487	23586 9	-	WP_000714879.1		DUF1427 family protein	58.8648507	1184333699	0.480201699	2.466328492	0.010650608	0.026020231	157 809692
ABUW_RS08430	ABUW_1731	NZ_CP008706.1	1727825	1728478	-	WP_000545879.1	adeN	multidrug efflux transcriptional repressor AdeN	1486.450187	1183748 08	0.232127369	5.0995483 87	3.40E-07	1.72E-06	5.97443 583
ABUW_RS1															

ABUW_R501545	ABUW_0274	NZ_CP008706.1	292407	293291	-	WP_001986587.1		hypothetical protein	147.1762873	1.12418041	0.264591666	4.248738635	2.165-05	7.856-05	4.105100343
ABUW_R50170	ABUW_3713	NZ_CP008706.1	3772479	3772554	-	WP_00071222.1		rRNA: Ala	3600.446472	1.12336957	0.273590615	4.10602378	4.03E-05	0.00018486	3.85856277
ABUW_R501790	ABUW_0773	NZ_CP008706.1	759531	760172	+	WP_000372122.1		hypothetical protein	57.06194162	1.123252916	0.258563039	4.320480996	1.53E-05	5.77E-05	4.23884167
ABUW_R501980	ABUW_2589	NZ_CP008706.1	2582072	2582075	-	WP_00118194.1		helic_tum-helic-transcriptional regulator	40.38100387	1.119583393	0.33369297	3.352354248	0.00080274	0.002103913	2.671434281
ABUW_R501940	ABUW_3767	NZ_CP008706.1	3819736	3820501	-	WP_000247733.1		alpha-beta fold hydrolase	41.91476444	1.11875537	0.233576015	4.78988429	1.67E-06	7.53E-06	5.52305024
ABUW_R502143	ABUW_9730	NZ_CP008706.1	9729792	9727712	-	WP_001070785.1	argF	ornithine carbamoyltransferase	7.900.903979	1.118626312	0.264062896	7.26084798	3.85E-13	5.08E-12	11.28416629
ABUW_R502445	ABUW_9553	NZ_CP008706.1	9555820	9555933	+	WP_001109332.1		hypothetical protein	37.25054444	1.118150335	0.478307564	2.37722458	0.0940165	0.03669179	14.03343663
ABUW_R502510	ABUW_2730	NZ_CP008706.1	2718780	2718715	-	WP_0001026486.1		OmpA family protein	759.8248155	1.117350361	0.20878074	5.351078484	8.71E-08	4.89E-07	6.31061914
ABUW_R502660	ABUW_1656	NZ_CP008706.1	184180	185088	-	WP_000098987.1	ydgG	aromatic amino acid DMF transporter YdgG	77.35532657	1.116477822	0.338706686	3.295269694	0.000979684	0.00258466	2.59202035
ABUW_R503935	ABUW_0804	NZ_CP008706.1	775451	783346	+	WP_000046172.1		tape measure protein	631.559343	1.1165193	0.105374443	10.58278601	3.58E-26	2.67E-24	23.57438874
ABUW_R504175	ABUW_2815	NZ_CP008706.1	2814453	2814944	-	WP_001195446.1		hypothetical protein	420.8285667	1.115060587	0.289748039	3.848380095	0.00018901	0.000372515	3.428856235
ABUW_R504400	ABUW_1312	NZ_CP008706.1	1241435	1250564	-	WP_0000650509.1		ORF49 domain-containing protein	182.400147	1.11421684	0.2262403	4.92517114	8.41E-07	4.00E-06	5.37940009
ABUW_R504345	ABUW_2955	NZ_CP008706.1	2968768	2969067	-	WP_000927114.1		hypothetical protein	116.0122662	1.113829491	0.215507635	5.163399222	2.36E-07	1.23E-06	5.91008489
ABUW_R503080	ABUW_2695	NZ_CP008706.1	2681857	2682328	+	WP_001185369.1		LexA family transcriptional regulator	690.1779394	1.111795753	0.13340643	8.33301918	6.65E-17	1.40E-16	14.86381967
ABUW_R503065	ABUW_9652	NZ_CP008706.1	958444	958969	+	WP_001056937.1		asymmetric-rhig-hydrolyzing deoxygenase subunit beta	7.14.8323945	1.112537775	0.45221067	2.460201555	0.01885901	0.02171585	1.565885027
ABUW_R503795	ABUW_0933	NZ_CP008706.1	1400694	1400921	-	WP_000043905.1		hypothetical protein	32.81096342	1.11264357	0.351296887	3.16047309	0.01575102	0.00388922	2.41105389
ABUW_R503650	ABUW_9776	NZ_CP008706.1	9774961	9775380	-	WP_000838063.1		heme-binding protein	546.9363457	1.109987696	0.24290832	4.56954618	4.89E-06	2.00E-05	6.69897004
ABUW_R503675	ABUW_2165	NZ_CP008706.1	2165699	2167585	-	WP_000249278.1		2'-5' RNA ligase family protein	350.0841259	1.108472089	0.221175455	5.016253217	5.27E-07	2.57E-06	5.950066677
ABUW_R503665	ABUW_9678	NZ_CP008706.1	969505	970747	-	WP_0001049720.1		SDR family NAD(P)-dependent oxidoreductase	62.35559783	1.10859103	0.271003948	4.090679568	4.30E-05	0.00014609	3.833303663
ABUW_R503755	ABUW_3256	NZ_CP008706.1	3287770	3287780	-			rRNA: Ala	3602.73212	1.10825846	0.27086023	4.094168377	4.24E-05	0.00014447	3.833990917
ABUW_R50305	ABUW_2531	NZ_CP008706.1	2522630	2523691	-	WP_0000177461.1		phenylacetate-CoA oxygenase/reductase subunit PaaK	1615.755334	1.107545638	0.167704728	19.53312917	0.0507780722	0.085283871	1.06910414
ABUW_R501745	ABUW_4299	NZ_CP008707.1	55860	6048	+	WP_000376692.1		conjugal transfer protein TraE	167.7603907	1.107545127	0.282166731	3.925142424	8.67E-05	0.00028179	3.55107118
ABUW_R5019490	ABUW_2571	NZ_CP008706.1	256145	2561812	-	WP_001072410.1		OmpA family protein	253.9073497	1.106720124	0.16345993	1.786599861	1.48E-12	1.17E-11	10.7474697
ABUW_R5014830	ABUW_0985	NZ_CP008706.1	9901436	9901436	-	WP_000800709.1		CSLRNA domain-containing protein	1770.04582	1.106560003	0.208988418	5.295298237	1.19E-07	6.50E-07	6.19708644
ABUW_R501740	ABUW_0299	NZ_CP008706.1	322914	324035	+	WP_000840834.1		FAD-dependent oxidoreductase	3029.08812	1.106570661	0.242190049	4.58910764	4.90E-06	2.01E-05	4.06803843
ABUW_R5018005	ABUW_0571	NZ_CP008706.1	570411	570758	+	WP_000887745.1		CPW025 family protein	40.4908163	1.104281312	0.351827639	3.18742356	0.00169746	0.04163213	2.381619795
ABUW_R501220	ABUW_0633	NZ_CP008706.1	671261	671425	+	WP_000710598.1		hypothetical protein	1709.89461	1.111206134	0.245520321	4.48519348	7.28E-06	2.87E-05	4.54219183
ABUW_R501825	ABUW_0368	NZ_CP008706.1	3371951	3373092	+	WP_000838837.1		inovasin-type Gp2 protein	271.1272943	1.11066803	0.22001696	5.000494634	5.72E-07	2.78E-06	5.559953204
ABUW_R5017910	ABUW_821	NZ_CP008706.1	816104	816525	-	WP_001029005.1		aldehyde dehydrogenase family protein	11798.24194	1.099590397	0.367414009	2.937762814	0.002755601	0.0064198	2.102883053
ABUW_R5017520	ABUW_3599	NZ_CP008706.1	3601766	3601766	-			rRNA: Thr	2945.731904	1.098767903	0.303616249	3.618900562	0.002295857	0.00080656	5.950170359
ABUW_R501470	ABUW_0256	NZ_CP008706.1	033631	033635	+	WP_000208716.1		lysocysteine	312.5601636	1.097554596	0.19154578	6.896338999	5.34E-12	5.94E-11	10.23921566
ABUW_R5017235	ABUW_3542	NZ_CP008706.1	3601752	3601326	-	WP_000532248.1	nusA	transcription termination/intermediation protein NusA	491.0715918	1.096361016	0.203129169	5.383914682	7.79E-09	4.16E-07	6.33299959
ABUW_R501665	ABUW_2377	NZ_CP008706.1	2363399	2365308	+	WP_001066271.1		HCS1 family nucleobase cation symporter-1	84.83074003	1.09230171	0.245810175	4.443822714	8.84E-06	3.42E-05	4.46973894
ABUW_R501930	ABUW_2452	NZ_CP008706.1	2430044	2440216	+	WP_001053639.1		isovaleryl-CoA dehydrogenase	2343.051086	1.090549622	0.36191581	3.010296199	0.00236597	0.002085789	2.15668139
ABUW_R501805	ABUW_3720	NZ_CP008706.1	377199	377198	+	WP_000231981.1		UDP-246 family protein	2347.172794	1.089221641	0.209753209	5.162871892	2.07E-07	1.08E-06	5.950651245
ABUW_R5014840	ABUW_1120	NZ_CP008706.1	1141571	1143157	+	WP_000166831.1		BlaPa protein-like domain-containing protein	4525.440612	1.08862639	0.200640892	5.29528552	1.20E-07	6.54E-07	6.18442232
ABUW_R5016020	ABUW_1148	NZ_CP008706.1	1141434	1170131	-	WP_010161044.1		BCTC family transporter	870.3374275	1.088078709	0.193268386	7.81281918	5.59E-15	9.27E-14	10.0320227
ABUW_R5014950	ABUW_3080	NZ_CP008706.1	3109320	3109396	-			rRNA: Met	45.02926697	1.087477263	0.417286306	2.600668953	0.009168778	0.01826896	17.2522192
ABUW_R5014945	ABUW_2160	NZ_CP008706.1	2140911	2142017	+	WP_000734917.1		poim	31.81080585	1.086164387	0.18474118	5.879310021	4.12E-09	2.99E-08	7.524328812
ABUW_R5017805	ABUW_1454	NZ_CP008706.1	1445528	1446361	-	WP_000744443.1		hypothetical protein	457.0234091	1.085490671	0.192671213	5.633901682	1.76E-08	1.02E-07	6.95057977
ABUW_R501895	ABUW_2445	NZ_CP008706.1	2431615	2431605	-	WP_001985862.1		hypothetical protein	39.76594994	1.083920321	0.415416652	2.621859369	0.008745151	0.018041072	1.74371367
ABUW_R501995	ABUW_0227	NZ_CP008706.1	2677126	2686675	-	WP_000576648.1		acyl-CoA dehydrogenase	2404.047217	1.08319162	0.337879171	3.205844931	0.01345618	0.003388835	2.609949574
ABUW_R501165	ABUW_0223	NZ_CP008706.1	277179	277139	+	WP_001037630.1		methionine/lanine import family NIS transporter small subunit	77.819216626	1.081708892	0.203270858	5.321914852	1.03E-07	6.69E-07	6.684487734
ABUW_R5019205	ABUW_0352	NZ_CP008707.1	21164	21700	+	WP_000731978.1		hypothetical protein	64.41631602	1.079559151	0.320271466	3.71307832	0.000749604	0.002001427	2.168660242
ABUW_R5017235	ABUW_0356	NZ_CP008706.1	371797	371918	+	WP_000797312.1	astA	arginine N-succinyltransferase	7234.677006	1.0787160057	0.255091639	4.229340151	2.38E-05	8.54E-05	4.068542129
ABUW_R501885	ABUW_3067	NZ_CP008706.1	3094580	3095440	+	WP_000838106.1		poim family protein	358.0537168	1.07825184	0.268889728	4.01014093	6.07E-05	0.000210168	3.69644162
ABUW_R502665	ABUW_0542	NZ_CP008706.1	544446	545739	-	WP_002101678.1	ssb	single-stranded DNA-binding protein	532.288048	1.078235926	0.232667002	4.034245162	3.58E-06	1.50E-05	4.423991741
ABUW_R501110	ABUW_0227	NZ_CP008706.1	247400	247735	-	WP_000108772.1		helic_tum-helic-transcriptional regulator	925.100451	1.076850218	0.280637285	3.837160194	0.000124465	0.00083941	3.04966986
ABUW_R501570	ABUW_2587	NZ_CP008706.1	2580666	2581400	-	WP_001118705.1		transcriptional regulator	23.4161506	1.076016168	0.40533756	2.654816	0.007393897	0.01549325	1.781219716
rRNA22	no	no	no	no	no	no	no	no	4.07502121	1.07501092	1.051161874	1.022440102	0.306569852	0.392241961	0.046445946
ABUW_R5019605	ABUW_2386	NZ_CP008706.1	2373057	2374448	-	WP_001986580.1		LLCMe flavin-dependent oxidoreductase	1019.61487	1.072737776	0.210819264	5.08842387	3.61E-07	1.81E-06	5.742321425
ABUW_R5017910	ABUW_2016	NZ_CP008706.1	2007144	2008865	-	WP_000996660.1		malonate decarboxylase subunit E2	264.6104911	1.071202346	0.201640492	5.131800081	1.06E-07	5.80E-07	6.236572006
ABUW_R501925	ABUW_2185	NZ_CP008706.1	2177566	2178117	+	WP_0011010029.1		tanase/esterase family alpha-beta hydrolase	148.1030492	1.071201533	0.347114469	3.088548827	0.002024705	0.00487891	2.311677193
ABUW_R5012990	ABUW_0466	NZ_CP008706.1	479247	4794909	+	WP_000877281.1		hypothetical protein	2209.100249	1.070544339	0.1429973	8.612603193	7.14E-18	5.67070389	
ABUW_R501935	ABUW_2453	NZ_CP008706.1	2440211	2441842	+	WP_001072771.1		hypothetical protein	219.0126352	1.070383178	0.34105332	3.10510083	0.01079608	0.004719838	2.37884055
ABUW_R501910	ABUW_0222	NZ_CP008706.1	266851	267163	+	WP_000102725.1		sodium-dependent transporter	10886.94454	1.070219163	0.18439887	6.335368215	2.13E-10	1.89E-09	8.72335196
ABUW_R5019205	ABUW_2375	NZ_CP008706.1	2308990	2309550	+	WP_000037185.1		TetR/AcrI family transcriptional regulator	124.0720834	1.069675963	0.45919169	2.329479824	0.018931661	0.037341837	14.27910621
ABUW_R5014425	ABUW_2171	NZ_CP0													

ABUW_RS18410	ABUW_3781	NZ_CP008706.1	3841207	3842856	-	WP_000969576.1		AMP-binding protein	693.1313288	1.010324428	0.400988016	2.519587589	0.01174924	0.023446107	1.629929257
ABUW_RS10130	ABUW_2086	NZ_CP008706.1	2067158	2067688	-	WP_000379658.1		flavin reductase family protein	5.36322968	1.008770966	0.522425659	1.930936668	0.05349086	0.089240031	1.049410288
ABUW_RS10550	ABUW_2171	NZ_CP008706.1	2152260	2153003	-	WP_000187501.1		adenosylcobinamide-GDP ribazoletransferase	273.7069471	1.008733349	0.164823298	6.120089571	9.35E-10	7.48E-09	8.126098402
ABUW_RS10800	ABUW_2221	NZ_CP008706.1	2205801	2207531	-	WP_001295038.1		ABC transporter ATP-binding protein	1177.883006	1.008683	0.154786307	6.918914571	4.55E-12	5.12E-11	10.29073004
ABUW_RS06065	ABUW_1241	NZ_CP008706.1	828739	8283191	-	WP_000835608.1		DUF1962 domain-containing protein	639.0061519	1.008387483	0.273793351	3.683023995	0.000203483	0.000684317	3.164742671
ABUW_RS15355	ABUW_3602	NZ_CP008706.1	3661033	3661108	-			IRNA-Thr	4673.477769	1.006457074	0.269539568	1.733986365	0.000188473	0.0005567436	3.24608315
ABUW_RS14955	ABUW_3800	NZ_CP008706.1	3860709	3861917	+	WP_000343018.1		IS256-like element ISAb26 family transposase	458.391884	1.00612166	0.290576923	3.462494738	0.000353192	0.001467863	2.83331477
ABUW_RS13110	ABUW_2701	NZ_CP008706.1	2685172	2685765	-	WP_000253373.1		lysine family transporter	259.1475051	1.0057663	0.294172434	3.419868543	0.00062859	0.001700886	2.7693299
ABUW_RS04945	ABUW_1008	NZ_CP008706.1	1021621	1022190	-	WP_001050712.1		CAP domain-containing protein	322.414122	1.004451898	0.186432789	5.387742691	7.5E-08	4.06E-07	6.391473966
ABUW_RS03880	ABUW_0791	NZ_CP008706.1	771487	772414	+	WP_000094258.1		hypothetical protein	17.64543608	1.001647252	0.440764203	2.272524049	0.023054877	0.042687546	1.361988811

Table S18. RNA-seq data: Absolute and relative expression (Col/MEP > 2-fold down)

ABUW_RS15475	ABUW_2775	NZ_CP008706.1	2768845	2769537	-	WP_005802836.1		GntR family transcriptional regulator	316.5831437	-1.000067844	0.161442837	-6.194563133	5.84E-10	4.85E-09	8.31425821
ABUW_RS10130	ABUW_2268	NZ_CP008706.1	2253727	2255037	+	WP_000850091.1		peptidylprolyl isomerase	4427.033963	-1.000900835	0.132653069	-7.545252007	4.27E-14	6.86E-13	12.9387588
ABUW_RS06610	ABUW_1555	NZ_CP008706.1	1568153	1568323	-	WP_000993415.1		hemin uptake protein HemP	362.5923692	-1.001148195	0.574655157	-2.187519245	0.02870515	0.051492899	1.288252657
ABUW_RS04410	ABUW_0899	NZ_CP008706.1	895188	897083	+	WP_001286662.1	ftsH	ATP-dependent zinc metalloprotease FtsH	66757.44407	-1.001954915	0.221856371	-4.154880097	6.34E-06	2.52E-05	4.598599459
ABUW_RS16610	ABUW_3417	NZ_CP008706.1	3465750	3466568	+	WP_000959085.1		protoprotein diacylglycerol transferase	1692.18671	-1.003559653	0.291577146	-3.441832342	0.000577788	0.00157504	2.802708412
ABUW_RS16120	ABUW_3318	NZ_CP008706.1	3352203	3352886	+	WP_001182927.1		hypothetical protein	872.3452918	-1.004469453	0.182014788	-5.516161538	3.42E-08	2.07E-07	6.684029655
ABUW_RS00665	ABUW_0194	NZ_CP008706.1	148163	1481708	+	WP_000955427.1		ankyrin repeat domain-containing protein	1912.052954	-1.005056078	0.118864242	-8.826792847	1.08E-18	2.91E-17	16.53610711
ABUW_RS01010	ABUW_0204	NZ_CP008706.1	229153	230601	+	WP_000615688.1		NAD-dependent succinate-semialdehyde dehydrogenase	4770.024141	-1.006107329	0.31588488	-3.228951448	0.00142445	0.003150302	2.50164781
ABUW_RS12105	ABUW_2487	NZ_CP008706.1	2483057	2484271	-	WP_000335523.1	pobA	4-hydroxybenzoate 3-monooxygenase	93.80805266	-1.007199253	0.3565005897	-2.757046695	0.005832602	0.012586799	1.900084703
ABUW_RS1840	ABUW_2433	NZ_CP008706.1	2420869	2422104	-	WP_000024222.1		stress-induced protein	101047.252	-1.008439403	0.53102156	-1.899055481	0.05757182	0.095079084	1.021915011
ABUW_RS15815	ABUW_2842	NZ_CP008706.1	2855958	2857601	+	WP_001289231.1		hypothetical protein	1714.662033	-1.008710684	0.199852779	-5.047268754	4.48E-07	2.21E-06	5.655607728
ABUW_RS1640	ABUW_3017	NZ_CP008706.1	3040090	3041319	-	WP_001091605.1		tyrosine-type recombinase/integrase	350.7219809	-1.008865904	0.199263123	-5.062983493	4.51E-07	2.05E-06	5.688246139
ABUW_RS01260	ABUW_0257	NZ_CP008706.1	270657	271421	-	WP_000060753.1	ompR	two-component system response regulator OmpR	10241.27743	-1.009701449	0.186475777	-5.141652067	6.14E-08	3.54E-07	6.450996738
ABUW_RS17340	ABUW_3563	NZ_CP008706.1	3620599	3621372	+	WP_001101836.1		transcriptional regulator	1188.109425	-1.010792664	0.180405221	-5.802901578	2.11E-08	1.32E-07	6.879426669
newcardsRNA1	no	no	no	no	no	no	no	no	238.6279859	-1.014586166	0.823031962	-1.232743018	0.21677857	0.29469056	0.530613377
ABUW_RS18875	ABUW_2440	NZ_CP008706.1	2429094	2429411	+	WP_000132046.1		hypothetical protein	33008.50582	-1.018017925	0.460518019	-2.210593035	0.02704032	0.048916239	13.10520308
ABUW_RS13210	ABUW_2722	NZ_CP008706.1	2708337	2708555	+	WP_000058246.1		DUF1653 domain-containing protein	170.8721715	-1.022972897	0.224399826	-4.558703363	5.5E-06	2.10E-05	4.677718075
ABUW_RS05510	ABUW_1126	NZ_CP008706.1	1148468	1149013	+	WP_001107199.1		gamma carbonic anhydrase family protein	627.0749455	-1.024678154	0.129784565	-7.896223558	2.90E-15	4.94E-14	13.30627305
ABUW_RS19370	ABUW_4074	NZ_CP008707.1	43471	43941	+	WP_000192272.1		hypothetical protein	96.73348833	-1.028300602	0.48094445	-2.138086016	0.032509763	0.057549106	12.39961192
ABUW_RS19660	no	NZ_CP008706.1	3109461	3109155	-		mpB	RNAse P RNA component class A	20781.41966	-1.029246227	0.289099986	-3.560173908	0.000370609	0.001493322	2.979091222
ABUW_RS08455	ABUW_1736	NZ_CP008706.1	1733894	1734448	+	WP_000610648.1	fr	ribosome recycling factor	5586.980737	-1.030943176	0.154582728	-2.57E-11	2.65E-10	1.24E-06	5.900578315
ABUW_RS13360	ABUW_2752	NZ_CP008706.1	2742498	2742887	+	WP_000735756.1		hypothetical protein	299.543435	-1.03552799	0.204739227	-5.038374002	4.70E-07	2.31E-06	5.56388802
ABUW_RS09205	ABUW_890	NZ_CP008706.1	891602	892018	-	WP_001026788.1		MerR family transcriptional regulator	286.2225447	-1.031859996	0.21851469	-4.847793628	1.25E-06	5.80E-06	5.236572008
ABUW_RS00520	ABUW_0105	NZ_CP008706.1	116879	116237	-	WP_000273188.1	phoR	phosphate regulon sensor histidine kinase PhoR	1072.405025	-1.032175585	0.176628639	-5.843768845	5.01E-09	3.61E-08	7.442492798
ABUW_RS04255	ABUW_0867	NZ_CP008706.1	846075	847349	+	WP_001287579.1	gltA	citrate (S)-synthase	34759.78554	-1.034263327	0.228545916	-4.525335898	6.03E-06	2.41E-05	4.677829697
ABUW_RS00810	ABUW_1163	NZ_CP008706.1	118609	118246	+	WP_000119870.1	gltM	phosphoglucosamine mutase	6879.82609	-1.035885492	0.128996407	-8.028793337	9.84E-16	1.79E-14	13.74714957
ABUW_RS17685	ABUW_3632	NZ_CP008706.1	3690522	3692375	-	WP_001278226.1		femA iron transporter B	9168.961091	-1.035888412	0.219286358	-3.558254466	0.0003716	0.001063599	2.97322208
ABUW_RS06030	ABUW_034	NZ_CP008706.1	1277293	1278120	-	WP_001084911.1	map	type I methionyl aminopeptidase	32.13.46037	-1.036508169	0.150194336	-6.91014387	5.1E-12	1.01E-11	10.23957752
ABUW_RS12660	ABUW_2522	NZ_CP008706.1	2512883	2514676	-	WP_000158322.1		AAA family ATPase	1542.724824	-1.037651419	0.200820252	-6.402831543	0.000666914	0.00179492	2.745914903
ABUW_RS18240	ABUW_3747	NZ_CP008706.1	3803233	3805023	+	WP_001092084.1		arginine-tRNA ligase	5864.710431	-1.038464392	0.10718248	-9.640740481	5.38E-22	2.31E-20	9.63638802
ABUW_RS18555	ABUW_3872	NZ_CP008706.1	3904402	3940999	-	WP_001866667.1		peptidyl-prolyl cis-trans isomerase	373.5754422	-1.038624143	0.180158863	-5.765044048	8.18E-09	5.57E-08	7.254144005
ABUW_RS16880	ABUW_3837	NZ_CP008706.1	3905458	3906027	-	WP_000810005.1	ampD	1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD	225.3413709	-1.038937787	0.220573554	-4.710164795	2.48E-06	1.08E-05	4.966576245
ABUW_RS15525	ABUW_3806	NZ_CP008706.1	3865436	3868042	-	WP_001095383.1	acnD	Fe/S-dependent 2-methylsulfite dehydrogenase AcnD	4507.353954	-1.041414897	0.320299162	-3.125138195	0.00114454	0.002937856	2.531969495
ABUW_RS00290	ABUW_0059	NZ_CP008706.1	63622	64341	-	WP_000197863.1	purC	phosphoribosylaminoimidazole succinocarboxamide synthase	10232.81424	-1.042981871	0.162496818	-6.418475668	1.38E-10	1.26E-09	8.89962545
ABUW_RS11155	ABUW_2293	NZ_CP008706.1	2279875	2280465	-	WP_000550334.1		polyisoprenoid-binding protein	2145.45552	-1.045140547	0.231288936	-4.519675863	6.22E-06	2.48E-05	4.605548319
sRNA95	no	no	no	no	no	no	no	no	126.2491262	-1.045257862	0.268744176	-3.889415868	0.00100486	0.00032106	3.493413799
ABUW_RS19800	no	NZ_CP008706.1	2051479	2051553	-	WP_001182218.1	pqqA	pyrroloquinoline quinone precursor peptide PqqA	870.2859197	-1.048328409	0.308075318	-6.402831543	0.000666914	0.00179492	2.745914903
ABUW_RS10065	ABUW_3307	NZ_CP008706.1	3341993	3342781	+	WP_001196724.1		crotonase/enoyl-CoA hydratase family protein	339.0483809	-1.049137087	0.187509044	-5.595127912	2.20E-08	1.37E-07	6.863279433
ABUW_RS17880	ABUW_3672	NZ_CP008706.1	3728668	3729621	+	WP_001172025.1	inxB	thiooxidin-disulfide reductase	100.58055	-1.052064604	0.263308396	-3.995560422	6.45E-05	0.000212971	3.67187953
ABUW_RS17695	ABUW_3634	NZ_CP008706.1	3692779	3693699	+	WP_000608735.1	xerD	site-specific tyrosine recombinase XerD	1343.215569	-1.05502624	0.137614782	-7.666518284	1.77E-14	2.83E-13	12.54821356
ABUW_RS05365	ABUW_1097	NZ_CP008706.1	1113160	1115771	+	WP_001214806.1		thiamine phosphate synthase	971.313968	-1.055078273	0.145745834	-7.239155892	4.51E-13	5.85E-12	11.22988471
ABUW_RS17720	ABUW_3639	NZ_CP008706.1	3698770	3699405	+	WP_000633799.1		response regulator	3946.076941	-1.055449058	0.183296554	-6.463388429	1.02E-10	9.50E-10	9.022276395
ABUW_RS05880	ABUW_1204	NZ_CP008706.1	1242291	1242875	-	WP_000925669.1		aminodeoxychorismate/antranilate synthase component II	1340.84241	-1.056635036	0.110047267	-9.60203985	7.84E-22	3.19E-20	19.49620932
ABUW_RS01155	ABUW_0236	NZ_CP008706.1	254791	255033	+	WP_000476050.1		hypothetical protein	337.0624544	-1.057583865	0.18782634	-5.630647248	1.80E-08	1.14E-07	6.813095149
ABUW_RS11710	ABUW_2407	NZ_CP008706.1	2394514	2395203	-	WP_001028704.1		LgB family protein	73.27774811	-1.058617812	0.2181625864	-3.758950965	0.000170627	0.000518054	3.285624969
ABUW_RS04865	ABUW_0992	NZ_CP008706.1	1004219	1004782	-	WP_000836015.1	pal	peptidoglycan-associated lipoprotein Pal	1270.619591	-1.061430534	0.205574056	-5.193251418	2.43E-07	1.26E-06	5.899629455
ABUW_RS17960	ABUW_3689	NZ_CP008706.1	3745849	3747528	-	WP_000411991.1		long-chain fatty-acid-CoA ligase	53752.16368	-1.061505445	0.158500703	-6.697195549	2.13E-11	2.21E-10	9.655607726
ABUW_RS01035	ABUW_0209	NZ_CP008706.1	25219	236046	+	WP_000640509.1		class IIASm-dependent methyltransferase	920.26502	-1.061795037	0.16680903	-6.365333078	1.95E-10	1.78E-09	8.754847332
ABUW_RS02450	ABUW_0499	NZ_CP008706.1	503936	510064	-	WP_000480818.1		LgB family protein	2130.15899	-1.063075805	0.21641913	-4.952804474	7.32E-07	5.62E-06	5.453457337
ABUW_RS01940	ABUW_0375	NZ_CP008706.1	398789	41092	+	WP_000550363.1		hypothetical protein	5027.339367	-1.068708584	0.118518097	-9.19191212	4.57E-20	1.88E-19	9.72524615
ABUW_RS15360	ABUW_3163	NZ_CP008706.1	318851	318944	+	WP_000806837.1		cold shock domain-containing protein	732.654885	-1.069159702	0.195216787	-5.476735485	4.34E-08	2.57E-07	6.590066877
ABUW_RS16030	ABUW_3300	NZ_CP008706.1	3331887	3334293	-	WP_000359493.1	magA	nucleoside triphosphate pyrophosphohydrolase	232.793531	-1.074962656	0.194884458	-5.321563787	3.38E-08	2.04E-07	6.890369833
ABUW_RS03110	ABUW_0632	NZ_CP008706.1	61333	63574	+	WP_001985920.1		hemolysin II family protein	966.9142932	-1.07538512	0.18255175	-5.890580783	3.84E-09	2.80E-08	7.552496384
ABUW_RS05370	ABUW_1098	NZ_CP008706.1	111304	111512	+	WP_000505923.1	hemL	glutamate-1-semialdehyde 2,1-aminomutase	4912.34148	-1.075919248	0.17170892	-6.722242473	3.42E-09	2.97E-09	8.724343551
ABUW_RS15375	ABUW_3370	NZ_CP008706.1	3410204	3410461	+	WP_000729828.1	grxC	glutaredoxin 3	4240.51042	-1.078445496	0.212261023	-5.071929665	3.95E-07	1.97E-06	5.705533774
ABUW_RS18320	ABUW_2843	NZ_CP008706.1	2857601	2858344	-	WP_001292948.1	nuoC	NAD(+)-diphosphate	1094.776218	-1.078004435	0.11832386	-7.529192136	5.11E-14	7.65E-13	1.12183586
ABUW_RS02300	ABUW_0468	NZ_CP008706.1	481271	481536	+	WP_000406284.1		DUF2789 domain-containing protein	2297.593528	-1.079082711	0.309592452	-4.148419174	0.000498722	0.001380048	2.86358058
ABUW_RS03440	ABUW_0699	NZ_CP008706.1	702919	703094	-	WP_000156491.1		SdiI family protein	3868.89451	-1.079197513	0.				

ABUW_RS330	ABUW_0295	NZ_CP008706.1	35037	35656	+	WP_00064372.1	aroK	shikimate kinase AroK	1559.02192	-1.084854294	0.035424027	-8.076796304	1.14E-15	2.06E-14	0.68610278
ABUW_RS340	ABUW_3355	NZ_CP008706.1	339272	3393278	-	WP_00186543.1	ivcC	ketol-acid reductoisomerase	33596.40446	-1.08923364	0.03005614	-8.06804947	7.14E-16	1.32E-14	0.87942670
ABUW_RS3400	ABUW_3171	NZ_CP008706.1	356589	357875	-	WP_00707098.1	nuoH	NADH-quinone oxidoreductase subunit NuoH	23369.85271	-1.090434048	0.28198098	-3.867046607	0.00019016	0.000348383	3.45793405
ABUW_RS3405	ABUW_3015	NZ_CP008706.1	303750	303865	-	WP_00016334.1			5.8464248	-1.091363343	0.693619709	-1.573438657	0.01269282	0.0725906	0.129292861
ABUW_RS3505	ABUW_0712	NZ_CP008706.1	719780	719339	-	WP_00706650.1	galB	Aap-(RNAse)Glu-(RNAse)Gln amidotransferase subunit GalB	6890.18704	-1.092232147	0.250470955	-4.209456234	2.56E-05	9.96E-05	0.42668489
ABUW_RS3560	ABUW_5220	NZ_CP008706.1	526964	5269674	-	WP_000342684.1		NADP-dependent malic enzyme	28718.8283	-1.084521561	0.0789353	-5.93201972	4.15E-12	4.71E-11	0.32697909
ABUW_RS1465	ABUW_2357	NZ_CP008706.1	2338870	2340300	+	WP_000078700.1		pyridoxal-phosphate-dependent aminotransferase	9096.88727	-1.094686953	0.245374691	-4.48102861	8.85E-06	3.17E-05	4.498940738
ABUW_RS4820	ABUW_3054	NZ_CP008706.1	3080842	3081789	+	WP_00276144.1	tsxB	thioredoxin-disulfide reductase	5167.262095	-1.098742374	0.075998439	-6.257101662	3.32E-12	3.38E-09	8.4710833
ABUW_RS2023	ABUW_0471	NZ_CP008706.1	482883	483740	+	WP_001090438.1		23S rRNA (adenine(2035)-N6)-methyltransferase RlmJ	2941526004	-1.00860838	0.02345493	-8.51010388	1.72E-17	3.80E-16	5.4154127
ABUW_RS3600	ABUW_5004	NZ_CP008706.1	1871	2389	-	WP_000447163.1		ser1repeat family protein	3451402254	-1.01434876	0.214749845	-5.02820466	2.91E-07	1.48E-06	5.82681732
ABUW_RS3860	ABUW_3873	NZ_CP008706.1	394143	3942215	-	WP_000023587.1		alpha/beta hydrolase	852.0312726	-1.02004656	0.03182859	-6.75318806	1.45E-11	1.54E-10	9.812479279
sRNA19	no	no	no	no	no	no	no	no	305.778355	-1.02718665	0.288790841	-3.818634435	0.000154192	0.000414936	3.382018884
sRNA10	no	no	no	no	no	no	no	no	305.778355	-1.02718665	0.288790841	-3.818634435	0.000154192	0.000414936	3.382018884
ABUW_RS5001	ABUW_0034	NZ_CP008706.1	40420	41920	+	WP_001050643.1		efflux RND transporter periplasmic adaptor subunit	6267.819798	-1.1031027	0.231718006	-4.76053941	1.93E-06	8.61E-06	5.064996849
ABUW_RS0860	ABUW_1782	NZ_CP008706.1	1780167	1781565	+	WP_000529940.1		aspartate aminotransferase family protein	118.134044	-1.03069857	0.07900967	-6.573338282	4.92E-11	4.81E-10	3.917854924
ABUW_RS210	ABUW_4337	NZ_CP008707.1	22237	22536	-	WP_001096429.1		helic-tum-helic transcriptional regulator	498.8094305	-1.04602047	0.347250588	-3.191864338	0.001466844	0.003650349	2.437685612
ABUW_RS245	ABUW_3748	NZ_CP008706.1	3805197	3805803	+	WP_000067262.1		SPOR domain-containing protein	2085.388125	-1.05418285	0.14883547	-7.427078224	1.11E-13	1.56E-12	1.1068754
ABUW_RS175	no	NZ_CP008706.1	851927	853056	-			hypothetical protein	529.59205	-1.05715773	0.174575595	-6.03239636	2.95E-10	2.61E-09	5.853335493
ABUW_RS3465	ABUW_4097	NZ_CP008707.1	59217	59570	+	WP_000424621.1		hypothetical protein	606.1980863	-1.059972779	0.273305094	-4.045493331	5.20E-05	0.00075142	3.756609995
ABUW_RS1670	ABUW_2236	NZ_CP008706.1	2225480	2225499	-	WP_000830354.1		AraC family transcriptional regulator	743.450414	-1.07011620	0.03798219	-7.98285536	6.16E-12	7.80E-12	11.0237291
ABUW_RS1035	ABUW_2269	NZ_CP008706.1	225616	2256163	-	WP_001074011		fructose-bisphosphate aldolase class II	8885.12851	-1.071022893	0.073844665	-6.368400557	191E-10	1.72E-09	8.76471653
ABUW_RS3560	ABUW_0723	NZ_CP008706.1	728645	728622	+	WP_000406999.1	thrH	l-thal phosphate-dependent phosphatase/homoserine phosphatase	1060.205949	-1.07606063	0.077836	-5.839584608	3.67E-09	2.68E-08	5.771865200
ABUW_RS3435	ABUW_3386	NZ_CP008706.1	3425871	3426890	+	WP_000578593.1	nagZ	beta-N-acetylhexosaminidase	1549.255862	-1.10427835	0.017570077	-8.094186559	5.73E-16	1.08E-14	0.1623735
ABUW_RS0665	ABUW_1366	NZ_CP008706.1	1380477	1382723	+	WP_000082052.1		bifunctional prephenate dehydrogenase/3-phosphoshikimate 1-carboxyvinyl	4200.558492	-1.119121211	0.15851919	-7.010710715	1.236E-12	2.81E-11	0.55109368
ABUW_RS4000	ABUW_0856	NZ_CP008706.1	836029	836589	+	WP_000071811.1		flavodoxin family protein	325.5110692	-1.112181623	0.216272195	-5.072150262	3.93E-07	1.96E-06	5.707743929
ABUW_RS0016	ABUW_0532	NZ_CP008706.1	54122	54151	-	WP_000051669.1	yajC	preprotein translocase subunit YajC	3581.023945	-1.15856932	0.19303987	-8.384265791	5.10E-17	1.08E-16	1.66657624
ABUW_RS3035	ABUW_0702	NZ_CP008706.1	66219	66663	+	WP_001980570.1	pncA	bifunctional nicotianamide/tryptophanase	460.7607337	-1.11474902	0.05054922	-7.399353457	1.37E-13	1.89E-12	11.723382
ABUW_RS1925	ABUW_2055	NZ_CP008706.1	2687963	2688370	+	WP_000331651.1		GFA family protein	269.52314	-1.18083366	0.20803051	-5.365009191	8.09E-08	4.55E-07	6.341988603
ABUW_RS2185	ABUW_0262	NZ_CP008706.1	279723	28184	+	WP_000090021.1	etfA	energy-dependent translocation thiolase protein EtfA	27429.05219	-1.0233592	0.1976778	-6.243254041	4.29E-10	3.67E-09	8.453333936
ABUW_RS1205	ABUW_2491	NZ_CP008706.1	2489449	2487433	-	WP_000064100.1		carboxymuconate dehydrogenase/3-phosphoshikimate family protein	95.40315455	-1.02453668	0.235500025	-4.750211916	2.03E-06	9.03E-06	5.0443125
ABUW_RS3169	ABUW_3169	NZ_CP008706.1	3169000	3169008	-	WP_010578792.1	nuoJ	NADH-quinone oxidoreductase subunit J	113150451	-1.02439387	0.261469705	-4.203260402	171E-05	6.36E-05	4.196542884
ABUW_RS1210	ABUW_2444	NZ_CP008706.1	2445228	2445228	+	WP_001094942.1	psbR	16S rRNA transcriptional regulator PsbR	224.0987496	-1.04363026	0.190376099	-5.640716142	1.69E-08	1.09E-07	6.926273502
ABUW_RS0955	ABUW_2180	NZ_CP008706.1	216259	2162782	-	WP_00101556.1		PeptS domain-containing protein	714.4884196	-1.0267533	0.314918845	-3.577791915	0.000344631	0.00099098	3.08393511
ABUW_RS0445	ABUW_1175	NZ_CP008706.1	115365	116336	+	WP_001028906.1		substrate-binding domain-containing protein	699.7235461	-1.07304675	0.27123132	-4.16709666	3.21E-05	0.000102622	3.948376764
ABUW_RS0700	ABUW_1677	NZ_CP008706.1	166519	166519	+	WP_000397471.1	gltS	sodium/glutamate symporter	4470.147107	-1.07530055	0.23480015	-5.860270449	1.57E-06	4.16E-07	5.82270402
ABUW_RS0795	ABUW_1807	NZ_CP008706.1	180312	1803884	+	WP_000061059.1	gpiA	ribose-5-phosphate isomerase GpiA	2847.905191	-1.0180358	0.19196392	-5.919988051	3.22E-09	2.38E-08	7.623423043
ABUW_RS0005	ABUW_0219	NZ_CP008706.1	571869	572581	+	WP_00117505.1	shA	Sh-specific NAD(P)+ transhydrogenase	7469.584491	-1.02297789	0.03050321	-8.384265791	5.10E-17	1.08E-16	1.66657624
ABUW_RS0245	ABUW_0452	NZ_CP008706.1	504336	504899	-	WP_00110146.1		glutathione S-transferase N-terminal domain-containing protein	484.8122393	-1.04336389	0.19098417	-5.998566199	1.99E-09	1.50E-08	7.623987614
ABUW_RS3440	ABUW_3058	NZ_CP008706.1	3084083	3084958	-	WP_000092293.1		malate dehydrogenase	506.2559932	-1.04503951	0.278057331	-4.08018039	4.50E-05	0.00012535	3.84630494
ABUW_RS0730	ABUW_1625	NZ_CP008706.1	1620422	1622104	+	WP_000086297.1		AAA family ATPase	1087.461035	-1.0562449	0.096946848	-11.7804522	1.02E-31	1.32E-29	28.87426705
ABUW_RS1705	ABUW_325	NZ_CP008706.1	359585	3561426	+	WP_000008979.1		cation channel antiporter	1075.45293	-1.07710531	0.14470722	-7.894889005	2.91E-15	4.94E-14	0.346273007
ABUW_RS0605	ABUW_1654	NZ_CP008706.1	1647233	1647429	-	WP_01019962.1		N-acetyltransferase	209.0185668	-1.03891681	0.34846609	-3.264161027	0.00197886	0.00283197	2.567026874
ABUW_RS1801	ABUW_0287	NZ_CP008706.1	305929	306261	+	WP_000165061.1		hypothetical protein	874.785375	-1.10264045	0.02955287	-8.842321005	9.38E-19	2.59E-17	5.84700008
ABUW_RS0493	ABUW_0170	NZ_CP008706.1	028367	0284655	-	WP_001034922.1		NF5-like dimeric metal center hexameric protein	0.401.49024	-1.114549887	0.05760316	-7.57189304	3.68E-14	5.63E-13	0.2249191
ABUW_RS1965	ABUW_3510	NZ_CP008706.1	351026	3750445	-	WP_000202252.1	parC	DNA topoisomerase IV subunit A	32.019932	-1.144244473	0.156891891	-7.293203859	3.70E-13	4.04E-12	11.39381963
ABUW_RS0140	ABUW_0288	NZ_CP008706.1	306264	307588	+	WP_001090541.1		methyltransferase domain-containing protein	1183.00014	-1.144905553	0.141873299	-8.087339379	6.16E-16	1.65E-14	0.593930216
ABUW_RS1430	ABUW_2760	NZ_CP008706.1	275019	2751741	+	WP_000459994.1		pin family protein	96.6784634	-1.145448536	0.228033206	-5.023604039	5.07E-07	2.48E-06	6.50554839
ABUW_RS0220	ABUW_0715	NZ_CP008706.1	101359	1021038	+	WP_000066269.1		hypothetical protein	91.4314567	-1.160254996	0.060597102	-1.188040336	0.000053329	0.098635979	1.009564611
ABUW_RS3265	ABUW_3348	NZ_CP008706.1	3383437	3384378	-	WP_000958109.1		DUF3298 domain-containing protein	1259.295566	-1.167143042	0.03616687	-7.467616499	3.87E-14	1.96E-12	11.93354201
ABUW_RS3395	ABUW_3170	NZ_CP008706.1	3195608	3196150	-	WP_000276693.1	nuoI	NADH-quinone oxidoreductase subunit NuoI	10274.49772	-1.16942452	0.276648915	-4.154512793	0.000114057	3.942878056	
ABUW_RS0740	ABUW_1616	NZ_CP008706.1	1602706	1603200	-	WP_000305020.1		chalcone isomerase family protein	37.63942864	-1.05226954	0.156430099	-2.038339423	0.0419E-06	0.07434384	1.94451736
ABUW_RS0800	ABUW_0528	NZ_CP008706.1	528246	528456	+	WP_000078452.1	eno	phosphoenolpyruvate hydratase	24287.51993	-1.05045857	0.16224932	-7.364186311	1.78E-13	2.44E-12	1.116102197
ABUW_RS1270	ABUW_3549	NZ_CP008706.1	3505887	3601759	+	WP_001274987.1	pilB	type IV-A pilus assembly ATPase PilB	0.238.801225	-1.1195811	0.20206913	-5.506300968	3.66E-08	2.21E-07	6.56560772
ABUW_RS0701	ABUW_2898	NZ_CP008706.1	2905472	2906917	-	WP_000479778.1		capsule assembly Waf family protein	7378.623707	-1.05309119	0.198064003	-5.805910098	6.40E-09	4.46E-08	7.350605141
ABUW_RS1795	ABUW_3542	NZ_CP008706.1	3741263	3756660	-	WP_000738515.1		ammonium transporter	3737.422396	-1.04605662	0.17333513	-6.604487956	2.73E-11	2.79E-10	9.5543395797
ABUW_RS1900	ABUW_2242	NZ_CP008706.1	2238039	2232512	-	WP_000140309.1	gtaA	53S ribosomal protein S1	206336.9575	-1.019100248	0.16198174	-7.185305306	9.38E-13	1.04E-11	0.18266666
ABUW_RS1000	ABUW_2362	NZ_CP008706.1	2347598	2347945	-	WP_000023429.1		ParB/RegB/SpdJ family partition protein	2035.032331	-1.059674622	0.148519015	-7.808256902	5.80E-16	9.97E-14	0.19008806
ABUW_RS0150	ABUW_0308	NZ_CP008706.1	331325	331708	-	WP_000009000.1		Rok family protein	674.7816872	-1.02294666	0.250798372	-4.543792287	5.53E-06		

ABUW_RS6430	ABUW_3381	NZ_CP008706.1	3420637	3421068	-	WP_00096385.1	nde	nucleoside-diphosphate kinase	19627.97567	-1223459576	0.21114971	-5.795228879	6.82E-09	4.74E-08	7.32422458
ABUW_RS00170	ABUW_0035	NZ_CP008706.1	41923	44648	+	WP_000671005.1		efflux RNAse transporter permease subunit	16662.05326	-1224036317	0.259056395	-4.72489051	2.30E-06	1.06E-05	4.956767826
ABUW_RS01780	ABUW_0363	NZ_CP008706.1	385237	385521	+	WP_000637648.1		hydropathic protein	790.3552533	-1224429676	0.208722956	-5.866291581	4.48E-09	3.21E-08	4.926494968
ABUW_RS61450	ABUW_3174	NZ_CP008706.1	320713	320722	-	WP_000973142.1	nuoE	NADH:quinone oxidoreductase subunit NuoE	13467.0391	-1225510657	0.287609095	-4.26104949	2.03E-05	7.47E-05	4.126737036
ABUW_RS04115	ABUW_0840	NZ_CP008706.1	819535	819569	-	WP_000369283.1		YnfJ family protein	2152.832471	-1229554574	0.224552556	-5.475576923	4.36E-08	2.59E-07	5.586703736
ABUW_RS02270	ABUW_0452	NZ_CP008706.1	3688.02287	446725	+	WP_000193835.1		YnfK family protein	3688.02287	-1232166806	0.1802592	-7.64824149	1.42E-06	2.27E-05	12.684924149
ABUW_RS1740	ABUW_3643	NZ_CP008706.1	3703634	3703911	-	WP_000128740.1		2,3-bisphosphoglycerate-independent phosphoglycerate mutase	7635.630303	-1232470195	0.826959564	-6.74651789	1.52E-11	1.81E-10	9.79371424
ABUW_RS00720	ABUW_0145	NZ_CP008706.1	959390	960334	+	WP_000126549.1	gshB	glutathione synthase	19112.09668	-1233746317	0.164865736	-7.483339737	7.25E-06	1.04E-12	1195290666
ABUW_RS6560	ABUW_3407	NZ_CP008706.1	3455344	3455937	+	WP_000127230.1	metW	methionine biosynthesis protein MetW	1425.23231	-1235140443	0.85947789	-6.642404585	3.09E-11	3.12E-10	9.505845406
ABUW_RS4095	ABUW_2903	NZ_CP008706.1	290589	2910770	+	WP_000553407.1		FAD-dependent oxidoreductase	145189893	-1235987018	0.20058318	-6.16969298	7.8E-06	5.88E-09	6.230622674
sRNA64	no	no	no	no	no	no	no	no	73.42638533	-1236333768	0.480428548	-2.573397799	0.010070538	0.02047942	1.688853686
ABUW_RS09145	ABUW_1678	NZ_CP008706.1	8776706	8785520	+	WP_000423293.1		LysR family transcriptional regulator	240.8648879	-1237783845	0.260862941	-4.744958561	2.09E-06	9.24E-06	5.932328029
ABUW_RS08100	ABUW_1662	NZ_CP008706.1	855514	855641	+	WP_000774578.1		hydropathic protein	12.02631539	-1239949704	0.708114421	-1.751058399	0.079935851	0.15364556	0.901825233
ABUW_RS02490	ABUW_5003	NZ_CP008706.1	639	1682	+	WP_000115246.1		hydropathic protein	3512526957	-1240951036	0.257366019	-4.871261942	1.62E-06	6.51E-06	5.96419011
ABUW_RS01360	ABUW_3668	NZ_CP008706.1	3726039	3726409	+	WP_000372102.1		metallorepressor Anr/SmbR family transcription factor	3417627471	-1246321066	0.20810846	-5.987298224	2.01E-09	1.60E-08	7.75988007
ABUW_RS00495	ABUW_5195	NZ_CP008706.1	827445	828338	-	WP_000110552.1		CysH family HTH-type transcriptional regulator	869.765051	-1247605447	0.14866756	-8.39191484	4.78E-17	1.03E-15	14.98776278
ABUW_RS01860	ABUW_0184	NZ_CP008706.1	218563	218587	-	WP_000899498.1	tnaA	thiaminase II	726.0604883	-1248863415	0.16015452	-7.80007414	6.91E-06	1.02E-13	12.99159983
ABUW_RS01570	ABUW_3127	NZ_CP008706.1	314968	3149204	-	WP_000118542.1	lgaA	NAD-dependent DNA ligase lgaA	2427.882349	-1249623353	0.14319357	-8.727395731	2.61E-06	6.77E-17	16.9241163
ABUW_RS01570	ABUW_0195	NZ_CP008706.1	92774	928389	+	WP_000145041.1		deifluide domain protein B	864.3654077	-1250625949	0.174507734	-7.86610435	7.69E-09	9.83E-12	1100744648
ABUW_RS18190	ABUW_3735	NZ_CP008706.1	3739319	3739349	-	WP_000818995.1		FGF1ATP synthase subunit delta	5007163558	-125174863	0.28220532	-4.450969310	8.55E-06	3.32E-05	4.17895191
ABUW_RS16480	ABUW_1913	NZ_CP008706.1	320091	3212925	+	WP_000111540.1		ribonucleoside-diphosphate reductase subunit alpha	44162.19303	-1251885896	0.85600063	-6.93072504	1.53E-11	1.62E-10	9.793484985
ABUW_RS4548	ABUW_2168	NZ_CP008706.1	219955	2140224	+	WP_000167927.1		YARH1 domain-containing protein	1267.619761	-1251925522	0.272727525	-5.512327893	3.54E-08	2.14E-07	6.659588227
ABUW_RS08030	ABUW_1645	NZ_CP008706.1	840257	840811	+	WP_000113191.1		TetR/AcrR family transcriptional regulator	10.2415457	-1266818517	1.00771419	-1.257084896	0.208722896	0.28489348	5.952081561
ABUW_RS19085	ABUW_2168	NZ_CP008706.1	218568	218587	-	WP_000167927.1		HuJ family DNA-binding protein	13.9312568	-1267583076	0.90829969	-6.642473835	3.08E-11	3.12E-10	9.504845406
ABUW_RS16435	ABUW_3382	NZ_CP008706.1	342182	342182	-	WP_000254329.1	hscX	Fe-S cluster assembly protein hscX	657.0273215	-1268452661	0.16505706	-7.48341878	7.24E-06	1.04E-12	119269666
ABUW_RS16710	ABUW_2378	NZ_CP008706.1	2365305	2366309	+	WP_000894033.1		aspartate/glutamate decarboxylase family protein	557.9893143	-1271774397	0.374388217	-3.396540231	0.00081438	0.0002919	2.737757039
ABUW_RS04500	ABUW_0927	NZ_CP008706.1	935673	936056	+	WP_000110178.1		SCP2 stent-binding domain-containing protein	4098.045421	-1271908336	0.174336492	-7.29581218	2.97E-13	3.97E-12	11.0401490
ABUW_RS01590	ABUW_5001	NZ_CP008706.1	1	951	+	WP_000120543.1	repM	replication initiation protein RepM	2709.803281	-1271954516	0.23352284	-5.446809888	5.01E-08	3.06E-07	5.65287745
ABUW_RS10325	ABUW_2165	NZ_CP008706.1	214781	214810	+	WP_000309176.1		hydropathic protein	94.97048432	-1272018893	0.596500279	-2.462765102	0.93787018	0.027004323	1.56856674
ABUW_RS01700	ABUW_3164	NZ_CP008706.1	3126065	3128739	-	WP_000985163.1		HADL-like family hydrolase	968.0784691	-1273705855	0.127979386	-9.952451021	2.46E-12	9.12E-20	2.042433034
ABUW_RS003005	ABUW_0610	NZ_CP008706.1	612007	613379	-	WP_000196959.1		acyl-CoA deuterase	11533.11517	-1274096173	0.324467779	-9.69605656	6.61E-22	2.75E-20	9.96066731
ABUW_RS17370	ABUW_3441	NZ_CP008706.1	3485500	3485949	-	WP_000358721.1		hydropathic protein	6337.999644	-1276430044	0.164812104	-8.245032683	1.65E-06	3.33E-16	14.47755577
sRNA91	no	no	no	no	no	no	no	no	255.279932	-127724162	0.23288329	-5.484470863	4.15E-08	2.48E-07	6.605548319
ABUW_RS02710	ABUW_0442	NZ_CP008706.1	454426	455105	-	WP_000745523.1		YnfJ family putative metal-binding protein	1766.887067	-1278426504	0.20902622	-6.116105922	9.59E-07	7.65E-09	1.16333656
ABUW_RS02710	ABUW_3848	NZ_CP008706.1	391469	391476	-	WP_000737570.1		thiol disulfide interchange protein DsbA/DsbL	7985.68479	-1281216822	0.24089339	-5.320394995	1.04E-07	5.71E-07	6.243363892
ABUW_RS16530	ABUW_3260	NZ_CP008706.1	329104	3292062	+	WP_000273589.1	glgA	RibU family protein phosphatase GlgA	1692.807685	-1282865591	0.125470283	-10.22445576	1.54E-24	9.15E-23	2.203952962
ABUW_RS01575	ABUW_1652	NZ_CP008706.1	165368	1653789	-	WP_000367186.1	cysB	cytochrome c ubiquinol oxidase subunit I	175014.1556	-1286799293	0.288292323	-4.463522588	8.06E-06	3.14E-05	4.520307032
ABUW_RS18515	ABUW_3128	NZ_CP008706.1	314919	3150156	+	WP_000405207.1		cell division protein ZipA	3904.018334	-1296654121	0.187078481	-6.93070387	4.8E-12	4.73E-11	10.32515886
ABUW_RS04465	ABUW_0941	NZ_CP008706.1	947466	948428	-	WP_000116164.1		SDR family oxidoreductase	14.056992	-129681661	0.28155641	-6.11449264	4.00E-06	1.66E-05	4.77899127
ABUW_RS02225	ABUW_0453	NZ_CP008706.1	465765	466406	+	WP_000857682.1		fumarate/acetoacetyl hydrolase family protein	2571.25978	-1302484297	0.147099643	-8.85459789	8.40E-10	2.35E-07	6.82892134
ABUW_RS14380	ABUW_2962	NZ_CP008706.1	2975235	297765	+	WP_000185269.1		YaeO family protein	614.5604144	-1307908456	0.23795595	-5.496538516	3.87E-08	2.33E-07	6.932644079
ABUW_RS02450	ABUW_0490	NZ_CP008706.1	503227	503883	-	WP_000863320.1		hydropathic protein	1762.96062	-1308689741	0.21363701	-6.15763301	9.02E-10	7.26E-09	8.59063579
ABUW_RS16565	ABUW_3408	NZ_CP008706.1	3455934	3456251	+	WP_000758932.1		serine repeat family protein	3229.399536	-1310263207	0.16124496	-9.16024496	5.88E-16	1.16E-14	13.95467702
ABUW_RS08125	ABUW_1668	NZ_CP008706.1	1660838	1662019	-	WP_000185938.1		benzoate/GlcY importer BenE family transporter	328.650101	-1311810057	0.239669777	-5.472517772	4.44E-08	2.62E-07	6.85898709
ABUW_RS08125	ABUW_0895	NZ_CP008706.1	893467	894837	+	WP_000936648.1	accC	acetyl-CoA carboxylase beta carboxylase subunit	23673.78733	-1313724371	0.23381571	-5.16010481	2.50E-09	1.86E-08	7.730487056
ABUW_RS03335	ABUW_0678	NZ_CP008706.1	683397	683780	+	WP_000389061.1	pIG	hitchhiking motility response regulator PIG	5491.783327	-1314281788	0.255368074	-5.16657458	2.65E-07	1.37E-06	5.883277943
ABUW_RS10115	ABUW_3162	NZ_CP008706.1	381742	381734	-	WP_000387256.1		SrB2 family protein	519.218761	-1315617653	0.231906682	-5.886958698	1.30E-08	8.58E-08	7.06051277
ABUW_RS10045	ABUW_2160	NZ_CP008706.1	2175766	2176230	-	WP_000106515.1	ybaK	Cys-RNA/protein deacylase	329.9024071	-1318503195	0.163995429	-8.027681776	9.93E-16	1.80E-14	13.74477429
ABUW_RS02140	ABUW_0435	NZ_CP008706.1	448800	449057	+	WP_000128820.1		succinate dehydrogenase assembly factor 2	262.4651899	-132500441	0.218076745	-6.250706403	4.09E-10	3.51E-09	8.454692884
ABUW_RS01290	ABUW_0874	NZ_CP008706.1	856133	857746	+	WP_000008260.1	lpcA	dihydropyridine dehydrogenase	63526.55558	-1325571697	0.24959199	-5.151552128	1.09E-07	5.96E-07	6.22475374
ABUW_RS14775	ABUW_3045	NZ_CP008706.1	307469	307212	-	WP_000120425.1		OmpA family protein	37602.89195	-1326670499	0.23945	-5.504090697	3.02E-08	1.85E-07	6.732828272
ABUW_RS01705	ABUW_1617	NZ_CP008706.1	163481	164104	+	WP_000528175.1		PAS domain-containing protein	114.017431	-1329218030	0.30545972	-4.35164617	1.35E-05	5.15E-05	4.289882636
ABUW_RS06870	ABUW_0481	NZ_CP008706.1	160585	161064	+	WP_000718711		femDoxin-NADP reductase	2150.862495	-133181901	0.19207713	-6.93377931	4.15E-12	1.03E-10	10.331646
ABUW_RS18015	ABUW_3471	NZ_CP008706.1	351919	3520218	+	WP_000423440.1	hcaR	DNA-binding transcriptional regulator HcaR	5060.10181	-1335653774	0.207103369	-6.449057459	1.01E-10	1.04E-09	6.826966681
ABUW_RS19115	ABUW_3618	NZ_CP008706.1	3676627	3678696	+	WP_000509996.1		oxidative damage protection protein	797.0023336	-1337866266	0.1166819	-11.55445993	6.24E-31	7.62E-29	28.1804503
ABUW_RS01970	ABUW_0401	NZ_CP008706.1	427321	428105	-	WP_000188881.1		flavohemoglobin	987.8301112	-1339607328	0.18383538	-6.74915112	1.48E-11	1.56E-10	13.94342918
ABUW_RS19385	ABUW_4077	NZ_CP008707.1	414943	419908	+	WP_000361811		hydropathic protein	4043.637669	-1340174495	0.32087018	-4.1766883	2.96E-05	0.000144445	3.98111346
ABUW_RS18185	ABUW_3738	NZ_CP008706.1	3739362	3743432	-	WP_000126489.1		F1F1ATP synthase subunit B	36085.43341	-1341990745	0.293320898	-4.57753191	4.84E-06	1.08E-05	4.70333481

ABUW_RS0320	ABUW_2124	NZ_CP008706.1	210672	2106943	+	WP_001096439.1	sigma-54-dependent Fis family transcriptional regulator	633.8649577	-1443373707	0.53247619	-9.48571812	4.57E-21	1.74E-19	8.75945075
ABUW_RS0775	ABUW_0362	NZ_CP008706.1	384299	385201	+	WP_01001828.1	Bank family transporter	925.7625006	-1449036993	0.289675607	-5.002274816	5.67E-07	2.76E-06	5.55909098
ABUW_RS1835	ABUW_3558	NZ_CP008706.1	3396481	339846	+	WP_001054464.1	DLF4 DUF40 domain-containing protein	521601916	-1452049138	0.25102607	-5.784585363	7.27E-09	5.03E-08	7.28943201
ABUW_RS0785	ABUW_0553	NZ_CP008706.1	9317993	9318945	-	WP_001250041.1	cysA	79095.44868	-1452196599	0.232525762	-6.172799553	6.7E-10	5.53E-09	8.25727489
ABUW_RS0105	ABUW_0246	NZ_CP008706.1	262407	263138	-	WP_000905533.1	hxA	3297.81621	-1454271917	0.17970124	-8.154576031	2.97E-16	5.81E-16	14.23562387
ABUW_RS0295	ABUW_0609	NZ_CP008706.1	690991	610567	+	WP_000608574.1	response regulator	131.8018953	-1455780858	0.176304194	-8.257216371	1.49E-16	3.02E-16	14.5999306
ABUW_RS0360	ABUW_2937	NZ_CP008706.1	2952192	2952584	-	WP_000117871.1	def	442.4433819	-1455981993	0.283293118	-5.09487342	2.75E-07	1.41E-06	5.55070887
ABUW_RS1425	ABUW_3176	NZ_CP008706.1	3203608	3204295	-	WP_000878003.1	NADH-quinone oxidoreductase subunit B	8071.788965	-1456454517	0.289227394	-5.03566266	4.76E-07	2.34E-06	6.53078413
ABUW_RS0070	ABUW_0514	NZ_CP008706.1	16160	17362	+	WP_000335558.1	tyrosine--RNA ligase	3456.529666	-1456688792	0.165769169	-9.14758862	7.69E-20	2.40E-18	17.60904689
ABUW_RS0065	ABUW_0165	NZ_CP008706.1	219500	220582	+	WP_000608201.1	DUF4145 domain-containing protein	5334.950811	-1458104065	0.193898464	-7.520009841	5.47E-14	8.10E-13	10.0951496
ABUW_RS18670	ABUW_3835	NZ_CP008706.1	3903094	3903789	+	WP_000724221.1	FKBP-type peptidyl-prolyl cis-trans isomerase	2235.095508	-1459973396	0.147554756	-9.89443952	4.40E-23	2.06E-21	20.68610278
ABUW_RS00870	ABUW_1655	NZ_CP008706.1	8448202	850178	+	WP_010189921.1	TollB-dependent siderophore receptor	3516875437	-1464753887	0.546658504	-2.67847849	0.007373928	0.0551429	18.09272602
ABUW_RS04990	ABUW_0117	NZ_CP008706.1	828440	829501	+	WP_000027499.1	surF ABC transporter ATP-binding protein	610.7820234	-1468322297	0.141789722	-10.35632814	3.95E-25	2.61E-23	22.58335949
ABUW_RS17705	ABUW_3636	NZ_CP008706.1	3694006	3696207	+	WP_000805827.1	homoserine dehydrogenase	5132.586541	-146892524	0.225803346	-6.510760744	7.43E-11	7.09E-10	9.14933765
ABUW_RS00795	ABUW_3800	NZ_CP008706.1	178603	179400	+	WP_000505317.1	MBL fold metallo-hydrolase	282.084104	-1471075266	0.208492951	-7.058784417	1.68E-12	2.06E-11	10.6863278
ABUW_RS1070	ABUW_3509	NZ_CP008706.1	3555321	3559502	-	WP_000865305.1	gspG type II secretion system major pseudopilin GspG	1642.303807	-1472204022	0.184993294	-9.933927347	2.96E-23	1.40E-21	20.85387160
ABUW_RS04855	ABUW_0990	NZ_CP008706.1	1003282	1003793	-	WP_000067970.1	class I fructose-bisphosphatase	2627.275444	-1476008411	0.170826283	-8.640405819	5.60E-18	1.38E-16	14.86071091
ABUW_RS017675	ABUW_1613	NZ_CP008706.1	1606764	1607393	-	WP_000221872.1	UDP-2-C,3-bisphosphoosamine dephosphatase	774.8095653	-147774635	0.178463987	-5.28036579	1.23E-16	2.15E-15	14.60032626
ABUW_RS02380	no	NZ_CP008706.1	2881956	2882114	-		hydrophobic protein	55.44343002	-1481632678	0.27356496	-5.423752222	5.84E-08	3.37E-07	6.42737099
ABUW_RS02620	ABUW_0770	NZ_CP008706.1	167219	1706937	-	WP_010162460.1	PTS transporter subunit EMC	853.739555	-1482922704	0.16618795	-8.92589169	4.42E-19	1.25E-17	8.30309990
ABUW_RS08825	ABUW_0771	NZ_CP008706.1	1768924	1769871	-	WP_010062810.1	phbB	739.5559454	-1495509857	0.183462157	-8.121163447	3.58E-16	8.89E-15	14.9187081
ABUW_RS10860	ABUW_2324	NZ_CP008706.1	2227120	2223885	+	WP_000160961.1	maleate synthase G	9216.426337	-1496595464	0.179990302	-8.314867216	9.19E-17	1.90E-15	14.722644
ABUW_RS1470	ABUW_2980	NZ_CP008706.1	2996929	2997365	-	WP_0003359021.1	YnfN family protein	34.31365574	-1491073786	0.445498947	-3.360188066	0.000776944	0.00207879	2.63637536
ABUW_RS14010	ABUW_3010	NZ_CP008706.1	3759186	3759339	+	WP_000218804.1	RsdA family protein	2361.872747	-1497526064	0.193435183	-10.92810511	5.06E-20	1.68E-18	17.74460727
ABUW_RS15450	ABUW_2150	NZ_CP008706.1	2143431	215148	-	WP_01076381.1	O-acyl-succinylhomoserine sulphydriase	2961042308	-1498543299	0.120505366	-1.98135193	4.34E-33	6.99E-31	30.15552282
ABUW_RS04645	ABUW_0441	NZ_CP008706.1	454843	454914	-	WP_010109891.1	hydrophobic protein	651.9803046	-1499456064	0.22199329	-6.768732854	1.32E-11	1.41E-10	9.85070887
ABUW_RS00770	ABUW_0755	NZ_CP008706.1	170216	172732	+	WP_000806433.1	aceE pyruvate dehydrogenase (acetyl-transfering), homodimeric type	41950.18742	-1500040703	0.238880327	-7.179465210	3.40E-10	2.96E-09	8.52807828
ABUW_RS18150	ABUW_3229	NZ_CP008706.1	3781961	3788106	+	WP_000914680.1	glutathione peroxidase	3340.40201	-1500196542	0.22579876	-6.66605193	2.63E-11	2.70E-10	9.568662636
ABUW_RS04465	ABUW_0704	NZ_CP008706.1	708980	710455	+	WP_001005371.1	alanine:citrate symporter family protein	7592.194519	-1512761362	0.250366324	-5.832528061	5.46E-09	3.85E-08	7.14453927
ABUW_RS18665	ABUW_2459	NZ_CP008706.1	2450498	2451001	+	WP_000959551.1	thioesterase family protein	487.3823714	-1515020566	0.253478126	-5.971405009	2.35E-09	1.76E-08	7.754457332
ABUW_RS01475	ABUW_0706	NZ_CP008706.1	71793	719028	+	WP_000615951.1	threonine ammonia-lyase	904.432457	-1520705949	0.140310561	-10.83090911	2.27E-27	1.99E-25	24.70149621
ABUW_RS14740	ABUW_3389	NZ_CP008706.1	3429724	3430999	+	WP_010161681.1	glutamate-5-semialdehyde dehydrogenase	4300.60118	-1527557987	0.130581029	-11.30843934	1.19E-29	1.22E-27	26.9100449
ABUW_RS05280	ABUW_0771	NZ_CP008706.1	1082637	1084340	+	WP_000903521.1	MB family metallophosphatase	5166.347497	-15280339	0.143697484	-10.63368735	2.08E-26	1.67E-24	23.7772833
ABUW_RS18265	ABUW_1697	NZ_CP008706.1	1694854	1695273	-	WP_000354611.1	accB acetyl-CoA carboxylase biotin:carboxyl carrier protein	7165.670055	-1530337444	0.214312645	-7.134201667	9.74E-13	1.23E-11	9.19004949
ABUW_RS14705	ABUW_3010	NZ_CP008706.1	3505033	3505725	-	WP_010108501.1	YggG family pyridoxal phosphate-dependent enzyme	616.19518	-1534486268	0.182256184	-8.1494388	3.78E-17	8.19E-16	5.08844239
ABUW_RS13745	ABUW_2828	NZ_CP008706.1	2833455	2833699	+	WP_000344462.1	TollB-dependent receptor	9231.342145	-1535817777	0.1418780425	-3.166750155	0.000244932	0.000722425	3.11407233
ABUW_RS05585	ABUW_1141	NZ_CP008706.1	1166163	1166722	+	WP_000035083.1	etp elongation factor P	33710.06363	-1537100957	0.207404744	-7.423030764	1.14E-13	1.59E-12	14.9807287
ABUW_RS00860	ABUW_0778	NZ_CP008706.1	1777226	1778020	+	WP_010202716.1	map type I methionyl aminopeptidase	9114.653488	-1539241632	0.152488335	-10.07035241	7.47E-24	4.10E-22	21.36858563
ABUW_RS18015	ABUW_3311	NZ_CP008706.1	36792	36794	-	WP_000205076.1	ppc phosphoenolpyruvate carboxylase	7098.510764	-1549281813	0.124409118	-6.349042337	2.17E-10	1.94E-09	11.970223
ABUW_RS18175	ABUW_2461	NZ_CP008706.1	2453066	2454055	+	WP_00094007.1	Psal family thioesterase	36.25344128	-1551049163	0.392026692	-3.95548864	7.61E-05	0.000248737	3.604259608
ABUW_RS00795	ABUW_3555	NZ_CP008706.1	1447765	1449303	+	WP_000441855.1	DUF3535 domain-containing protein	5004.678972	-1554183638	0.15693827	-11.14141027	3.67E-30	3.99E-28	27.3990271
ABUW_RS01460	ABUW_0747	NZ_CP008706.1	1054773	1055474	+	WP_001004984.1	uvrB excruclease ABC subunit UvrB	3748.387079	-155687543	0.248933444	-6.254183472	3.40E-10	3.44E-09	8.46341057
ABUW_RS01825	ABUW_0581	NZ_CP008706.1	763564	766118	+	WP_01027844.1	hydrophobic protein	99.19703954	-156017865	0.28247473	-5.524666216	3.00E-08	2.01E-07	6.65840393
ABUW_RS01960	ABUW_2191	NZ_CP008706.1	2195421	2197223	+	WP_00098571.1	hydrophobic protein	532.831793	-1563395806	0.300478215	-5.202659178	1.96E-07	1.03E-06	5.98727775
ABUW_RS17300	ABUW_3555	NZ_CP008706.1	3610991	3612417	-	WP_000309685.1	pyrimidin:pyrroline nucleoside phosphorylase	2164.914021	-1563488992	0.18304061	-8.598930371	8.82E-32	3.46E-20	19.4821809
ABUW_RS10285	ABUW_2737	NZ_CP008706.1	2724819	2727398	-	WP_010210050.1	cspB ATP-dependent chaperone CspB	14167.99303	-1564339778	0.208033518	-7.519748702	5.49E-14	8.10E-13	12.0951498
ABUW_RS01330	ABUW_0677	NZ_CP008706.1	682476	683114	-	WP_000959411.1	hydrophobic protein	93.5595824	-1565545168	0.244648071	-6.351050408	2.10E-10	1.91E-09	8.71896633
ABUW_RS00885	ABUW_0179	NZ_CP008706.1	116216	116357	-	WP_000145860.1	meuE	53.4222782	-1566755536	0.281271593	-5.570286897	2.54E-08	1.57E-07	6.80403048
ABUW_RS02560	ABUW_0521	NZ_CP008706.1	530083	530097	+	WP_000619820.1	sulfurtransferase	2343.500924	-1567519219	0.2253016	-6.957436527	3.47E-12	4.00E-11	10.3974001
ABUW_RS18230	ABUW_3745	NZ_CP008706.1	380074	380094	+	WP_000103779.1	Dyp-type peroxidase	2600.016644	-1568061335	0.126419423	-10.50130799	7.16E-36	1.6E-33	32.7931742
ABUW_RS11015	ABUW_2707	NZ_CP008706.1	2688875	2691046	-	WP_000377525.1	copcoo-translocating P-type ATPase	1657.208891	-1568779727	0.237474223	-6.608105308	3.95E-11	3.93E-10	9.40560745
ABUW_RS14145	ABUW_2913	NZ_CP008706.1	2922146	2922763	+	WP_001141692.1	carbonic anhydrase	1423.18559	-1585088986	0.1704816	-9.29774116	1.43E-20	5.02E-19	18.29073004
ABUW_RS01265	ABUW_0287	NZ_CP008706.1	1308740	1308976	+	WP_000152667.1	hydrophobic protein	16.58330551	-1586573723	0.385701864	-4.10471754	3.90E-05	0.00014791	3.810739105
ABUW_RS00770	ABUW_0318	NZ_CP008706.1	272077	274425	+	WP_000111981.1	RNA-binding transcriptional accessory protein	14293.87794	-1589501468	0.243407452	-6.530208727	6.57E-11	6.33E-10	9.5898269
ABUW_RS01795	ABUW_1515	NZ_CP008706.1	1506193	1502688	-	WP_000205634.1	response regulator transcription factor	26116229304	-1594296765	0.233040908	-6.841274266	7.85E-12	8.64E-11	10.05428662
ABUW_RS18185	ABUW_2279	NZ_CP008706.1	2284176	2284176	+	WP_000240310.1	DUF2058 domain-containing protein	546.2721627	-1597688842	0.254106445	-6.287478623	3.23E-10	2.83E-09	6.84621564
ABUW_RS01575	ABUW_0380	NZ_CP008706.1	297514	298515	+	WP_000985981.1	sulfate ABC transporter substrate-binding protein	290.2902415	-1604118924	0.211384443	-7.601103364	2.94E-14	6.53E-13	12.343901
ABUW_RS07870	ABUW_1611	NZ_CP008706.1	1605864	1606307	-	WP_000365034.1	oxygen-insensitive NAD(P)H reductase	284.9070096	-1610352932	0.326903072	-4.939623128	7.33E-07	3.75E-06	5.422968732
ABUW_RS17945	ABUW_3616	NZ_CP008706.1	3744267	3744794	-	WP_000124443.1	ppa inorganic diphosphatase	9635.394249	-16117336406	0.173769005	-8.95888797	1.2		

ABLUW_RS4446	ABLUW_0910	NZ_CP008706.1	903722	905053	-	WP_00188654.1		MFS transporter	3451342625	-1.793591679	0.238476778	-7.520026046	5.48E-14	8.10E-13	12.0915498
ABLUW_RS0630	ABLUW_1400	NZ_CP008706.1	403464	104147	-	WP_00009688.1		hella-tum-hella domain-containing protein	346.231844	-1.79749154	0.97446663	-9.0588487	8.55E-20	2.7E-9	17.56703071
ABLUW_RS1920	ABLUW_2682	NZ_CP008706.1	267236	267782	-	WP_00024027.1		hella-tum-hella transcriptional regulator	71.844983	-1.801556177	0.29082612	-6.9460559	5.84E-10	4.85E-09	8.31425261
ABLUW_RS0300	ABLUW_3696	NZ_CP008706.1	375470	375372	+	WP_00108956.1		TGD02730 family Rossmann fold protein	2141.12396	-1.808466955	0.220613379	-8.9744914	2.46E-16	4.83E-15	14.9005287
ABLUW_RS0526	ABLUW_3972	NZ_CP008706.1	108741	108978	+	WP_00089667.1		NAD(P)-dependent succinate dehydrogenase	48159.08892	-1.81445849	0.91079378	-9.47736515	8.41E-22	3.32E-20	19.4788992
ABLUW_RS0100	ABLUW_5161	NZ_CP008706.1	19333	19347	+	WP_00071457.1	pnfB	nicotinate phosphoribosyltransferase	1536.04517	-1.82569849	0.9182336	-10.0251509	2.62E-33	4.40E-31	30.56654732
ABLUW_RS0490	ABLUW_809	NZ_CP008706.1	102231	1022774	-	WP_00193620.1		perlecanidin	665.929238	-1.82624588	0.90479325	-9.1888933	4.56E-24	2.59E-22	21.68670024
ABLUW_RS0430	ABLUW_0878	NZ_CP008706.1	859075	859965	+	WP_000114637.1	sucD	succinate--CoA ligase subunit alpha	49529.37226	-1.827665707	0.227383911	-8.639409902	9.03E-16	1.66E-14	13.7789191
ABLUW_RS1600	ABLUW_2181	NZ_CP008706.1	216273	2163076	-	WP_000018791.1		hydrolytic protein	60.86691226	-1.840340783	0.52963667	-3.474721072	0.000510385	0.00191947	2.849812659
ABLUW_RS1406	ABLUW_2896	NZ_CP008706.1	2904183	2905091	-	WP_000140408.1	cysD	sulfate adenylyltransferase subunit CysD	7026.503791	-1.841209317	0.22936064	-8.647164485	5.28E-18	1.30E-16	15.88805665
ABLUW_RS0705	ABLUW_0142	NZ_CP008706.1	155897	156547	+	WP_00021030.1	pyrE	ornate phosphoribosyltransferase	1411.926369	-1.842591048	0.179410582	-10.27024732	9.60E-25	5.77E-23	22.23882419
ABLUW_RS0905	ABLUW_1650	NZ_CP008706.1	1846320	1847564	+	WP_000446246.1		acyl-CoA dehydrogenase family protein	324.893565	-1.84474868	0.170618579	-10.44481956	1.05E-25	1.11E-23	22.95467702
ABLUW_RS1670	ABLUW_3453	NZ_CP008706.1	350053	350115	+	WP_000967566.1		hydrolytic protein	1224.585304	-1.850281649	0.21609373	-8.702728502	3.24E-18	8.22E-17	16.0851281
ABLUW_RS0550	ABLUW_3405	NZ_CP008706.1	3452403	3454100	+	WP_00097884.1	leuA	2-isopropylmalate synthase	8761.899879	-1.852194051	0.21609285	-8.547656171	1.26E-17	2.88E-16	15.04060751
ABLUW_RS0690	ABLUW_1551	NZ_CP008706.1	163763	165520	+	WP_00102091.1	tsdA	F1p plus assembly complex ATPase component TsdA	494.7244338	-1.854323884	0.98434879	-10.05910237	8.38E-24	4.33E-22	21.3635121
ABLUW_RS1690	ABLUW_3433	NZ_CP008706.1	3478521	3478799	-	WP_000027403.1		hydrolytic protein	2965.486317	-1.856599238	0.344541858	-5.38802857	7.10E-08	4.05E-07	6.392544977
ABLUW_RS0255	ABLUW_0502	NZ_CP008706.1	57715	58452	-	WP_000100787.1		dienelactone hydrolase family protein	902.252445	-1.860921007	0.26187917	-7.10853669	1.17E-12	1.46E-11	10.83564714
ABLUW_RS0540	ABLUW_1522	NZ_CP008706.1	1146331	1145919	+	WP_000593084.1	purB	5-phosphoribosylase	9530.79736	-1.874558232	0.535197726	-10.21555817	2.54E-34	5.36E-32	31.9629172
ABLUW_RS1140	ABLUW_2708	NZ_CP008706.1	2697513	2697119	+	WP_00181651.1		heavy-metal-associated domain-containing protein	146.196303	-1.880822078	0.370651979	-5.074364009	3.89E-07	1.94E-06	17.5192827
ABLUW_RS0130	ABLUW_0208	NZ_CP008706.1	233916	235214	+	WP_000350212.1		FAD-dependent oxidoreductase	93614.84475	-1.887905222	0.61022419	-11.79228041	4.82E-32	6.89E-30	29.1745738
ABLUW_RS0250	ABLUW_0510	NZ_CP008706.1	526947	527282	-	WP_001023924.1		TIGR0144 family phosphatase	162.943448	-1.891973657	0.206054974	-9.18408166	5.48E-20	1.81E-18	17.74223143
ABLUW_RS1210	ABLUW_2486	NZ_CP008706.1	248259	2482881	-	WP_000434318.1		UTRA domain-containing protein	320.320314	-1.900449389	0.9467495	-10.29078051	7.75E-25	4.73E-23	22.3251886
ABLUW_RS1325	ABLUW_2725	NZ_CP008706.1	2710666	2711677	-	WP_000781042.1		glutathione S-transferase N-terminal domain-containing protein	211.81943	-1.907066045	0.210222411	-8.616682324	6.89E-18	1.66E-16	15.7789191
ABLUW_RS0440	ABLUW_0987	NZ_CP008706.1	1000005	1001025	-	WP_001016071.1		hydrolytic protein	642.7993	-1.90784362	0.21937623	-8.63360788	1.00E-18	7.27E-17	16.5654311
ABLUW_RS0960	ABLUW_1674	NZ_CP008706.1	1875742	1879332	+	WP_001819096.1	adeA	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	18712.17969	-1.91546646	0.32756826	-6.87128857	1.00E-09	1.97E-09	6.808541879
ABLUW_RS1860	ABLUW_3666	NZ_CP008706.1	372646	372889	+	WP_000670219.1		arsenite reductase ArsC	594.6205399	-1.918633498	0.282473269	-6.792272792	1.10E-11	1.20E-10	9.940281874
ABLUW_RS1075	ABLUW_2075	NZ_CP008706.1	2056937	2057578	-	WP_000026856.1		isochromatase family protein	469.7438191	-1.936555793	0.574164096	-3.37262365	0.000744009	0.00987805	2.71620221
ABLUW_RS0390	ABLUW_2179	NZ_CP008706.1	2180924	2181062	-	WP_000006591.1		hydrolytic protein	35.267197341	-1.937328791	0.449850885	-4.306534202	1.06E-05	6.19E-05	4.203303951
ABLUW_RS0540	ABLUW_2169	NZ_CP008706.1	250929	2509178	+	WP_000018784.1		sulfate exporter TsdA/SdcE family protein	1667.46087	-1.955443003	0.378307279	-5.98827775	2.35E-07	1.23E-06	5.91094889
ABLUW_RS0540	ABLUW_0169	NZ_CP008706.1	178375	178375	-	WP_000194085.1		TollB-dependent endophore receptor	1568.219191	-1.957806276	0.378812072	-5.938610793	2.35E-07	1.23E-06	5.91094889
ABLUW_RS0540	ABLUW_0959	NZ_CP008706.1	967105	968057	+	WP_000035983.1		FAD-binding protein	29476.92565	-1.96182519	0.206898398	-9.57728934	9.96E-22	3.86E-20	19.4134127
ABLUW_RS0810	ABLUW_1671	NZ_CP008706.1	1673430	1664191	-	WP_000196941.1	tal	transaldolase	4363.726706	-1.987949608	0.20139923	-8.77396884	1.46E-22	6.87E-21	20.1781147
ABLUW_RS1400	ABLUW_2895	NZ_CP008706.1	2902539	2904152	-	WP_0001001495.1	cysN	sulfate adenylyltransferase subunit CysN	7728.310994	-1.990590383	0.12842742	-11.51677758	1.09E-30	1.25E-28	27.93008999
ABLUW_RS00710	ABLUW_0143	NZ_CP008706.1	165588	165787	-	WP_001819818.1		TollB-dependent endophore receptor	689.0208509	-2.006835124	0.383192526	-5.24333619	1.58E-07	8.47E-07	6.07219659
ABLUW_RS1185	ABLUW_2422	NZ_CP008706.1	2410633	2410633	-	WP_001033059.1		amino acid ABC transporter ATP-binding protein	93.9656982	-2.009226102	0.374510325	-5.384005078	6.87E-08	3.92E-07	6.406710933
ABLUW_RS01250	ABLUW_0255	NZ_CP008706.1	267476	268890	-	WP_000039344.1		acyl-CoA hydrolase/transferase family protein	9966.206656	-2.02073884	0.31965553	-6.375263239	1.83E-10	1.65E-09	8.782519056
ABLUW_RS12935	ABLUW_2665	NZ_CP008706.1	2659934	2660566	-	WP_001140766.1		hydrolytic protein	570.1711918	-2.028194579	0.21776533	-9.31433496	1.24E-20	4.49E-19	8.34773658
ABLUW_RS06165	ABLUW_184	NZ_CP008706.1	1871810	1873074	-	WP_001818380.1		alpha/beta hydrolase	280.3388866	-2.033373064	0.308274893	-6.95997794	4.22E-11	4.18E-10	9.378823718
ABLUW_RS03170	ABLUW_0644	NZ_CP008706.1	650510	650995	+	WP_000093547.1		DUF3168 domain-containing protein	1621350918	-2.053606626	0.221846008	-9.343414429	2.16E-20	7.49E-19	8.25514318
ABLUW_RS1870	ABLUW_2439	NZ_CP008706.1	2428766	2428887	+	WP_000100365.1		hydrolytic protein	109.948858	-2.055272445	0.63466665	-3.238250108	0.00102653	0.003060954	2.51434197
ABLUW_RS1945	ABLUW_2363	NZ_CP008706.1	2349370	2350311	+	WP_00019738.1		hydrolytic protein	48.81671673	-2.077221107	0.16585402	-10.24601411	4.71E-40	2.1E-37	36.6716204
ABLUW_RS1920	ABLUW_1668	NZ_CP008706.1	1679141	1679623	-	WP_000103995.1		peptidylglyoxylase	6945.332805	-2.088647277	0.200516467	-10.4163886	2.09E-25	1.45E-23	22.838032
ABLUW_RS1370	ABLUW_3573	NZ_CP008706.1	3632075	3633247	+	WP_000021712.1	tsdA	acyl-CoA C-acyltransferase TsdA	5429.800059	-2.02305558	0.259737107	-8.92836685	3.27E-16	6.34E-14	19.971974
ABLUW_RS1045	ABLUW_1193	NZ_CP008706.1	1154233	1156851	-	WP_000186277.1		ATP-binding protein	5097.738301	-2.16997445	0.17719635	-10.31971023	6.71E-34	1.23E-31	30.93009489
ABLUW_RS19545	ABLUW_2170	NZ_CP008706.1	2181966	2182184	+	WP_000102808.1		3-deoxy-7-phosphoglutamate synthase	4506.74442	-2.169793055	0.21799068	-11.81529205	5.45E-17	2.20E-07	16.85757732
ABLUW_RS18890	ABLUW_3879	NZ_CP008706.1	3846285	3848225	+	WP_001062607.1	dnaK	molecular chaperone DnaK	66577.39885	-2.220745124	0.230172639	-9.64819932	5.00E-22	2.17E-20	19.68354027
ABLUW_RS01950	ABLUW_0377	NZ_CP008706.1	402100	403050	-	WP_001816461.1	hemF	oxygen-dependent coproporphyrinogen oxidase	3810.627263	-2.233665277	0.301774877	-9.470147633	1.35E-13	1.87E-12	11.72818639
ABLUW_RS021975	ABLUW_0605	NZ_CP008706.1	605611	605451	-	WP_001023422.1		acyl-CoA dehydrogenase C-terminal domain-containing protein	4097.43323	-2.23681035	0.9788818	-11.90341253	1.28E-29	1.27E-27	26.89619628
ABLUW_RS00695	ABLUW_0140	NZ_CP008706.1	154228	154578	-	WP_000091165.1		arsenite reductase	1303.452954	-2.239018849	0.22278945	-10.04953062	9.23E-24	4.65E-22	21.33245705
ABLUW_RS14740	ABLUW_3037	NZ_CP008706.1	3063650	3064105	+	WP_000078297.1		bachemethemoglobin	78.15187815	-2.242409979	0.32274856	-6.948364642	3.70E-12	4.23E-11	10.37360963
ABLUW_RS03435	ABLUW_0698	NZ_CP008706.1	700215	702761	-	WP_000473052.1		PspF5 domain-containing protein	1695.93703	-2.24391157	0.33441219	-6.70078865	1.95E-11	2.03E-10	9.69250362
ABLUW_RS1808	ABLUW_1769	NZ_CP008706.1	1766667	1767173	+	WP_000734811.1		PEGA domain-containing protein	206.5046345	-2.251884076	0.285882757	-7.87416295	3.43E-15	5.73E-14	13.24196138
ABLUW_RS0470	ABLUW_0958	NZ_CP008706.1	966358	967107	+	WP_000045190.1		electron transfer flavoprotein subunit beta/FixA family protein	24391.33267	-2.25485154	0.904190091	-12.50754598	6.79E-36	1.68E-33	32.7937147
ABLUW_RS17185	ABLUW_3572	NZ_CP008706.1	3623969	3623062	+	WP_0000580492.1	fadB	fatty acyl oxidase complex subunit beta/FixA family protein	10697.51077	-2.259807385	0.284356691	-7.94487983	1.94E-15	3.38E-14	14.078933
ABLUW_RS18105	ABLUW_2283	NZ_CP008706.1	2268551	2268925	+	WP_001816343.1	gcvH	glycine clearance system protein GcvH	864.4193304	-2.26140451	0.170856446	-10.23415363	5.57E-40	2.24E-37	6.644971598
ABLUW_RS01765	ABLUW_0605	NZ_CP008706.1	1792699	1793058	+	WP_000081238.1		TollB-dependent endophore receptor	1957.479374	-2.262698878	0.268475722	-8.42794597	3.52E-17	6.16E-15	16.8045031
ABLUW_RS1865	ABLUW_3834	NZ_CP008706.1	3903232	3903404	+	WP_000030403.1		PKBP_Tyr-peptidyl-glyoxyl-coA-trans isomerase	3588.460895	-2.266163123	0.315974431	-8.66609917	2.31E-62	4.86E-59	58.3311608
ABLUW_RS11780	ABLUW_2423	NZ_CP008706.1	2410066	2410731	-	WP_000100417.1		amino acid ABC transporter permease	108.884913	-2.284330903	0.474509643				

ABUW_RS02305	ABUW_0469	NZ_CP008706.1	481665	482092	-	WP_000021434.1		hypothetical protein	1430.738018	-3.17560157	0.398302241	-7.962697242	168E-15	2.95E-14	10.5307798
ABUW_RS05000	ABUW_1019	NZ_CP008706.1	1030394	1031227	-	WP_0000083117.1	cysT	sulfate ABC transporter permease subunit CysT	16.0387869	-3.178663881	0.442575357	-7.182198087	6.88E-13	8.83E-12	11.0540393
ABUW_RS10220	ABUW_2104	NZ_CP008706.1	2086545	2087963	+	WP_0000980437.1		asparilate ammonia-lyase	5497.212832	-3.230478295	0.332432088	-9.717708994	2.53E-22	1.10E-20	19.94692166
ABUW_RS08730	ABUW_1793	NZ_CP008706.1	1787286	1787387	-	WP_0002070276.1	cydX	cytochrome bd-oxidase subunit CydX	364.1533744	-3.344309648	0.474912677	-7.041946462	1.90E-12	2.31E-11	10.63638802
ABUW_RS08735	ABUW_1794	NZ_CP008706.1	1787401	1788546	-	WP_000575152.1	cydB	cytochrome d ubiquinol oxidase subunit II	4867.989219	-3.347141068	0.417930718	-6.008841947	1.18E-15	2.08E-14	10.68193667
ABUW_RS18445	ABUW_3788	NZ_CP008706.1	3850235	3851338	-	WP_001137881.1	alt	alanine racemase	4405.282926	-3.360765663	0.282039767	-11.91592837	9.78E-33	1.46E-30	29.83564714
sRNA48	no	no	no	no	no	no	no	no	160.425978	-3.393922402	0.428710562	-7.916582203	2.44E-15	4.22E-14	13.37468755
ABUW_RS05005	ABUW_1020	NZ_CP008706.1	1031308	1031916	-	WP_000141921.1		alpha/beta hydrolase	280.8572397	-3.466790281	0.542889538	-6.365811549	1.70E-10	1.55E-09	8.80968302
ABUW_RS07450	ABUW_1506	NZ_CP008706.1	1512329	1512532	-	WP_0007558190.1		hypothetical protein	1037.75093	-3.556888384	0.445853362	-7.977709005	1.49E-15	2.65E-14	10.5767314
ABUW_RS16650	ABUW_3425	NZ_CP008706.1	3471050	3471670	-	WP_001011864.1		MoA/TolQ/EtdB proton channel family protein	4560.680571	-3.630058445	0.350110565	-10.3683202	3.46E-25	2.32E-23	22.6345102
ABUW_RS05475	ABUW_1119	NZ_CP008706.1	1140333	1141295	+	WP_000897187.1	sohB	protease SohB	9116.455687	-3.680822475	0.254671854	-14.4331913	2.39E-47	2.41E-44	43.67982196
ABUW_RS05010	ABUW_1021	NZ_CP008706.1	1031947	1032964	-	WP_001212600.1		sulfate ABC transporter substrate-binding protein	524.9851964	-3.823569229	0.587758766	-6.505337649	7.75E-11	7.37E-10	9.132532512
ABUW_RS05680	ABUW_1345	NZ_CP008706.1	1356538	1357908	-	WP_000845861.1	yegQ	lRNA 5'-hydroxyuridine modification protein YegQ	1012.726209	-3.896463582	0.310830196	-12.53566621	4.76E-36	1.20E-33	32.92081875
ABUW_RS09450	ABUW_1942	NZ_CP008706.1	194185	1942269	+	WP_001007514.1		ribose-phosphate pyrophosphokinase	1577.014582	-3.972360345	0.640942485	-6.107686128	5.73E-10	4.77E-09	8.32148121
ABUW_RS08740	ABUW_1795	NZ_CP008706.1	1788543	1790129	-	WP_000621645.1		cytochrome ubiquinol oxidase subunit I	7232.816896	-4.177536807	0.40020325	-10.43853793	1.65E-25	1.17E-23	22.9315114
ABUW_RS18450	ABUW_3789	NZ_CP008706.1	3851359	3852624	-	WP_001263980.1		D-amino acid dehydrogenase	9131.384796	-4.372245658	0.322329172	-13.56453601	6.50E-42	4.36E-39	38.36051931
ABUW_RS1585	ABUW_2381	NZ_CP008706.1	2367863	2368657	-	WP_000114471.1		ATP-binding cassette domain-containing protein	719.963052	-4.378279922	0.459016905	-9.538384916	1.45E-21	5.57E-20	19.2544418
ABUW_RS16540	ABUW_3403	NZ_CP008706.1	3448925	3451156	+	WP_000052885.1		TonB-dependent siderophore receptor	7747.738344	-4.447352483	0.53303193	-8.343505767	7.21E-17	1.51E-15	40.82102305
ABUW_RS06555	ABUW_1344	NZ_CP008706.1	1356272	1356535	-	WP_001196305.1		YHl family 4Fe-4S cluster farnesin	132.2757823	-4.464562777	0.499504475	-8.937983544	3.96E-19	1.14E-17	16.34039515
ABUW_RS08745	ABUW_1796	NZ_CP008706.1	1790129	1790323	-	WP_000053889.1		hypothetical protein	1533.908964	-4.655549674	0.421675649	-11.04321298	2.36E-28	2.22E-26	25.65364703
ABUW_RS12180	ABUW_2319	NZ_CP008706.1	2304179	2304616	-	WP_001161759.1		PACE efflux transporter	486.7408237	-4.733014866	0.545687441	-8.673490554	4.19E-18	1.04E-16	15.88266666
ABUW_RS12115	ABUW_2489	NZ_CP008706.1	2485285	2485881	-	WP_001062883.1		NAD(P)H-dependent oxidoreductase	443.6515256	-4.820002906	0.419550055	-11.888505	151E-30	1.69E-28	27.7721133
ABUW_RS15890	ABUW_2382	NZ_CP008706.1	2368667	2369707	-	WP_000651495.1	tauA	taurine ABC transporter substrate-binding protein	782.0023615	-5.03565188	0.549721154	-9.283909786	1.63E-20	5.72E-19	18.24260397
ABUW_RS17440	ABUW_3583	NZ_CP008706.1	3641934	3642515	-	WP_000472947.1		outer membrane beta-barrel protein	17177.01318	-7.204195817	0.479789408	-15.01530816	5.83E-51	7.83E-48	47.06238224

Table S19. RNA-seq data: Absolute and relative expression (TS/AT > 2-fold up)

locus_tag	old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	-log10
ABUW_RS02475	ABUW_2443	NZ_CP008706.1	2430503	2430646	-	WP_000251635.1		hypothetical protein	1153.102491	9.804485991	0.857810712	11.42966141	2.97E-30	5.79E-29	28.2376283
ABUW_RS07145	ABUW_1466	NZ_CP008706.1	1456445	1456678	-	WP_001094391.1		DUF2171 domain-containing protein	16057.06702	9.13327517	0.589921619	15.78756238	3.79E-56	2.21E-54	53.6550778
ABUW_RS07170	ABUW_1471	NZ_CP008706.1	1460237	1460599	+	WP_000721827.1		NrdYgWYdeI family stress tolerance protein	865.07839	8.247520031	0.490054122	16.82981464	1.48E-63	1.29E-61	60.88858218
ABUW_RS18175	ABUW_2440	NZ_CP008706.1	2429094	2429411	+	WP_000102046.1		hypothetical protein	33008.50582	7.799139145	0.420102677	18.56404497	6.28E-77	1.05E-74	73.97709762
ABUW_RS18150	ABUW_2435	NZ_CP008706.1	2423144	2424022	+	WP_000432325.1		glucose 1-dehydrogenase	1873.767352	7.456206146	0.432727577	17.23071636	1.56E-66	1.70E-64	63.76931008
ABUW_RS18170	ABUW_2439	NZ_CP008706.1	2428766	2428987	+	WP_000101365.1		hypothetical protein	139148.8858	7.446851216	0.584518745	12.74014587	3.54E-37	9.37E-36	10.8218641
ABUW_RS07960	ABUW_1631	NZ_CP008706.1	1628562	1629092	+	WP_000750672.1		spore coat protein U domain-containing protein	7973.259285	7.394418441	0.393167213	18.80731198	6.58E-79	1.33E-76	75.8776715
ABUW_RS00260	ABUW_0053	NZ_CP008706.1	58624	58782	-	WP_000490267.1		DUF128 domain-containing protein	5808.425003	7.205181497	0.332725826	21.6550112	5.45E-104	5.49E-101	10.2603231
ABUW_RS18140	ABUW_2433	NZ_CP008706.1	2420869	2422104	-	WP_000024222.1		stress-induced protein	10147.252	7.141422782	0.493778327	14.6281132	2.08E-47	8.39E-46	45.07648794
ABUW_RS10025	ABUW_2064	NZ_CP008706.1	2045977	2046213	-	WP_000044010.1		hypothetical protein	395.3538908	7.182717148	0.679153313	10.48109699	1.06E-25	1.60E-24	23.79474395
ABUW_RS12975	ABUW_2673	NZ_CP008706.1	2666136	2666784	-	WP_001138417.1		hypothetical protein	4617.200979	7.106444096	0.36582396	19.42585742	4.67E-84	1.25E-81	80.90201508
ABUW_RS07155	ABUW_1468	NZ_CP008706.1	1457939	1458733	+	WP_000053984.1		PGI-L family deacetylase	1565.51356	7.103552219	0.417248451	17.02475398	5.38E-65	5.29E-63	62.27665749
ABUW_RS18155	ABUW_2436	NZ_CP008706.1	2424078	2426222	-	WP_001985865.1	katE	catalase HPI	40275.84518	7.07446583	0.36063478	19.61870426	1.11E-85	3.20E-83	82.4942723
ABUW_RS15160	ABUW_3122	NZ_CP008706.1	3142445	3143296	+	WP_001064773.1	otsB	trehalose-phosphatase	1639.033208	6.963316164	0.548011953	12.70650418	5.44E-37	1.41E-35	34.85222435
ABUW_RS07160	ABUW_1467	NZ_CP008706.1	1456977	1457951	+	WP_000947654.1		hypothetical protein	1143.003934	6.934944454	0.420044652	16.49587943	3.93E-61	2.83E-59	58.54882005
ABUW_RS18160	ABUW_2437	NZ_CP008706.1	2426277	2427686	-	WP_001145690.1		iron-containing redox enzyme family protein	6730.665542	6.870223655	0.38952855	17.6371298	1.27E-69	1.66E-67	66.78107838
sRNA29	no	no	no	no	no	no	no	no	394.2856283	6.788594433	0.494925821	13.76336788	8.10E-43	2.77E-41	40.55819084
ABUW_RS07160	ABUW_1469	NZ_CP008706.1	1458708	1459307	+	WP_0001581927.1		class ISAM-dependent methyltransferase	1136.371545	6.773058971	0.410120463	16.51480297	2.91E-59	2.10E-58	67.8771367
ABUW_RS12725	ABUW_2621	NZ_CP008706.1	2618549	2619007	-	WP_001127331.1		hypothetical protein	4941.499428	6.704432108	0.348592892	19.23284225	1.97E-82	4.95E-80	79.30543911
ABUW_RS07965	ABUW_1632	NZ_CP008706.1	1629165	1629869	+	WP_000739311.1		molecular chaperone	944.5360155	6.640853729	0.412704906	10.50169225	2.95E-58	1.89E-56	55.22459766
ABUW_RS07500	ABUW_1536	NZ_CP008706.1	1522327	1522575	+	WP_000850008.1		hypothetical protein	5416.89278	6.533053858	0.384531855	16.98962977	9.80E-65	9.18E-63	62.03701935
ABUW_RS15165	ABUW_3123	NZ_CP008706.1	3143284	3144714	+	WP_000045106.1		trehalose-6-phosphate synthase	9244.358405	6.502010551	0.388505638	16.73594901	7.17E-63	6.15E-61	60.2195046
ABUW_RS20165	ABUW_1657	NZ_CP008706.1	1651777	1651908	+	WP_000161254.1		hypothetical protein	513.5381563	6.48972066	0.571532819	11.549246	7.01E-30	1.33E-28	27.8751843
ABUW_RS18185	ABUW_2442	NZ_CP008706.1	2429805	2430233	-	WP_001136759.1		hypothetical protein	253.3190753	6.427455316	0.49058281	10.167251	3.22E-39	9.16E-38	37.03912598
ABUW_RS12605	ABUW_2594	NZ_CP008706.1	2588077	2589240	-	WP_001027394.1		glutathione-dependent formaldehyde dehydrogenase	678.6762962	6.399490575	0.433147719	14.77438386	2.14E-49	9.49E-48	47.02286057
ABUW_RS18145	ABUW_2434	NZ_CP008706.1	2422589	2423002	+	WP_000983536.1		hypothetical protein	38.63620481	6.302008016	1.021459244	6.169612791	6.85E-10	2.84E-09	8.546474605
ABUW_RS15330	ABUW_3167	NZ_CP008706.1	3183396	3185072	-	WP_001001666.1		mechanosensitive ion channel	41419.22788	6.248735412	0.282350119	22.3151914	1.58E-108	2.13E-105	104.6720277
ABUW_RS07970	ABUW_1633	NZ_CP008706.1	1629879	1632338	+	WP_000873962.1		fimbrial biogenesis outer membrane usher protein	2618.722312	6.16839053	0.329592852	18.71518296	3.72E-78	6.82E-76	75.16628489
ABUW_RS15280	ABUW_3147	NZ_CP008706.1	3173306	3173806	-	WP_000208132.1		hypothetical protein	6879.766036	6.150966855	0.358608717	17.16230714	6.04E-66	6.40E-64	63.9350712
sRNA65	no	no	no	no	no	no	no	no	3728.887349	6.102218942	0.4140059742	14.733753502	3.70E-49	1.60E-47	46.79502916
ABUW_RS07165	ABUW_1470	NZ_CP008706.1	1459304	1459948	+	WP_000690470.1		glycosyltransferase	1075.612586	6.015411715	0.384156504	15.56875275	2.90E-55	1.60E-53	52.79644783
ABUW_RS18145	ABUW_2455	NZ_CP008706.1	2442667	2444658	+	WP_000461820.1		acetyl(propionyl)methylcrotonyl-CoA carboxylase subunit alpha	3837.508829	5.936254494	0.274328179	21.63920174	7.68E-104	6.19E-101	100.2082891
ABUW_RS12980	ABUW_2674	NZ_CP008706.1	2667054	2667332	-	WP_000072985.1		hypothetical protein	324.4144914	5.897261129	0.438636854	13.4445111	3.32E-41	1.00E-39	38.99809402
ABUW_RS18165	ABUW_2438	NZ_CP008706.1	2428002	2428481	+	WP_000402801.1		Cna family protein	165.370782	5.892747696	0.742845504	7.932669257	2.14E-15	1.46E-14	13.8372731
ABUW_RS08050	ABUW_1651	NZ_CP008706.1	1645792	1646622	+	WP_001127311.1		hypothetical protein	984.5032291	5.138664021	0.36806701	12.037361	3.26E-32	1.34E-31	14.4869519
ABUW_RS13010	ABUW_2679	NZ_CP008706.1	2670707	2671300	-	WP_000461336.1		DUF142 domain-containing protein	255.376196	5.8535119	0.56708972	10.28929229	7.82E-25	1.10E-23	22.95777432
ABUW_RS15335	ABUW_3168	NZ_CP008706.1	3185300	3185527	-	WP_000543705.1		hypothetical protein	2621.945201	5.829959294	0.323935625	17.99127737	2.05E-72	2.84E-70	69.54622214
ABUW_RS18980	ABUW_3898	NZ_CP008706.1	3965352	3965783	+	WP_000269927.1		GlabYeaQ/YmgE family stress response membrane protein	885.08856	5.714999018	0.32738957	17.53873532	7.25E-69	9.13E-67	66.0394742
ABUW_RS13040	ABUW_2686	NZ_CP008706.1	2675924	2676382	-	WP_00127319.1		hypothetical protein	1931.96074	5.709042499	0.39140539	15.82747618	2.54E-56	1.51E-54	53.82224399
ABUW_RS18140	ABUW_2454	NZ_CP008706.1	2441852	2442655	+	WP_000127219.1		enoyl-CoA hydratase/isomerase family protein	1247.63873	5.66636086	0.305024919	18.57827258	4.83E-78	8.44E-77	74.0369572
ABUW_RS00340	ABUW_0069	NZ_CP008706.1	71348	71780	-	WP_000781235.1	malA	malicylacetoacetate isomerase	4444.186904	5.644097727	0.35017345	12.1058872	1.82E-58	1.98E-56	55.92507825
ABUW_RS00335	ABUW_0068	NZ_CP008706.1	72466	73130	-	WP_001001451.1		VOC family protein	294.196693	5.55229409	0.331798364	6.7334442	7.48E-63	6.22E-60	60.20222491
ABUW_RS18160	ABUW_2456	NZ_CP008706.1	2445553	2445557	+	WP_000128890.1		hydroxymethylglutaryl-CoA lyase	1690.797706	5.5315389	0.27015659	20.4791697	3.30E-92	3.87E-90	85.6410065
ABUW_RS16140	ABUW_3322	NZ_CP008706.1	3357517	3357882	-	WP_000853613.1		hypothetical protein	526.5195002	5.499546372	0.37817671	14.54226614	6.54E-48	2.69E-46	45.57050737
ABUW_RS03380	ABUW_0687	NZ_CP008706.1	695949	696092	-	WP_001984261.1		entericidin A/B family lipopeptide	1286.695798	5.478000988	0.29574466	14.914793	6.74E-67	1.57E-63	72.80413466
ABUW_RS01040	ABUW_0233	NZ_CP008706.1	252171	252714	+	WP_000581866.1		hypothetical protein	8292.890922	5.70492394	0.320540864	17.06643403	2.94E-75	6.73E-73	62.56460943
ABUW_RS09210	ABUW_0811	NZ_CP008706.1	892175	892867	+	WP_000044208.1		type 1 glutamine amidotransferase domain-containing protein	1710.05375	5.416329503	0.38484913	10.7225571	5.62E-45	2.12E-43	42.67409272
newcasRNA1	no	no	no	no	no	no	no	no	238.6279859	5.41075811	0.35791927	8.51548197	1.66E-17	1.39E-16	15.58800296
ABUW_RS00345	ABUW_0070	NZ_CP008706.1	73767	75074	-	WP_000435854.1	fahA	fumaroylcoarboxate	12767.00428	5.405967895	0.343527552	13.7636558	8.48E-56	5.31E-54	53.37148149

ABLUW_RS085	ABLUW_RS86	NZ_CP008706.1	1887347	1888177	+	WP_000542602.1		alpha/beta hydrolase	3697.71742	5.300610565	0.260085703	20.3802458	2.505-92	1.445-89	88.84127554
ABLUW_RS1935	ABLUW_RS2453	NZ_CP008706.1	2440241	2441842	+	WP_001072777.1		methylecristonyl CoA carboxylase	2910.262352	5.238846504	0.317006379	6.5259972	2.385-61	1.785-59	58.74977482
ABLUW_RS0070	ABLUW_RS259	NZ_CP008706.1	274727	274915	+	WP_001110063.1		bifunctional SuP family organic anion transporter/carbonic anhydrase	5543.887225	5.233623993	0.26418748	9.8079979	2.545-87	7.875-85	45.7303895
ABLUW_RS0730	ABLUW_RS191	NZ_CP008706.1	1932461	1932841	-	WP_000720499.1		hypothetical protein	932.909218	5.224781877	0.35823271	0.7306205	4.175-48	1.755-46	64.7679417
ABLUW_RS0480	ABLUW_RS191	NZ_CP008706.1	1758355	1758993	-	WP_000332547.1		SDS response-associated peptidase family protein	5617.360635	5.18282677	0.340224269	9.23333481	2.515-52	1.075-50	49.9782033
ABLUW_RS0340	ABLUW_RS253	NZ_CP008706.1	2947306	2948451	-	WP_000073756.1		galactose mutarotase	433.777944	5.165068318	0.256774479	20.1714505	5.225-90	1.915-87	86.7826926
ABLUW_RS0595	ABLUW_RS27	NZ_CP008706.1	106720	1069675	-	WP_000576645.1		acyl-CoA dehydrogenase	2404.047217	5.118733195	0.318739905	8.28973425	1.175-59	8.115-58	57.0910206
ABLUW_RS1920	ABLUW_RS2450	NZ_CP008706.1	2436477	2438197	-	WP_001181733.1		AMP-binding protein	1761.17043	5.107345252	0.29578023	17.2700095	7.785-67	8.715-65	64.0602286
ABLUW_RS0480	ABLUW_RS1015	NZ_CP008706.1	920616	9227356	+	WP_000866525.1	carO	ornithine uptake porin CarO type 3	40059.38539	5.064394356	0.248601021	20.3756683	2.595-92	1.915-89	88.8222897
ABLUW_RS00325	ABLUW_RS0065	NZ_CP008706.1	70383	71438	+	WP_000035193.1	hpdD	4-hydroxyphenylpyruvate dioxygenase	9314.533215	5.005623445	0.30458745	6.6705286	5.115-62	4.85-60	59.3783703
ABLUW_RS1915	ABLUW_RS328	NZ_CP008706.1	350523	350566	+	WP_001018905.1		hemerythrin domain-containing protein	1429.973452	5.026851807	0.250360527	20.0784594	1.115-89	3.825-87	86.4750257
ABLUW_RS1930	ABLUW_RS2452	NZ_CP008706.1	2439044	2440216	+	WP_001053639.1		isovaleryl-CoA dehydrogenase	2343.051086	5.008276727	0.336778747	14.871187	5.085-50	2.305-48	47.6386787
ABLUW_RS0805	ABLUW_RS159	NZ_CP008706.1	1652339	1652770	+	WP_000720296.1		hypothetical protein	280.6947332	4.984527519	0.481873266	0.34406321	4.455-25	6.455-24	23.1902448
ABLUW_RS06270	ABLUW_RS196	NZ_CP008706.1	1906188	1906541	+	WP_001039306.1		hypothetical protein	504.7512917	4.978182056	0.542431093	9.17496209	4.415-20	4.515-19	8.34563294
ABLUW_RS05710	ABLUW_RS173	NZ_CP008706.1	1461930	1461956	+	WP_001046924.1		hypothetical protein	1524.7782	4.96627385	0.218962129	22.89004847	5.845-116	1.115-925991	
ABLUW_RS1724	ABLUW_RS274	NZ_CP008706.1	2710557	2710901	+	WP_001037898.1		hypothetical protein	7937.004811	4.882547197	0.360093126	0.55912358	7.905-42	2.235-40	39.65249055
ABLUW_RS1475	ABLUW_RS126	NZ_CP008706.1	218934	2189134	-	WP_000564581.1		hypothetical protein	2939.365429	4.84733244	0.336102338	14.2278701	3.725-47	1.485-45	44.8285675
ABLUW_RS075	ABLUW_RS134	NZ_CP008706.1	1533239	1533348	+	WP_000055766.1		spore coat protein Udoamin-containing protein	1453.5572	4.816584254	0.265220752	17.8919051	1.365-71	1.835-69	68.7370551
ABLUW_RS1960	ABLUW_RS2458	NZ_CP008706.1	2486955	2490347	+	WP_001017562.1		indolepyruvate ferredoxin oxidoreductase family protein	6779.54997	4.788689595	0.283477755	8.69328304	5.045-64	4.625-62	63.1335617
ABLUW_RS0070	ABLUW_RS197	NZ_CP008706.1	1793245	1793605	+	WP_000185571.1		hypothetical protein	4077.391926	4.787335951	0.334880717	14.2956431	2.235-46	9.025-45	44.04545846
ABLUW_RS1915	ABLUW_RS2449	NZ_CP008706.1	2435735	2436406	+	WP_001021902.1		class I SAM-dependent methyltransferase	578.580408	4.750106444	0.279200199	17.0126381	6.555-65	6.285-63	62.2018049
ABLUW_RS085	ABLUW_RS211	NZ_CP008706.1	211856	211918	-	WP_001017517.1		thiamine pyrophosphate-dependent dehydrogenase E1c component	638.366658	4.74810092	0.557892416	9.80710747	1.785-17	1.495-16	15.6278173
ABLUW_RS1935	ABLUW_RS1346	NZ_CP008706.1	1371744	1382500	+	WP_001015180.1	acnA	acetyl-CoA dehydrogenase AcnA	5478.736844	4.694437277	0.248183582	18.9158002	8.555-80	2.035-77	76.0931458
ABLUW_RS1935	ABLUW_RS1317	NZ_CP008706.1	1243531	1250346	+	WP_000862903.1	add	adenosine deaminase	9.15.2527994	4.691890561	0.388470772	0.7784704	1.385-33	3.155-32	3.150927362
ABLUW_RS0310	ABLUW_RS046	NZ_CP008706.1	651474	651917	-	WP_001016585.1		VOC family protein	1234.266871	4.657052314	0.331754512	14.0394543	8.945-45	3.345-43	42.4768995
ABLUW_RS010	ABLUW_RS261	NZ_CP008706.1	2047554	2043221	+	WP_001018176.1		hypothetical protein	1239.277092	4.55195487	0.289435598	0.72700424	9.885-56	5.535-54	53.25748772
ABLUW_RS160	ABLUW_RS1306	NZ_CP008706.1	1329650	1310123	+	WP_000522216.1	lysM	peptidoglycan-binding protein LysM	110.15.1442	4.547584369	0.247665888	18.36171929	2.665-75	4.125-73	72.3841435
ABLUW_RS1825	ABLUW_RS2451	NZ_CP008706.1	2438282	2438899	-	WP_000102693.1		TerR/AcrR family transcriptional regulator	3367.16207	4.478533461	0.237446786	9.81610205	2.385-79	5.045-77	26.2947883
ABLUW_RS0875	ABLUW_RS172	NZ_CP008706.1	1650275	1651405	+	WP_000071635.1		3-hydroxyacyl-CoA dehydrogenase	810.953237	4.44544726	0.309277177	14.7336271	7.585-47	2.975-45	44.5278975
ABLUW_RS1925	ABLUW_RS287	NZ_CP008706.1	2848092	2849471	+	WP_000491978.1		copper resistance protein NtpE	12285.46824	4.44128559	0.308105337	14.4131888	4.215-47	1.665-45	44.77595702
ABLUW_RS1930	ABLUW_RS2730	NZ_CP008706.1	2716760	2718175	+	WP_000026496.1		OmpA family protein	7519.248195	4.41493537	0.19222644	22.95057888	1.045-116	4.205-10	10.3770954
ABLUW_RS0005	ABLUW_RS260	NZ_CP008706.1	2041677	2041842	-	WP_001017338.1		hypothetical protein	3287.187005	4.342318393	0.450251022	9.6442197	5.205-32	6.025-21	20.22025956
ABLUW_RS1015	ABLUW_RS2097	NZ_CP008706.1	2079357	2077996	+	WP_000310583.1		CoA transferase subunit B	6393.215324	4.300182414	0.318480962	13.5021912	1.525-41	4.705-40	39.32752233
ABLUW_RS11270	ABLUW_RS2317	NZ_CP008706.1	2301891	2303245	+	WP_001046928.1		hypothetical protein	7.19.2993559	4.238817237	0.340766837	12.6161791	1.745-36	4.425-35	34.34506608
ABLUW_RS1910	ABLUW_RS2098	NZ_CP008706.1	2080116	2081524	+	WP_000414829.1		short-chain fatty acid transporter	1402.192529	4.25301809	0.334684669	12.7449264	5.175-37	1.345-35	34.81767952
ABLUW_RS0785	ABLUW_RS173	NZ_CP008706.1	166104	1662200	+	WP_000602467.1		acyl-CoA dehydrogenase family protein	1217.664098	4.247968098	0.308474761	0.170880055	3.825-43	1.335-41	40.8777724
ABLUW_RS1010	ABLUW_RS2096	NZ_CP008706.1	2078151	2077935	+	WP_001045567.1		CoA transferase subunit A	2383.511861	4.243340968	0.306701095	0.18340559	1.065-43	5.575-42	41.25416237
ABLUW_RS03030	ABLUW_RS011	NZ_CP008706.1	75433	76821	+	WP_000107088.1		amino acid permease	2930.899722	4.2366724	0.283359144	14.9519938	1.525-50	7.045-49	48.1623271
ABLUW_RS03030	ABLUW_RS028	NZ_CP008706.1	629733	629914	-	WP_000107532.1		peroxiredoxin	1819.451528	4.122374417	0.345964151	11.9161149	9.815-33	2.105-31	30.67245422
ABLUW_RS1945	ABLUW_RS2460	NZ_CP008706.1	243817	244053	+	WP_000097195.1		hypothetical protein	249.4369006	4.114659734	0.316818438	12.8805514	5.785-38	1.605-36	35.76686031
ABLUW_RS19400	ABLUW_RS3575	NZ_CP008706.1	3634322	3634669	-	WP_000201800.1		serine hydroxylase family protein	563.3272485	4.077334632	0.380023911	0.17291286	7.435-27	1.215-25	24.91656323
ABLUW_RS03045	ABLUW_RS149	NZ_CP008706.1	1645128	1645379	+	WP_000179474.1		hypothetical protein	1723.980466	4.06833271	0.305056865	0.14809494	1.755-39	4.995-38	37.3021365
ABLUW_RS1905	ABLUW_RS210	NZ_CP008706.1	2119323	2118842	-	WP_0010133050.1		alpha-ketoadid dehydrogenase subunit beta	780.155966	4.009370926	0.33778453	7.45520316	8.975-14	5.475-10	12.2617026
ABLUW_RS05925	ABLUW_RS103	NZ_CP008706.1	903508	903933	-	WP_000176933.1		hypothetical protein	18.19.96649	3.960060709	0.448533889	8.83012444	1.055-19	9.555-19	17.098669
ABLUW_RS05925	ABLUW_RS1723	NZ_CP008706.1	1721401	1721697	-	WP_000070184.1		hypothetical protein	89.8443279	3.934433732	0.403924418	9.740599222	2.025-32	2.435-21	20.035999
ABLUW_RS0995	ABLUW_RS258	NZ_CP008706.1	2038281	2040182	-	WP_000632243.1		hypothetical protein	2580.471181	3.931810451	0.271683922	14.47734984	1.685-47	6.865-46	45.8391847
ABLUW_RS1015	ABLUW_RS2099	NZ_CP008706.1	2081960	2082762	+	WP_000095311.1		thioester family protein	6876.388232	3.930529235	0.323044694	12.16713758	4.635-34	1.072-32	3.197028667
ABLUW_RS1010	ABLUW_RS289	NZ_CP008706.1	2713608	2715392	-	WP_001016890.1		sidechain bicyclic thioester protein	6455.57795	3.92888048	0.585326336	0.675722363	2.465-11	1.195-10	9.925003083
ABLUW_RS1005	ABLUW_RS2678	NZ_CP008706.1	2696967	2670326	-	WP_000247196.1		hypothetical protein	772.2938274	3.924603462	0.371187326	0.57426689	3.925-26	6.205-25	24.2077016
ABLUW_RS0590	ABLUW_RS163	NZ_CP008706.1	1760845	1761288	-	WP_000102025.1		universal stress protein	1077.488021	3.922454257	0.344258006	0.139367949	4.505-30	8.635-29	28.06420084
ABLUW_RS1010	ABLUW_RS2703	NZ_CP008706.1	2687016	2687371	+	WP_001086862.1		four-helix bundle copper-binding protein	7279.866477	3.89454273	0.428586532	0.08673735	1.025-19	1.015-18	17.9666381
ABLUW_RS05435	ABLUW_RS1111	NZ_CP008706.1	1129545	1130975	+	WP_001013471.1		aldehyde dehydrogenase family protein	4291.91369	3.887182403	0.252490661	0.35927202	1.765-53	9.215-52	51.0355773
ABLUW_RS19420	ABLUW_RS3579	NZ_CP008706.1	3637192	3638266	+	WP_000848679.1		hypothetical protein	4553.25005	3.76805158	0.218095553	17.2818268	6.475-67	7.455-65	64.8200305
ABLUW_RS1010	ABLUW_RS2639	NZ_CP008706.1	2637592	2638434	-	WP_001082436.1		universal stress protein	4035.481308	3.7634387	0.250702882	0.51954939	6.175-51	2.895-49	48.53908866
ABLUW_RS19174	ABLUW_RS324	NZ_CP008706.1	3580463	3580699	+	WP_000868735.1		hypothetical protein	3336.22511	3.752704173	0.304816856	12.3048185	8.535-35	2.035-33	32.6191348
ABLUW_RS19174	ABLUW_RS2639	NZ_CP008706.1	2644476	2625780	+	WP_000559371.1		MF5 transporter	811163458	3.735663696	0.277025716	0.48489867	19325-41	5.905-40	39.22893342
ABLUW_RS07425	ABLUW_RS21	NZ_CP008706.1	906545	907192	+	WP_000095779.1		sorbose dehydrogenase family protein	7814867356	3.705683898	0.229350885	8.9726879	10.15-58	6.785-57	56.889079
ABLUW_RS19420	ABLUW_RS373	NZ_CP008706.1	384380	3845357	+	WP_001093234.1		CoA-acylating methyltransferase-semialdehyde dehydrogenase	1549.02384	3.673876389	0.386897573	9.96447138	2.115-52	2.795-22	2.15545952
ABLUW_RS201															

ABLUW_R01620	ABLUW_0206	NZ_CP008706.1	231701	232327	-	WP_000046566.1		hydrolyase	42.0	509722	3.12993623	0.20469539	16.2906728	8.786-53	4.54E-51	50.34322581
ABLUW_R01425	ABLUW_2349	NZ_CP008706.1	233033	232092	+	WP_000084500.1		tautomerase family protein	1324	073987	3.05753392	0.22885429	13.66058926	1.75E-42	5.88E-41	40.2320258
ABLUW_R0245	ABLUW_2519	NZ_CP008706.1	250039	250665	-	WP_000700328.1		hypothetical protein	9.7	6040661	0.09620452	0.34433975	8.99170261	2.43E-19	2.32E-18	9.763481016
ABLUW_R0190	ABLUW_2448	NZ_CP008706.1	243429	243492	-	WP_00191598.1		hypothetical protein	36.2	5669837	0.088829817	0.283720856	10.87891284	1.44E-27	2.40E-26	25.61888567
ABLUW_R00555	ABLUW_0652	NZ_CP008706.1	945451	946732	+	WP_000503375.1		hypothetical protein	14.8	5893581	0.084503201	0.339764195	9.078365274	1.95E-19	1.08E-19	9.7653535
ABLUW_R00220	ABLUW_0563	NZ_CP008706.1	907261	914255	+	WP_000705588.1		hypothetical protein	9709	858461	0.084444095	0.237327643	13.56827551	6.95E-42	2.01E-40	39.69753138
ABLUW_R017430	ABLUW_0522	NZ_CP008706.1	1607940	1608392	+	WP_00186574.1		GNA1 family N-acetyltransferase	306	4885917	3.04884693	0.298021325	16.23029787	1.45E-24	2.01E-23	22.69618796
ABLUW_R0059	ABLUW_0888	NZ_CP008706.1	888590	890657	+	WP_000180179.1		saccharopine dehydrogenase NADP-binding domain-containing	397	5036773	3.033707082	0.27149556	11.8648983	4.73E-29	8.74E-28	27.00867919
ABLUW_R0167	ABLUW_3438	NZ_CP008706.1	348272	348284	-	WP_000859455.1		HsdR family auto-resistance protein	116	710402	0.023999924	0.28366094	10.66050872	1.56E-26	2.49E-25	24.60379421
ABLUW_R01500	ABLUW_3320	NZ_CP008706.1	3354427	3355329	-	WP_001068077.1		copper resistance protein B	833	9744303	0.023340809	0.283194619	10.67584129	1.32E-26	2.0E-25	24.6737882
ABLUW_R0185	ABLUW_2093	NZ_CP008706.1	207499	2076340	-	WP_000263726.1		GnpI family permease	788	2064039	0.022034567	0.250376112	12.06997961	1.52E-33	3.37E-32	31.47259394
ABLUW_R01480	ABLUW_3587	NZ_CP008706.1	3645893	3646249	-	WP_001334851.1		hypothetical protein	928	718039	0.299918872	0.289595788	10.49048486	9.55E-26	1.46E-24	23.83623569
ABLUW_R017820	ABLUW_0601	NZ_CP008706.1	691760	691768	+	WP_000351525.1		hypothetical protein	12.3	817892	0.072188729	0.424044525	7.009166615	2.40E-12	1.28E-11	10.86243028
ABLUW_R01705	ABLUW_3518	NZ_CP008706.1	3564335	3564664	+	WP_000207459.1		MerR family transcriptional regulator	924	2330037	0.218708124	0.3051972848	9.738715593	2.10E-22	2.52E-21	20.59842728
ABLUW_R0085	ABLUW_0237	NZ_CP008706.1	255242	255931	-	WP_001845986.1		aqpZ	6712	921277	0.2197042169	0.270296358	9.3914251	4.20E-28	7.33E-27	26.13419197
ABLUW_R0085	ABLUW_1762	NZ_CP008706.1	1759348	1760790	+	WP_001332848.1		PQQ-dependent sugar dehydrogenase	2276	90416	0.295264302	0.174058519	17.03601969	4.44E-65	4.47E-63	62.34954251
ABLUW_R00580	ABLUW_1188	NZ_CP008706.1	121942	1220581	+	WP_000983826.1		baeJ	175	9262843	0.2961670082	0.461877295	6.42243439	1.43E-10	9.19E1005	
ABLUW_R01520	ABLUW_2784	NZ_CP008706.1	2719143	2719332	+	WP_000374131.1		Paal family thioesterase	33	8152834	0.295947042	0.54057661	5.174651924	4.38E-08	1.52E-07	6.98557790
ABLUW_R00300	ABLUW_0190	NZ_CP008706.1	97994	912576	-	WP_0003040497.1		amidohydrolase	280	5165312	0.2941655538	0.3502241966	8.399074625	4.50E-17	3.61E-16	16.44228354
ABLUW_R018470	ABLUW_3054	NZ_CP008706.1	309587	3092412	-	WP_000160012.1		EucC family protein	5108	911190	0.2924185742	0.217794567	12.42632441	4.24E-41	1.27E-39	38.94060645
ABLUW_RS0200	ABLUW_2143	NZ_CP008706.1	2120710	2120974	+	WP_000086293.1		hypothetical protein	2812	697964	0.292099249	0.319750005	9.99812884	3.59E-20	3.69E-19	18.43351047
ABLUW_R01105	ABLUW_2293	NZ_CP008706.1	2279875	2280465	-	WP_0005050334.1		polyspermin-binding protein	2445	43552	0.2905856111	0.21010198	12.8295518	1.68E-43	5.94E-42	41.22607147
ABLUW_R01060	ABLUW_2606	NZ_CP008706.1	2599973	2600737	-	WP_000460677.1		Lamb/Yic family protein	1243	95541	0.2885197	0.333287082	8.564374005	1.19E-17	1.00E-16	15.9986546
ABLUW_RS0160	ABLUW_0307	NZ_CP008706.1	330921	331115	-	WP_000289091.1		bacterioferritin-associated ferredoxin	600	0857499	0.2879624222	0.677274087	4.251958803	2.12E-05	5.43E-05	6.246332806
ABLUW_R00380	ABLUW_1721	NZ_CP008706.1	1718751	1718758	+	WP_0000604789.1		SDR family NAD(P)-dependent oxidoreductase	2742	637338	0.287531473	0.217979949	13.9073034	9.92E-40	2.86E-38	37.54433453
ABLUW_R00430	ABLUW_0944	NZ_CP008706.1	950665	950763	+	WP_000370435.1		FdhH/Yoaf family oxidoreductase	1111	842605	0.287472461	0.236027357	12.221643	2.38E-34	5.60E-33	32.2520132
ABLUW_R01455	ABLUW_2355	NZ_CP008706.1	2337728	2338210	-	WP_000066032.1		glutathione peroxidase	698	417007	0.28683733	0.239995524	11.92037787	9.27E-33	2.02E-31	30.6949547
ABLUW_R001765	ABLUW_1181	NZ_CP008706.1	121029	121098	+	WP_001918265.1		baeF	81843	9734	0.285827286	0.575632994	4.965433384	6.85E-07	2.08E-06	5.681552608
ABLUW_R00570	ABLUW_1540	NZ_CP008706.1	1626390	1627840	+	WP_001295000		circularly permuted type 2 ATP-gasp protein	880	105564	0.282678367	0.232861912	12.14781482	5.89E-34	1.33E-32	31.67496491
ABLUW_R00270	ABLUW_0604	NZ_CP008706.1	904447	904743	-	WP_001277236.1		antibiotic biosynthesis monooxygenase	316	8657159	0.28200545	0.247047424	11.44924052	2.37E-30	4.64E-29	28.33332987
ABLUW_R00325	ABLUW_0677	NZ_CP008706.1	673231	673690	+	WP_001005094.1		SRPBC family protein	567	959535	0.2825752	0.286385957	10.9198729	9.89E-28	1.66E-26	25.77960253
ABLUW_R01070	ABLUW_2062	NZ_CP008706.1	2065673	2066017	-	WP_001804872.1		hypothetical protein	70	1672331	0.281603573	0.53285195	5.328047922	9.39E-08	3.29E-07	6.482918075
ABLUW_RS0820	ABLUW_3865	NZ_CP008706.1	393369	3934181	+	WP_0000944180.1		NAD(P)-dependent oxidoreductase	7913	5208805	0.280917185	0.240220685	11.69383806	1.37E-31	2.83E-30	29.54795799
ABLUW_RS00445	ABLUW_1110	NZ_CP008706.1	115168	115339	+	WP_000408453.1		alpha-keto acid decarboxylase family protein	4938	374743	0.2792420249	0.397219447	17.029916266	2.07E-12	1.1E-11	10.9545901
ABLUW_RS00210	ABLUW_0561	NZ_CP008706.1	607054	6071930	+	WP_000718056.1		ecpB	19151	81954	0.2784496711	0.2504388653	13.62533861	2.90E-42	9.60E-41	40.01649976
ABLUW_RS07105	ABLUW_1472	NZ_CP008706.1	1460763	1461233	+	WP_001028851.1		BLUF domain-containing protein	695	8784372	0.277321897	0.197774424	16.41055118	1.29E-53	8.82E-52	11.5061959
ABLUW_RS01725	ABLUW_0542	NZ_CP008706.1	526462	5262941	+	WP_000772583.1		transglutaminase family protein	1111	563833	0.27616674	0.21616362	12.77594794	2.23E-37	6.00E-36	35.22179313
ABLUW_RS01990	ABLUW_0637	NZ_CP008706.1	633040	6335723	+	WP_000209704.1		SDR family NAD(P)-dependent oxidoreductase	232	5891053	0.276140075	0.297524977	9.281639379	1.67E-20	1.77E-19	18.75195628
ABLUW_RS01860	ABLUW_2425	NZ_CP008706.1	241866	241950	-	WP_001225680.1		N-acetyltransferase	284	57772	0.275641834	0.226470979	12.0718801	4.43E-34	1.03E-32	31.98924061
rRNA2									no							
ABLUW_RS02235	ABLUW_2516	NZ_CP008706.1	2507870	2508022	+	WP_001279164.1		hypothetical protein	141	8609751	0.2746849128	0.71951491	3.81763732	0.000194738	0.000309317	3.050996704
ABLUW_RS04485	ABLUW_0914	NZ_CP008706.1	910874	911012	+	WP_001247651.1		NAD(+)/NADH kinase	725	0380992	0.2742287353	0.395680043	14.01413915	1.28E-44	4.68E-43	42.32987604
ABLUW_RS0625	ABLUW_2168	NZ_CP008706.1	218869	219710	-	WP_000511932.1		siderophore autohemolysin biosynthesis protein AcsC	4196	402731	0.2732821562	0.27198819	10.05008058	9.91E-24	1.19E-22	21.02274864
ABLUW_RS0620	ABLUW_2185	NZ_CP008706.1	218649	218689	-	WP_000993042.1		lucA/lucC family siderophore biosynthesis protein	4238	665621	0.27278191	0.264679068	10.30607314	6.16E-25	9.42E-24	23.02606447
ABLUW_RS00295	ABLUW_0500	NZ_CP008706.1	951431	917051	+	WP_001869306.1		hypothetical protein	833	053233	0.272097062	0.218793619	12.5164828	3.90E-36	9.76E-35	34.01977771
ABLUW_RS02710	ABLUW_2861	NZ_CP008706.1	2871422	2871535	-	WP_001186305.1		hypothetical protein	933	3494449	0.2718652254	0.277864206	9.799910099	1.67E-22	2.03E-21	20.69244873
ABLUW_RS01435	ABLUW_2129	NZ_CP008706.1	211486	211621	-	WP_001289782.1		2-oxo acid dehydrogenase subunit E2	734	842135	0.2718723021	0.401906669	16.764832405	1.33E-11	6.59E-11	10.810095
ABLUW_RS00545	ABLUW_0110	NZ_CP008706.1	124445	124599	-	WP_000393852.1		pyridoxal phosphate-dependent aminotransferase	1728	205827	0.2716619321	0.255643009	10.62658787	2.24E-26	3.57E-25	24.44735705
ABLUW_RS01875	ABLUW_1720	NZ_CP008706.1	171837	171887	+	WP_001005178.1		sulfurtransferase complex subunit TusD	3942	661932	0.271067167	0.303741054	8.91270453	5.05E-19	4.72E-18	17.32649502
ABLUW_RS01880	ABLUW_2441	NZ_CP008706.1	2424396	2429717	-	WP_000498474.1		hypothetical protein	94	1224227	0.2704929622	0.404065352	16.754466037	1.43E-11	7.05E-11	10.165194
ABLUW_RS0950	ABLUW_3485	NZ_CP008706.1	3533892	3534353	+	WP_001984522.1		DMF family transporter	497	9645164	0.269998857	0.289433254	10.4071079	2.30E-25	3.41E-24	23.60775757
ABLUW_RS01840	ABLUW_0333	NZ_CP008706.1	356034	356402	+	WP_001189303.1		hypothetical protein	1049	19822	0.269073296	0.229726102	11.7127887	1.10E-31	2.30E-30	29.638238
ABLUW_RS01950	ABLUW_3525	NZ_CP008706.1	3580992	3582410	+	WP_000003544.1		polyphosphate-AMP phosphatransferase	239	475915	0.2680038067	0.18147146	14.77277328	2.19E-49	9.61E-48	47.0173859
ABLUW_RS00270	ABLUW_0055	NZ_CP008706.1	59548	60717	-	WP_001990830.1		PQQ-dependent sugar dehydrogenase	1979	193379	0.267187802	0.319764511	8.35542216	6.62E-17	5.95E-16	9.27851934
ABLUW_RS01190	ABLUW_2862	NZ_CP008706.1	287143	2871884	-	WP_0007182311		hypothetical protein	242	0235090	0.266340381	0.309814829	8.596758281	8.20E-18	7.01E-17	16.154027
ABLUW_RS01230	ABLUW_2534	NZ_CP008706.1	2525000	2525290	-	WP_000339648.1		paalB	2333	557698	0.2658292302	0.56484207	4.705257633	2.52E-06	7.21E-05	6.1796179
ABLUW_RS00275	ABLUW_0905	NZ_CP008706.1	990473	990542	-	WP_000200064.1		hydrolyase	833	8099465	0.2649047235	0.19147019	13.83523863	1.56E-43	5.57E-42	41.25415237
ABLUW_RS01840	ABLUW_3781	NZ_CP008706.1	384107	3												

ABUW_RS1265	ABUW_2336	NZ_CP008706.1	230049	2301878	+	WP_001637930.1			DMT family transporter	175.036632	2.362241248	0.310404224	7.561484958	3.98E-14	2.50E-13	12.60210093
ABUW_RS12330	ABUW_2336	NZ_CP008706.1	2268927	2528629	+	WP_000802952.1	paaZ	phenylacetate: acid degradation bifunctional protein PaaZ	4627.007606	2.360889542	0.376632472	6.268417398	3.65E-10	1.56E-09	8.80595936	
ABUW_RS18985	ABUW_3874	NZ_CP008706.1	3942434	3942750	+	WP_001274778.1		hypothetical protein	1618107049	2.356150051	0.282415162	8.342877613	7.25E-17	5.68E-16	15.24542272	
ABUW_RS100420	ABUW_1008	NZ_CP008706.1	1025993	1025993	-	WP_001259423.1		SMF1 domain-containing protein	1059.21077	2.336390775	0.223438088	0.45564658	137E-25	2.05E-24	23.68862999	
ABUW_RS100575	ABUW_0585	NZ_CP008706.1	581551	582819	+	WP_000941010.1		HAMP domain-containing histidine kinase	4046.784549	2.335003585	0.243064412	9.81224582	7.24E-22	8.29E-21	20.086101	
ABUW_RS152815	ABUW_2783	NZ_CP008706.1	2776566	2777912	+	WP_000758290.1		DUF3337 domain-containing protein	23.86100691	2.334059944	0.555310170	4.20311863	2.63E-05	4.17421967		
ABUW_RS160619	ABUW_055	NZ_CP008706.1	056163	056323	-	WP_000993415.1		hemin uptake protein HmpP	362.5923692	2.331953228	0.410705256	5.636772397	1.73E-08	6.26E-08	7.20371145	
ABUW_RS103495	ABUW_0710	NZ_CP008706.1	718525	717043	+	WP_000108643.1		hypothetical protein	6215008335	2.319703917	0.162223693	12.71800982	4.77E-37	1.26E-35	34.9102327	
ABUW_RS10510	ABUW_2782	NZ_CP008706.1	2777259	2778509	+	WP_000041032.1		CyD family protein	152.4745652	2.316072653	0.328531935	7.049768429	1.79E-12	9.69E-12	10.1055273	
ABUW_RS107410	ABUW_1518	NZ_CP008706.1	1503894	1504400	-	WP_000894317.1		GNAT family N1-acyltransferase	25.36516504	2.31610271	0.584324493	3.95859105	7.54E-05	0.000719209	23.46640259	
ABUW_RS18565	ABUW_3814	NZ_CP008706.1	3876585	3878252	-	WP_01857993.1	ldp	L-lactate permease	5075.973923	2.310278674	0.32410261	7.131525768	9.81E-13	5.43E-12	11.26519946	
ABUW_RS10480	ABUW_0301	NZ_CP008706.1	325229	325819	+	WP_000846931.1		LemA family protein	2088.037787	2.299059014	0.182036763	12.62934465	1.45E-36	3.71E-35	34.43064211	
ABUW_RS105890	ABUW_1016	NZ_CP008706.1	1041971	1045612	-	WP_000872627.1		peptide MFS transporter	139.1449105	2.293982674	0.214138881	10.7134287	8.91E-27	1.45E-25	24.83948197	
ABUW_RS12230	ABUW_2514	NZ_CP008706.1	2507184	2507484	-	WP_000338517.1		hypothetical protein	200.4946675	2.291921614	0.641314409	3.573164397	0.000332693	0.000714801	3.11645138	
rRNA77																
ABUW_RS12730	ABUW_2623	NZ_CP008706.1	2619612	2620262	-	WP_000398495.1		3-hydroxyacyl-CoA dehydrogenase	448.312448	2.284407752	0.188241779	12.10549182	0.65E-34	1.54E-32	318.1201629	
ABUW_RS12745	ABUW_2627	NZ_CP008706.1	2623944	2624381	+	WP_000760328.1		DUF2147 domain-containing protein	59.144426	2.284406014	0.337362243	6.771974269	1.28E-11	6.31E-11	10.20022951	
ABUW_RS100385	ABUW_0078	NZ_CP008706.1	83915	85453	+	WP_000421600.1	huhH	histidine ammonia-lyase	47.6175973	2.278770902	0.337590258	6.149886628	1.44E-11	7.26E-11	10.9330475	
ABUW_RS11910	ABUW_2294	NZ_CP008706.1	2280680	2281087	+	WP_000348280.1		OsmC family protein	34.11705182	2.278397208	0.308705938	7.38041743	1.58E-10	9.40E-10	12.02684544	
ABUW_RS102550	ABUW_0175	NZ_CP008706.1	0189442	0189602	-	WP_000443551.1		hypothetical protein	39.98401575	2.266708466	0.426041656	5.320302896	1.04E-07	3.43E-07	6.46521632	
ABUW_RS18560	ABUW_3810	NZ_CP008706.1	387818	3878565	-	WP_001022772.1	lslR	transcriptional regulator LslR	1028.841217	2.25310445	0.305529088	7.33514282	2.21E-10	1.30E-12	11.88515367	
ABUW_RS105040	ABUW_027	NZ_CP008706.1	103894	1039570	+	WP_000842416.1		Do family serine endopeptidase	6454.739462	2.243191662	0.217225296	10.32987687	5.16E-25	7.43E-24	3.23190548	
ABUW_RS11895	ABUW_2485	NZ_CP008706.1	2457319	2457986	-	WP_000608703.1		3-oxoacyl-CoA transferase subunit A	34.94059084	2.240011304	0.466216246	4.804635888	1.55E-05	4.53E-06	5.343941787	
ABUW_RS108325	ABUW_1710	NZ_CP008706.1	171082	171136	+	WP_000181765.1		MoadT3 family protein	238.2220708	2.218101075	0.1823191	12.6659091	4.69E-34	1.07E-32	31.91694177	
ABUW_RS16440	ABUW_3179	NZ_CP008706.1	3206785	3207138	-	WP_001847855.1		hypothetical protein	50.1815851	2.216740406	0.305682324	7.23218768	4.75E-13	2.69E-12	11.57082305	
ABUW_RS17465	ABUW_3588	NZ_CP008706.1	3646463	3646828	-	WP_000373863.1		hypothetical protein	843.7289397	2.210066299	0.281803838	7.842656909	4.41E-15	2.97E-14	15.02665404	
ABUW_RS107405	ABUW_017	NZ_CP008706.1	1503187	1503739	-	WP_000692365.1		nuclear transport factor 2 family protein	82.9493349	2.208741238	0.341339033	6.644954275	1.01E-10	4.81E-10	9.335007594	
rRNA30																
ABUW_RS18550	ABUW_3811	NZ_CP008706.1	3871632	3871338	-	WP_001019301.1	dd	D-lactate dehydrogenase	5286.122384	2.192444748	0.238661228	9.13121819	0.78E-20	6.83E-19	16.1657718	
ABUW_RS100845	ABUW_0715	NZ_CP008706.1	714456	7147101	+	WP_000494568.1		hypothetical protein	2649.474744	2.174386125	0.246780009	8.81018885	1.24E-18	1.02E-17	16.94962724	
ABUW_RS18545	ABUW_2603	NZ_CP008706.1	2595821	2597539	-	WP_001016100.1		ATP-gas domain-containing protein	22.02234466	2.173156004	0.28641482	3.913376617	2.28E-13	1.33E-12	11.8714351	
ABUW_RS18480	ABUW_2187	NZ_CP008706.1	2193065	2196990	-	WP_000065521.1		GTA family protein	72.482609	2.161916068	0.372841421	5.81303998	6.24E-09	2.36E-08	7.627214566	
ABUW_RS18555	ABUW_3812	NZ_CP008706.1	3874665	387518	-	WP_000518728.1	ldd	FMN-dependent L-lactate dehydrogenase Lld	2830.650487	2.160553769	0.317292864	6.809316144	9.81E-12	4.91E-11	10.30861057	
ABUW_RS18710	ABUW_1174	NZ_CP008706.1	1162122	1164727	-	WP_000420477.1		LysE family translocator	32.8782485	2.153720534	0.4531435	4.757257991	1.96E-08	5.69E-06	5.245029327	
ABUW_RS18710	ABUW_3489	NZ_CP008706.1	3538557	3539585	+	WP_000396920.1		ABC transporter	9176.547017	2.150295568	0.192244508	11.78959947	3.95E-32	8.42E-31	30.14744832	
ABUW_RS180485	ABUW_0302	NZ_CP008706.1	325841	326923	-	WP_001042387.1		TPM domain-containing protein	2347.529646	2.147848911	0.162361036	15.08711817	1.96E-51	9.30E-50	49.03105141	
ABUW_RS180360	ABUW_1509	NZ_CP008706.1	1504532	1495503	+	WP_000303270.1		acyl-CoA deacylase	82.15000026	2.13210116	0.339281021	6.284262898	3.29E-10	1.42E-09	8.847874052	
ABUW_RS18425	ABUW_2145	NZ_CP008706.1	2104117	2103683	-	WP_000183702.1		hypothetical protein	1494.68286	2.128343051	0.265509399	7.897101398	2.85E-15	1.94E-14	13.7003762	
ABUW_RS102130	ABUW_2532	NZ_CP008706.1	2523716	2524216	-	WP_000177936.1	paaJ	phenylacetate-CoA oxygenase subunit PaaJ	2571070063	2.107741961	0.502384364	4.235286694	2.28E-05	5.83E-05	4.234471941	
ABUW_RS107525	ABUW_1624	NZ_CP008706.1	1610919	1620191	-	WP_000874704.1		iron-containing alcohol dehydrogenase	2045.830793	2.102281914	0.271882224	7.803014704	6.04E-15	4.03E-14	13.3958141	
ABUW_RS107375	ABUW_1512	NZ_CP008706.1	1497572	1498771	+	WP_000598001.1		class I SAM-dependent methyltransferase	12.1110193	2.10152683	0.30364024	6.968094085	2.83E-12	1.50E-11	10.82380387	
ABUW_RS185700	ABUW_3395	NZ_CP008706.1	3438237	3439439	+	WP_000236000.1		acyl kinase	893.1029219	2.10525443	0.255833457	8.283730576	1.16E-16	9.07E-16	15.0428336	
ABUW_RS187100	ABUW_2216	NZ_CP008706.1	2201452	2202197	-	WP_000164085.1		nucleoside-diphosphate sugar epimerase	303.4214736	2.118965397	0.200536926	10.56645997	4.26E-26	6.71E-25	24.7334447	
ABUW_RS180780	ABUW_1184	NZ_CP008706.1	1215153	1215123	+	WP_001018155.1	baaA	actin export ABC transporter permease/ATP-binding subunit	216.33050317	2.118441752	0.355193384	5.897167487	3.68E-09	1.42E-08	7.846073103	
ABUW_RS18355	ABUW_2957	NZ_CP008706.1	2959912	2970700	+	WP_000071453.1		citronellal:monop-CoA hydratase family protein	160.5196267	2.1146054373	0.254236634	8.176616983	8.97E-17	6.90E-16	15.056366	
rRNA73																
ABUW_RS18585	ABUW_3291	NZ_CP008706.1	3324165	3325793	+	WP_000253062.1		acyl-CoA synthetase	358.5162198	2.103251726	0.163368377	3.231925265	0.00129592	0.00249712	2.603876432	
ABUW_RS180285	ABUW_1507	NZ_CP008706.1	1506891	1509133	+	WP_0001832870.1		PQQ-dependent sugar dehydrogenase	1705.026247	2.108019419	0.159336453	13.22988832	5.89E-40	1.7E-38	37.7677279	
ABUW_RS14490	ABUW_2184	NZ_CP008706.1	2100533	2100124	-	WP_000181910.1		transferin-binding protein-like solute binding protein	71.4589986	2.105953511	0.423403812	4.97185355	5.66E-07	2.00E-06	5.69889107	
ABUW_RS107175	ABUW_1173	NZ_CP008706.1	1169938	1200879	+	WP_0001210792.1	bauD	acetylcholinesterase ABC transporter permease subunit BauD	55.64408605	2.10187285	0.816344651	2.577718998	0.00943441	0.01720881	1.74424902	
ABUW_RS100660	ABUW_0153	NZ_CP008706.1	147654	148004	+	WP_000193161.1		HPF/Rak family ribosome-associated protein	7874.214608	2.099983264	0.274270297	7.656619348	1.91E-14	1.22E-13	12.91068712	
ABUW_RS120035	ABUW_2531	NZ_CP008706.1	2522630	2523691	-	WP_000671461.1	paaK	phenylacetate-CoA oxygenase:reductase subunit PaaK	91.5755354	2.098935062	0.528666184	3.938181584	6.78E-05	0.000182355	3.789534605	
ABUW_RS100440	ABUW_0109	NZ_CP008706.1	102071	102338	-	WP_001035124.1		MAT E family accessory	913711007	2.098736287	0.19540712	10.52022411	0.64E-26	1.06E-24	23.97640904	
ABUW_RS185435	ABUW_0945	NZ_CP008706.1	953162	953943	+	WP_000187642.1	mdh	gamma dehydrogenase:acyl-sulfurtransferase Fdh	96.36323002	2.096972629	0.318224188	6.652321449	2.89E-11	1.39E-10	9.858416266	
ABUW_RS180190	ABUW_0360	NZ_CP008706.1	382756	383175	-	WP_000105414.1		hypothetical protein	541.5244468	2.094309194	0.219500063	9.703218176	2.92E-22	3.47E-21	20.45941575	
ABUW_RS180945	ABUW_0303	NZ_CP008706.1	3269197	327477	+	WP_000251894.1		TPM domain-containing protein	193.8158324	2.094427109	0.163414885	12.16241134	1.32E-37	3.60E-36	35.44337896	
ABUW_RS18500	ABUW_211	NZ_CP008706.1	214234	214274	-	WP_000183456.1		DUF337 domain-containing protein	1594.584944	2.089241546	0.102756788	9.30123486	4.60E-67	5.46E-65	64.26310362	
ABUW_RS107105	ABUW_1644	NZ_CP008706.1	163227	1647495	-	WP_000181772.1		CoA-acylating methylmalonate-semialdehyde dehydrogenase	524.0297573	2.085197345	0.26164858	7.999489878	1.24E-18	8.56E-16	14.10763295	
ABUW_RS100605	ABUW_0411	NZ_CP008706.1														

ABLW_RS740	ABLW_3849	NZ_CP008706.1	391703	3917879	+	WP_000877608.1	YcK family oxidoreductase	2577.502109	189997.912	0.219669	86	8.6492426	5.18E-18	4.50E-17	6.34660365
ABLW_RS0885	ABLW_0205	NZ_CP008706.1	1243172	1244974	-	WP_000999140.1	aminopeptidase F family protein	2804.592122	1898653871	0.80334	173	1184129268	2.39E-32	5.0E-31	30.21927271
ABLW_RS1030	ABLW_3161	NZ_CP008706.1	317437	3178006	+	WP_000044599.1	TerR(Au) family transcriptional regulator	795.0830233	1897280303	0.276948	99	6.85070536	7.35E-12	3.75E-11	0.42622088
ABLW_RS0375	ABLW_074	NZ_CP008706.1	108085	109341	+	WP_000542117.1	NADP-dependent isocitrate dehydrogenase	2005.382013	189454595	0.85680288	11	117206258	5.09E-29	1.02E-27	26.91900016
ABLW_RS0990	ABLW_2675	NZ_CP008706.1	266782	266919	-	WP_00134729.1	hypothetical protein	3881.700127	1887595289	0.232507979	8	118385007	4.72E-16	3.39E-15	14.46942922
ABLW_RS1765	ABLW_3508	NZ_CP008706.1	354710	3550504	-	WP_000643174.1	hypothetical protein	1335.933238	1.88	80058	0.409133612	4.598988024	4.25E-06	1.98E-05	4.92724476
ABLW_RS0690	ABLW_1784	NZ_CP008706.1	178389	1782362	-	WP_001300584.1	DUF2750 domain-containing protein	602.0140716	1878948256	0.223973758	8	3.89146465	4.90E-17	3.02E-16	6.40644779
ABLW_RS0270	ABLW_0684	NZ_CP008706.1	670429	671253	-	WP_000734697.1	ser1 repeat family protein	4319565547	1876688969	0.16	933559	12.35203716	4.73E-35	1.6E-33	32.9382771
ABLW_RS0845	ABLW_1754	NZ_CP008706.1	1749578	1750194	-	WP_000573225.1	CNAT family N-acetyltransferase	304.760239	1864540865	0.230481919	8	8.089748956	5.98E-16	4.20E-15	14.37100636
ABLW_RS0526	ABLW_1662	NZ_CP008706.1	107198	1072703	-	WP_000744219.1	hypothetical protein	573.6837546	186224994	0.83912271	10	12575141	4.20E-24	5.70E-23	22.24383769
ABLW_RS1690	ABLW_3473	NZ_CP008706.1	3521217	3521822	-	WP_000053846.1	glutathione S-transferase family protein	1229.767908	186088537	0.68897597	11	11010649	3.35E-28	5.88E-27	26.21368784
ABLW_RS0730	ABLW_1463	NZ_CP008706.1	145174	145316	+	WP_001865538.1	aspartate aminotransferase family protein	367.755596	1857576595	0.347743678	5	5.347198327	9.20E-08	3.05E-07	6.51009681
ABLW_RS0760	ABLW_0359	NZ_CP008706.1	382230	382661	+	WP_001880601.1	hypothetical protein	1058.801739	185252967	0.225059036	8	8.231005441	1.85E-16	1.39E-15	14.8571733
ABLW_RS0735	ABLW_1608	NZ_CP008706.1	149349	149442	+	WP_000770558.1	IpoCalm family protein	97.91582499	1851915362	0.338884635	5	4.647336943	4.64E-08	1.60E-07	6.716077986
ABLW_RS00516	ABLW_0164	NZ_CP008706.1	15613	158809	+	WP_000619878.1	alpha-beta fold hydrolase	628.886829	1850264265	0.83905255	11	112862076	1.49E-29	2.79E-28	26.5550333
ABLW_RS10095	ABLW_2698	NZ_CP008706.1	2683223	2684855	+	WP_001283235.1	exodeoxyribonuclease VI large subunit	319.4895929	1847489161	0.91318299	9	6.66625461	4.61E-22	5.37E-21	20.2707313
ABLW_RS1475	ABLW_0192	NZ_CP008706.1	609131	608488	+	WP_000688053.1	glycyl-3-phosphate dehydrogenase	1006.105178	1835122904	0.96459026	9	9.34091564	9.54E-21	1.03E-19	8.96787834
sRNA45	no	no	no	no	no	no	no	633.2776015	1834210617	0.28182615	6	6.95555448	7.10E-11	3.30E-10	9.461638746
ABLW_RS01665	ABLW_0338	NZ_CP008706.1	355689	361739	-	WP_001819261.1	ycsS	740.36361	1831055616	0.8039547	9	10067478	4.46E-23	2.23E-22	32.35035754
ABLW_RS02630	ABLW_1794	NZ_CP008706.1	1229578	1227909	-	WP_001171005.1	class C enteric-spectrum beta-lactamase ADC-11	759.1165548	1829190364	0.86395992	9	9.36191641	7.89E-21	8.52E-20	8.06975259
ABLW_RS10360	ABLW_2162	NZ_CP008706.1	211893	2119169	+	WP_000364058.1	IspA	500.7776	1825008879	0.320490408	5	6.6946841	1.24E-08	4.53E-08	7.344188163
ABLW_RS02385	ABLW_1488	NZ_CP008706.1	1497507	1499120	+	WP_000154085.1	acetyl-CoA carboxylase carboxyltransferase subunit	92.74162579	1817354148	0.366248797	4	3.66210694	6.97E-07	2.12E-06	5.074503371
ABLW_RS10075	ABLW_2003	NZ_CP008706.1	2341675	2344469	+	WP_000532899.1	TMBare1 protein	687.589601	1817311916	0.90673562	9	2.402281909	2.46E-20	2.55E-19	8.99260661
ABLW_RS1870	ABLW_2460	NZ_CP008706.1	2451498	2453300	-	WP_001101921.1	acyl-CoA dehydrogenase C-terminal domain-containing protein	184.7320181	1812343486	0.247667866	7	3.71637678	5.26E-13	1.47E-12	11.83286194
sRNA76	no	no	no	no	no	no	no	2018.95062	1804003291	0.279121509	6	6.46314681	1.03E-10	4.65E-10	9.332294971
ABLW_RS04175	ABLW_0851	NZ_CP008706.1	83131	832161	+	WP_001177768.1	DUF3298 domain-containing protein	108.029615	1803073627	0.62269872	11	110473027	1.9E-28	2.16E-27	26.66764194
ABLW_RS1825	ABLW_2390	NZ_CP008706.1	2371890	2371954	+	WP_000566413.1	cytochrome b ubiquinol oxidase subunit 8	1418.1735	1802261235	0.404963104	4	4.5073047	8.56E-06	2.30E-05	4.637386664
ABLW_RS1885	ABLW_3899	NZ_CP008706.1	3960337	3966535	-	WP_000502161.1	DacC family protein	771.616579	1801834218	0.14360649	12	5.47005	4.15E-36	1.02E-34	33.9192756
ABLW_RS0420	ABLW_0216	NZ_CP008706.1	236055	236477	+	WP_000141353.1	GFA family protein	93.12171109	1795651083	0.23191104	7	7.63963193	8.23E-15	5.43E-14	13.2653602
sRNA41	no	no	no	no	no	no	no	55.76865547	1791689779	0.452523364	3	3.959330992	7.52E-05	0.000719077	3.746995906
ABLW_RS01735	ABLW_1175	NZ_CP008706.1	120123	1202593	+	WP_000582112.1	baeE	51.076947	1782745991	0.532987869	3	3.44915335	0.000823374	0.00170368	2.76673525
ABLW_RS00959	ABLW_1165	NZ_CP008706.1	119130	1200106	-	WP_000995337.1	pilin family protein	345.1720603	1774866638	0.238539648	7	4.40509998	1.00E-10	6.08E-10	3.01235932
ABLW_RS03905	ABLW_3166	NZ_CP008706.1	3183097	3183287	+	WP_000742883.1	hypothetical protein	226.3425816	1774195201	0.301971688	5	5.892324226	3.81E-09	1.47E-08	7.83322086
sRNA100	no	no	no	no	no	no	no	3166.530264	1772477272	0.240991724	7	7.35356071	1.93E-13	1.14E-12	11.94240316
sRNA185	no	no	no	no	no	no	no	103.619108	1770576297	0.327188643	5	5.11484577	6.25E-08	2.12E-07	6.67370873
ABLW_RS02025	ABLW_2391	NZ_CP008706.1	2373969	2380153	+	WP_000748814.1	hypothetical protein	256.47899	1767934293	0.382033828	4	4.626278948	3.72E-06	1.04E-05	4.19810494
sRNA93	no	no	no	no	no	no	no	524.999025	176658411	0.375232767	4	4.07968662	2.50E-06	7.9E-06	5.10512233
ABLW_RS01895	ABLW_1683	NZ_CP008706.1	1678464	1679080	-	WP_000186580.1	acyl-CoA thioesterase	93.5828837	1765414861	0.90575842	9	9.26358176	1.98E-20	2.07E-19	18.6831552
ABLW_RS02075	no	no	no	no	no	no	no	10184305	1759394427	0.332771004	5	5.287099379	1.24E-07	4.06E-07	6.391841761
ABLW_RS00745	ABLW_1177	NZ_CP008706.1	1203564	1205567	+	WP_00116286.1	baaA	748.5593257	1756001222	0.334577263	5	5.248656783	1.53E-07	4.97E-07	6.303980466
ABLW_RS01645	ABLW_0940	NZ_CP008706.1	947003	947608	-	WP_001007011.1	nitroreductase family protein	504.955484	1754948428	0.27923193	8	8.284929967	3.28E-10	1.41E-09	8.849273753
ABLW_RS10335	ABLW_2127	NZ_CP008706.1	212600	212845	-	WP_000238448.1	acetylase	222.5969389	1750273262	0.361007669	4	4.848299386	1.25E-06	3.67E-06	5.434399608
ABLW_RS18720	ABLW_0885	NZ_CP008706.1	861406	861448	+	WP_073938453.1	lp-like domain-containing protein	50908.24393	1742532396	0.9127019	9	9.18319725	8.21E-20	8.9E-19	8.9866319
ABLW_RS03295	ABLW_0479	NZ_CP008706.1	497128	492058	+	WP_000458157.1	GFA family protein	103.9145629	1734147386	0.367893327	4	4.733731508	2.20E-06	6.38E-06	5.96418977
ABLW_RS17775	ABLW_3045	NZ_CP008706.1	3071469	3072122	-	WP_001302411.1	OmpA family protein	378602.89175	1714917204	0.223709091	7	7.77869303	7.27E-16	4.83E-14	3.17051911
ABLW_RS11255	ABLW_2314	NZ_CP008706.1	2299784	2299963	+	WP_000905609.1	hypothetical protein	14.54781678	1740809804	0.584250028	2	2.979563062	0.002888598	0.005561682	2.254777045
sRNA164	no	no	no	no	no	no	no	427.5802554	1729975179	0.373973368	4	4.62588216	7.37E-06	1.05E-05	4.980844168
ABLW_RS12390	ABLW_2738	NZ_CP008706.1	2727699	2728505	+	WP_001237338.1	peptidoglycan DD-metabolite depeptidase family protein	5311551463	1729875323	0.92202077	9	9.000294649	2.25E-19	2.15E-18	17.66664843
ABLW_RS14750	ABLW_3039	NZ_CP008706.1	3065316	3066097	-	WP_000890283.1	CNAT family N-acetyltransferase	103.185804	1723740652	0.250201885	6	6.88939919	5.60E-12	2.90E-11	10.5793094
ABLW_RS16415	ABLW_2373	NZ_CP008706.1	2358676	2360550	-	WP_001010619.1	aminochrysidase	403.0680616	1722886017	0.203934606	8	8.22693749	1.92E-17	1.44E-15	14.84231433
ABLW_RS01750	ABLW_0357	NZ_CP008706.1	380432	380740	+	WP_000457408.1	hypothetical protein	96.23866246	171548825	0.368760007	4	4.148347031	1.01E-05	2.70E-05	4.569800356
ABLW_RS01300	ABLW_1684	NZ_CP008706.1	1678380	1680237	-	WP_000017859.1	iron-containing alcohol dehydrogenase	445.2221516	1708678343	0.14878193	11	1148449525	1.58E-30	3.12E-29	28.50617541
ABLW_RS19315	ABLW_2868	NZ_CP008706.1	2877568	2878777	+	WP_000566025.1	META and DUF4377 domain-containing protein	9392.94382	1704415369	0.22912637	7	7.438910568	1.02E-13	6.14E-12	11.2711995
ABLW_RS14760	ABLW_3041	NZ_CP008706.1	3067141	3068559	-	WP_001102848.1	phosphononmannosyl-phosphoglucomutase	2323.972996	1702580123	0.31821894	11	1106810045	1.79E-28	3.9E-27	26.4971921
ABLW_RS14460	ABLW_2878	NZ_CP008706.1	295619	2956326	-	WP_001193533.1	DUF1975 domain-containing protein	47.50594831	1693502954	0.315453373	5	5.420018162	5.96E-08	2.03E-07	6.692259243
ABLW_RS14900	ABLW_2778	NZ_CP008706.1	2771867	2772506	+	WP_002040868.1	p-hydroxycinnamoyl-CoA hydratase/lyase	2146.63844	1686271168	0.27758439	6	6.068819723	1.29E-09	5.23E-09	8.282017601
ABLW_RS02190	no	no	no	no	no	no	no	3173.757184	1679618066	1.164450848	1	1.465058944	0.162904837	0.930399504	7.03067676
ABLW_RS07895	ABLW_1818	NZ_CP008706.1	1811128	1811843	-	WP_000774022.1	ethanolamine ammonia-lyase subunit EutC	125.9156749	1672522023	0.25765895	6	6.49224249	8.81E-11	3.92E-10	9.406868801
ABLW_RS01875	ABLW_0203	NZ_CP008706.1	1234946	1241825	+	WP_000905544.1	Mit family metalloprotease	918.060745	1665577711	0.22741724	7	7.323885009	2.41E-13	1.40E-12	11.85245637
ABLW_RS10255	ABLW_2785	NZ_CP008706.1	2775666	2781517	+	WP_001100029.1	laminase/fenylolase family alpha-beta hydrolase	148.1930492	1661641639	0.32011191	5	5.9763629	2.08E-07	6.68E-07	6.176425054
ABLW_RS16330	ABLW_3807	NZ_CP008706.1	3868042	38691											

ABLUW_RS00045	ABLUW_0009	NZ_CP008706.1	1106	12133	+	WP_000724996.1		hypothetical protein	6087.483227	154.028034	0.21800024	7.034596819	2.00E-12	1.08E-11	10.96802626
ABLUW_RS04360	ABLUW_0889	NZ_CP008706.1	885766	886095	+	WP_00066539.1		MGMT family protein	172.5077069	1539776361	0.24410933	6.307639448	2.83E-10	1.23E-09	8.908662126
ABLUW_RS00116	ABLUW_0023	NZ_CP008706.1	27176	27319	+	WP_000597630.1		methionine/alanine import family NES transporter small subunit	778.9276026	1534950451	0.18779659	8.15765621	3.04E-16	2.23E-15	14.65087933
ABLUW_RS14515	ABLUW_2989	NZ_CP008706.1	3007583	3008627	+	WP_0005050879.1		dihydrodipicolinate synthase family protein	48.6902462	153180205	0.36854685	4.45643197	3.26E-05	8.20E-05	4.086265198
ABLUW_RS17395	ABLUW_3574	NZ_CP008706.1	3632392	3633763	-	WP_0001910211		GNAT family N-acetyltransferase	748.0260994	1530882092	0.21007393	7.218636094	5.25E-13	2.96E-12	11.52883379
ABLUW_RS17320	ABLUW_3238	NZ_CP008706.1	326780	3268406	-	WP_0002000136.1		CoxA pyrophosphatase	816.7795029	152761837	0.209370784	7.29623407	2.96E-13	1.71E-12	11.76806629
ABLUW_RS19340	ABLUW_4968	NZ_CP008707.1	40571	40885	+	WP_00070874.1		hypothetical protein	53.1146116	1525882272	0.586520586	2.683932544	0.00727543	0.019695046	1.887225927
ABLUW_RS08180	ABLUW_875	NZ_CP008706.1	867840	8689231	+	WP_000102116.1		3-oxoacyl-ACP reductase	910.570218	1525361081	0.182104977	8.37399854	5.48E-17	4.37E-16	15.35962512
ABLUW_RS01862	ABLUW_862	NZ_CP008706.1	855844	855869	+	WP_00056937.1		aromatic-rh-g-hydroxylating dioxygenase subunit beta	714.8232945	151191604	0.1465529	3.644417579	0.000267998	0.000589069	3.229833645
ABLUW_RS01615	ABLUW_0205	NZ_CP008706.1	230706	231880	-	WP_000912176.1		LyxR family transcriptional regulator	558.8023826	150688693	0.154016715	9.784630948	1.13E-22	1.60E-21	20.7871889
ABLUW_RS19340	ABLUW_2739	NZ_CP008706.1	2728502	2728927	-	WP_0001626236.1		GNAT family N-acetyltransferase	2316.18286	1506798006	0.208264895	7.235007147	4.66E-13	2.64E-12	11.51870708
ABLUW_RS05450	ABLUW_1114	NZ_CP008706.1	113350	1134909	+	WP_0003833010.1		amino acid permease	1396.508443	150580102	0.268027318	5.161808874	1.93E-08	6.95E-08	7.16793131
ABLUW_RS19900	no	NZ_CP008706.1	2843929	2844051	+			glutathione S-transferase	1413323059	1504008627	0.226076537	6.652923411	2.87E-11	1.38E-10	9.859198444
ABLUW_RS19340	ABLUW_2106	NZ_CP008706.1	210072	2102030	-	WP_0006442315.1		2,3-butanediol dehydrogenase	837.2140566	1496555161	0.225867508	6.625809859	3.45E-11	1.64E-10	9.783914292
ABLUW_RS12895	no	NZ_CP008706.1	2653604	2654148	-			hypothetical protein	34.27594609	1496308808	0.387729462	3.859156851	0.00010779	0.000264674	3.577288901
ABLUW_RS19170	ABLUW_1304	NZ_CP008706.1	314782	3145975	-	WP_0001992131.1		MFS transporter	835.9160838	1487181732	0.267186893	5.566868823	2.59E-08	9.24E-08	7.034360548
ABLUW_RS03730	ABLUW_603	NZ_CP008706.1	489909	490016	+	WP_000791069.1		membrane integrity-associated transporter subunit PgC	656.8022025	1486391655	0.1748641	8.500264254	1.89E-17	1.57E-16	16.80281973
ABLUW_RS07905	ABLUW_820	NZ_CP008706.1	813636	814792	-	WP_0001705439.1	eat	ethanolamine permease	85.25975536	1485530529	0.346550044	4.285418009	1.62E-05	4.72E-05	4.336208965
ABLUW_RS16760	ABLUW_890	NZ_CP008706.1	890470	893190	+	WP_000109432.1		outer membrane protein assembly factor	3874.665882	1484463268	0.155928655	0.92081977	8.17E-38	1.55E-26	25.80917762
ABLUW_RS16450	ABLUW_3395	NZ_CP008706.1	3423495	3425676	-	WP_0001769302.1		carboxy-terminal processing peptidase	10534.4189	1479941694	0.146652465	0.10914687	6.02E-24	7.96E-23	22.00772812
ABLUW_RS18835	ABLUW_2432	NZ_CP008706.1	2420572	2420808	-	WP_0007365915.1		hypothetical protein	219.5339958	1478344644	0.285353307	5.107581025	2.21E-07	7.05E-07	6.1514336
ABLUW_RS16440	ABLUW_3383	NZ_CP008706.1	3421482	3422003	-			phosphatase PAP2 family protein	303.0802445	1477147783	0.251699261	5.046605327	1.64E-08	5.92E-08	7.277780081
ABLUW_RS02240	no	NZ_CP008706.1	2508189	2508305	+	WP_000514392.1		hypothetical protein	198.0471592	1475771888	0.430389809	3.358604832	0.000783143	0.001030038	2.71674247
ABLUW_RS07180	ABLUW_1645	NZ_CP008706.1	1645499	16454296	+	WP_0001028165.1		amino acid permease	6115931751	1474693859	0.255392328	5.707189016	1.15E-08	4.23E-08	7.373661787
ABLUW_RS18715	ABLUW_3658	NZ_CP008706.1	3717569	3719365	+	WP_0001041958.1		hypothetical protein	2025.442237	1472775689	0.191429131	7.693581845	1.43E-14	9.28E-14	13.03233394
ABLUW_RS17615	ABLUW_2214	NZ_CP008706.1	2200933	2201439	-	WP_0001038826.1	naA	ribonuclease E activity regulator RnaA	1700.377994	1469344482	0.18806656	7.812980646	5.59E-15	3.74E-14	13.02717529
ABLUW_RS18400	ABLUW_3779	NZ_CP008706.1	3839273	3840046	-	WP_0001886911		enoyl-CoA hydratase	234.409076	1468035481	0.310375012	4.681495468	2.81E-06	7.96E-06	5.099232923
ABLUW_RS18400	ABLUW_3351	NZ_CP008706.1	3387175	3388038	-	WP_0000377364.1		hypothetical protein	980.7425242	1467377355	0.400473498	3.66391868	0.000248325	0.000549193	3.260330572
ABLUW_RS08505	ABLUW_1764	NZ_CP008706.1	17614	1763507	-	WP_0002031491.1		GGDase domain-containing protein	967.1298172	1466390474	0.189919006	7.71215977	1.16E-14	7.52E-14	13.1297143
ABLUW_RS12000	ABLUW_2656	NZ_CP008706.1	2651223	2654996	-	WP_0002309934.1		DUF4882 family protein	375.14818	145516039	0.216222284	6.794265643	1.08E-11	4.54E-11	10.28750304
ABLUW_RS16090	ABLUW_2078	NZ_CP008706.1	2054065	2060097	-	WP_0000976581.1	modB	mycylate ABC transporter permease subunit	68.9416177	1453280963	0.250319329	5.845626205	5.04E-09	1.92E-06	7.71667679
ABLUW_RS16090	ABLUW_832	NZ_CP008706.1	827946	828599	+	WP_0001002179.1		CoA transferase subunit B	94.29694727	145045194	0.330274047	4.421862697	9.78E-06	2.81E-05	4.582017875
ABLUW_RS07090	ABLUW_1435	NZ_CP008706.1	1446735	1447818	-	WP_0001001808.1		ATP-binding protein	531.6085288	1448014927	0.195929236	7.451748124	9.21E-14	5.61E-13	12.25088396
ABLUW_RS16475	ABLUW_848	NZ_CP008706.1	847325	848785	+	WP_000063670.1	isaH	indoleacetamide hydrolase	97.1636057	1435125116	0.25418238	5.724728913	1.04E-08	3.83E-08	7.417277673
ABLUW_RS16440	ABLUW_2474	NZ_CP008706.1	2468141	2468422	-	WP_0000850368.1		nitrate monooxygenase	226.6071258	145434086	0.242164617	0.005587793	1.91E-09	7.54E-09	8.122762895
ABLUW_RS03230	ABLUW_0656	NZ_CP008706.1	663238	663669	+	WP_000022555.1	mscL	gate conductance channel-associated channel protein MscL	4212.464846	1453801635	0.19719961	8.510710911	1.66E-17	1.39E-16	15.88502966
ABLUW_RS00019	ABLUW_0184	NZ_CP008706.1	104004	2001319	+	WP_000087185.1		carbon acetate symporter	3826.19546	144981921	0.362096023	4.00161924	6.29E-05	0.000191213	3.820241113
ABLUW_RS03595	ABLUW_0730	NZ_CP008706.1	736530	737423	-	WP_0001888885.1		AraC family transcriptional regulator	405.912333	144889996	0.16070937	9.192407719	7.08E-22	8.12E-21	20.0901667
ABLUW_RS18375	ABLUW_2795	NZ_CP008706.1	2793499	2793837	-	WP_0000711211		hypothetical protein	37.7325294	1446676722	0.581918658	2.486046293	0.010291116	0.02196622	1657651909
ABLUW_RS05445	ABLUW_1167	NZ_CP008706.1	1163382	11632757	-	WP_0001076822.1	xshB	xanthine dehydrogenase molybdopter binding subunit	366.271051	1444448756	0.197588238	7.300412525	2.87E-13	1.66E-12	11.77971407
ABLUW_RS18165	ABLUW_2803	NZ_CP008706.1	2807703	2802473	+	WP_0001041177.1		nuclear transport factor 2 family protein	1259.732836	1443510891	0.322603646	4.44747059	7.66E-06	2.07E-05	4.684256887
ABLUW_RS02180	ABLUW_1918	NZ_CP008706.1	1917241	1917381	-	WP_000770264.1		hypothetical protein	87.0192377	1442696937	0.43681954	3.302744981	0.000957434	0.001978206	2.703273425
ABLUW_RS02180	ABLUW_0386	NZ_CP008706.1	307638	3080093	+	WP_000101667.1		hypothetical protein	784.5427279	1440416069	0.359319727	4.00882846	6.11E-05	0.000146865	3.833080851
ABLUW_RS18025	ABLUW_3806	NZ_CP008706.1	3805348	3808042	-	WP_0001393583.1	acnD	Fe/S-dependent 2-methylglutamate dehydratase AcnD	45007.353954	1439078267	0.298589201	4.819592484	1.44E-06	4.22E-06	5.375192063
ABLUW_RS17615	no	NZ_CP008706.1	2628331	2628676	-			SAL domain-containing protein	68.16964	1436887037	0.23343716	6.025640188	1.68E-09	6.71E-09	8.1739146
ABLUW_RS06885	ABLUW_030	NZ_CP008706.1	1862207	1863475	-	WP_0001652957.1		Mg/Ca/SigB family protein	216.0618863	1435238956	0.231669132	6.16521412	5.82E-10	2.43E-09	8.61832455
ABLUW_RS01380	no	NZ_CP008706.1	1498801	1499580	+	WP_000149738.1		DUF1295 domain-containing protein	97.1604677	1430192284	0.300977617	4.73181428	2.02E-06	5.85E-06	5.233208909
ABLUW_RS16760	ABLUW_2464	NZ_CP008706.1	2465665	2467318	+	WP_000106039.1		3-oxoacyl-CoA transferase subunit B	74.4200576	1427907125	0.29318601	4.87031252	1.1E-06	3.32E-06	5.149448137
ABLUW_RS02225	ABLUW_0459	NZ_CP008706.1	47117	471860	-	WP_0000201647.1		DUF3108 domain-containing protein	13918.93503	1421015971	0.193426452	10.19251333	2.14E-24	2.92E-23	22.53389694
ABLUW_RS16875	ABLUW_3269	NZ_CP008706.1	3269425	3301322	-	WP_0000276867.1		DUF2339 domain-containing protein	2260.401498	1416628738	0.10088289	10.8379954	2.27E-27	3.79E-26	25.42182927
ABLUW_RS08190	ABLUW_1831	NZ_CP008706.1	1827256	1827927	-	WP_0005606027.1		3-oxoacyl-CoA transferase subunit A	93.0885272	141849879	0.31878618	4.452766893	8.48E-06	2.28E-05	4.641258496
ABLUW_RS00090	ABLUW_0162	NZ_CP008706.1	177676	21819	+	WP_000058168.1		DUF104 domain-containing protein	93.2808992	1416264379	0.247857188	5.72619154	1.03E-08	3.80E-08	7.42047756
ABLUW_RS10235	ABLUW_2883	NZ_CP008706.1	2878274	2876408	+	WP_0006418020.1		MFS transporter	64.1727819	1416480701	0.386580094	3.664126847	0.000248184	0.000549193	3.260333295
ABLUW_RS18375	ABLUW_3706	NZ_CP008706.1	3764885	3765470	+	WP_0001008177.1		DUF2338 domain-containing protein	59.2599375	141533263	0.355604611	3.980077384	6.89E-05	0.00014683	3.782964365
ABLUW_RS03175	ABLUW_0645	NZ_CP008706.1	651978	651431	-	WP_0004517783.1		guanylate ammonium transporter	132.151407	1416053562	0.314227391	4.503278919	6.69E-06	1.83E-05	4.738672898
ABLUW_RS19175	ABLUW_2702	NZ_CP008706.1	2686206	2688633	+	WP_000980459.1		hypothetical protein	90.167281	1412954201	0.422036881	3.347842483	0.00081939	0.001932532	2.71457192
ABLUW_RS19160	ABLUW_3729	NZ_CP008706.1	3787561	3788196	+	WP_000194680.1		glutathione peroxidase	3340.40201	1410432549	0.209398173	6.14935638	1.53E-11	7.41E-11	10.2569723
ABLUW_RS18995	ABLUW_2404	NZ_CP008706.1	2391629	2392222	-	WP_000006033.1		GNAT family N-acetyltransferase	230.084805	1410161468	0.19145161	7.369744877	1.71E-13	1.02E-12	11.99131626
ABLUW_RS191															

ABUW_RS0650	ABUW_291	NZ_CP008706.1	216421	216723	+	WP_00198575.1		hythopetial protein	532.5213793	1.31817476	0.267527727	4.903482317	9.426-07	2.826-06	5.54696392
ABUW_RS0305	ABUW_382	NZ_CP008706.1	3193003	3193646	+	WP_000047790.1		MFS transporter	530.9016642	1.307498668	0.290365703	4.50239769	6.706-06	1.836-05	4.738269254
ABUW_RS0760	ABUW_210	NZ_CP008706.1	2200126	2200908	-	WP_000592589.1		glutathione S-transferase N-terminal domain-containing pro	366.584102	1.306371058	0.148085307	8.821748666	1.10E-08	1.02E-17	6.99031692
ABUW_RS0330	ABUW_174	NZ_CP008706.1	253419	2534995	+	NZ_CP00932294.1		aldehyde dehydrogenase (NAD(P)+)	89.3306006	1.306216193	0.27614471	4.730165497	2.24E-06	6.46E-06	5.8971977
ABUW_RS0070	ABUW_8077	NZ_CP008706.1	9072032	9074911	+	WP_000588779.1		serine hydrolase	857.8575919	1.304661167	0.197097605	8.306252362	9.88E-17	7.58E-16	5.0322977
ABUW_RS0345	ABUW_981	NZ_CP008706.1	986868	987577	+	WP_000377262.1		hythopetial protein	924.283302	1.301655981	0.196051938	6.6404137	3.10E-11	1.50E-10	9.82464261
ABUW_RS0725	ABUW_3846	NZ_CP008706.1	3914859	3914746	-	WP_000737570.1		flavin disulfide interchange protein DdaA/DaL	7995.68479	1.299431891	0.23484722	5.7791976	7.9E-09	2.82E-08	7.54991856
ABUW_RS0240	ABUW_3343	NZ_CP008706.1	3376884	3377493	+	WP_000558782.1		hythopetial protein	447.0977319	1.297162267	0.347490365	3.73378601	0.000188623	0.000423897	3.372740045
ABUW_RS0570	ABUW_102	NZ_CP008706.1	920879	920826	+	WP_001223581.1	bauC	ric acetylcholin ABC transporter permease subunit Ba	41.7618632	1.292274511	0.543879109	2.736074811	0.017497916	0.029019575	1.537422709
ABUW_RS0350	ABUW_2541	NZ_CP008706.1	2531691	2532362	+	WP_000203777.1		APC family permease	9198001097	1.291289795	0.28309626	4.561009977	5.08E-06	1.40E-05	4.852988752
ABUW_RS0445	ABUW_0190	NZ_CP008706.1	903722	905053	-	WP_001986541.1		MFS transporter	3451134625	1.285690017	0.220878524	5.820801379	5.86E-09	2.22E-08	7.6540978
ABUW_RS0505	ABUW_3366	NZ_CP008706.1	3434882	3441626	+	WP_001502295.1	pta	phosphatase acetyltransferase	106.173529	1.284416158	0.251559383	5.95810298	3.29E-07	1.03E-06	5.985338271
ABUW_RS0485	ABUW_2777	NZ_CP008706.1	2770187	2771419	-	WP_000411716.1	mhpT	3-(3-hydroxy-phenyl)propionate transporter MhpT	107.681282	1.284085892	0.284445788	4.51434345	6.35E-06	1.73E-05	4.760730002
ABUW_RS0470	ABUW_2888	NZ_CP008706.1	2905472	2906917	-	WP_000479778.1		capsule assembly Wzi family protein	7378.623707	1.282285417	0.194861748	6.936456187	4.02E-12	2.11E-11	6.67644051
ABUW_RS0574	ABUW_1076	NZ_CP008706.1	1023660	1023568	+	WP_001014131.1	baaB	siderophore-binding periplasmic lipoprotein BaaB	238.2229561	1.281779323	0.327850297	3.909648192	9.24E-05	0.000217271	3.662997602
ABUW_RS0585	ABUW_182	NZ_CP008706.1	1188482	1189510	-	WP_000868943.1		hythopetial protein	4.85995034	1.281708421	0.218962455	5.907512534	3.47E-09	1.35E-08	7.67098601
ABUW_RS0965	ABUW_3287	NZ_CP008706.1	331966	3320394	+	WP_000954162.1		DedA family protein	93.21776723	1.278572824	0.203686089	6.277173012	3.45E-10	1.48E-09	8.82894767
ABUW_RS0216	no	NZ_CP008706.1	2044647	2053038	-			TeR/AuR family transcriptional regulator	134.5420867	1.27619710	0.47902368	2.66424484	0.007718639	0.01066408	1.06441966
ABUW_RS02390	ABUW_0487	NZ_CP008706.1	499163	500320	+	WP_000673016.1		acyl-CoA dehydrogenase family protein	363.1200255	1.275405376	0.27103723	4.703971754	2.59E-06	7.29E-06	9.57228719
ABUW_RS0655	ABUW_3486	NZ_CP008706.1	3534387	3536733	+	WP_000073358.1	abeM	multidrug efflux MATE transporter AbeM	686.78869	1.274987803	0.221294235	5.76701595	8.32E-09	3.16E-08	7.50870462
ABUW_RS0350	ABUW_0711	NZ_CP008706.1	77192	771700	-	WP_000303736.1		DU-1/PP1 family protein	750.1525465	1.274102031	0.197908669	7.1026921	1.16E-12	6.20E-12	11.0364607
ABUW_RS0240	ABUW_0052	NZ_CP008706.1	51715	51842	-	WP_000100767.1		detonectone hydrolase family protein	902.252445	1.273214749	0.24166472	5.277251617	1.31E-07	4.27E-07	6.36919005
ABUW_RS0465	ABUW_3018	NZ_CP008706.1	3044022	3044007	-	WP_001542911.1	ggt	gamma-glutamyltransferase	449.0713353	1.272803766	0.249991667	5.099544301	3.40E-07	1.07E-06	5.91762432
ABUW_RS0790	ABUW_3574	NZ_CP008706.1	3632075	3632347	+	WP_000207121.1	fadA	acyl-CoA-C4 acyltransferase FadA	5429.80059	1.272225541	0.241621884	5.27842658	1.30E-07	4.23E-07	6.371206124
ABUW_RS0515	ABUW_058	NZ_CP008706.1	601730	601836	-	WP_000555193.1		nitronate monooxygenase	663.2602768	1.27061189	0.20676032	6.14273595	8.11E-10	3.34E-09	8.47588562
ABUW_RS0450	ABUW_3181	NZ_CP008706.1	3208842	3209558	-	WP_000107640.1	bfnR	response regulator transcription factor BfnR	1212.02799	1.264102903	0.224702288	5.62810076	1.86E-08	6.66E-08	7.17653536
ABUW_RS0710	ABUW_0511	NZ_CP008706.1	4468784	4471575	+	WP_000292586.1		DUF065 domain-containing protein	31.0395807	1.264003544	0.33808117	3.73875818	0.000184932	0.000417967	3.38059351
ABUW_RS0230	no	NZ_CP008706.1	3870899	3871033	+			hythopetial protein	5.51458729	1.262052426	0.360027674	1.328437541	0.84033605	0.242073866	0.60052597
ABUW_RS0880	ABUW_2654	NZ_CP008706.1	261056	2612094	+	WP_000407345.1		hythopetial protein	124.618945	1.26069257	0.339955229	3.70842732	0.000208551	0.000466029	3.3158722
ABUW_RS0330	ABUW_0368	NZ_CP008706.1	101130	101915	-	WP_000367670.1		DUF362 domain-containing protein	252.0192526	1.260253779	0.194918995	6.46552572	1.01E-10	4.60E-10	9.27631592
ABUW_RS0060	ABUW_2077	NZ_CP008706.1	205777	2053852	-	WP_000202696.1	ppk1	polyphosphatase kinase 1	1455.564746	1.258718668	0.209630695	5.995757234	2.03E-09	7.99E-09	8.89731841
ABUW_RS0935	ABUW_0208	NZ_CP008706.1	824553	825230	-	WP_000366882.1		DUF421 domain-containing protein	837.842101	1.256835925	0.22617752	5.555971805	2.79E-08	9.82E-08	7.00877176
ABUW_RS0840	ABUW_837	NZ_CP008706.1	833377	833790	+	WP_000997505.1	pcdA	4-carboxymuconolactone decarboxylase	56.0108362	1.256175725	0.303568876	4.109733586	3.96E-05	9.84E-05	4.007208623
ABUW_RS0570	ABUW_1076	NZ_CP008706.1	1020021	1020733	-	WP_000717766.1	basC	putative histamine N-monooxygenase	110.0105642	1.255690029	0.300195491	4.933047042	2.88E-05	7.27E-05	4.51875707
ABUW_RS0240	ABUW_0456	NZ_CP008706.1	468138	468565	-	WP_000893466.1		YRY family inner membrane protein	1434.719714	1.254688891	0.127710595	9.450015406	3.39E-21	3.75E-20	9.42588528
ABUW_RS0430	ABUW_005	NZ_CP008706.1	619738	620053	-	WP_000109102.1		NFS 1	843.1942831	1.254013937	0.155207166	8.079777707	6.49E-16	4.59E-15	14.33853368
ABUW_RS0200	ABUW_2063	NZ_CP008706.1	2044222	2045809	-	WP_000582742.1		uracil-DNA glycosylase family protein	258.6883308	1.25148188	0.246601965	5.074005544	3.88E-07	12.1E-06	5.91740191
ABUW_RS0515	ABUW_076	NZ_CP008706.1	669306	671016	+	WP_001507352.1		hythopetial protein	503.748639	1.250410259	0.15885422	8.02104829	1.05E-15	7.23E-15	14.1088884
ABUW_RS0425	ABUW_0822	NZ_CP008706.1	779195	779386	-	WP_000397562.1	Ndc family protein	2194.789324	1.245388882	0.16243967	1.02730292	5.25E-34	1.9E-32	3.192292879	
ABUW_RS0160	ABUW_2292	NZ_CP008706.1	2272329	2278829	+	WP_00181972.1		lectin histidine acyltransferase family protein	438.235189	1.245089568	0.276806688	4.49799885	6.86E-06	1.87E-05	4.72905567
ABUW_RS0360	ABUW_0980	NZ_CP008706.1	985828	986901	+	WP_001508628.1		FAD-binding oxidoreductase	120.101716	1.244110757	0.193061507	6.240474734	4.36E-10	1.85E-09	8.73370936
ABUW_RS0285	ABUW_0485	NZ_CP008706.1	477246	477819	+	WP_000792527.1		lytic transglycosylase domain-containing protein	2985.96109	1.239320492	0.11945398	10.92422884	8.83E-28	1.50E-26	25.8236361
ABUW_RS0685	ABUW_3181	NZ_CP008706.1	388217	3883979	+	WP_000686101.1		UDP-glucose/GDP-mannose dehydrogenase family protein	540.171826	1.238170603	0.19180423	8.94164266	2.52E-16	1.88E-15	14.726706
ABUW_RS0785	ABUW_2474	NZ_CP008706.1	248195	2481992	+	WP_000991611.1		hythopetial protein	124.5089825	1.237014623	0.321993783	3.84937898	0.000212047	0.00028938	3.55000973
ABUW_RS0120	ABUW_3937	NZ_CP008706.1	372419	3727398	-	WP_001505051.1	cjdB	ATP-dependent chaperone CjdB	14.8719993	1.236910802	0.194303894	3.946031035	1.61E-10	7.19E-10	9.43378159
ABUW_RS0145	ABUW_0274	NZ_CP008706.1	292407	293291	+	WP_001866587.1		hythopetial protein	147.1762873	1.23305874	0.24445806	5.04218674	4.60E-07	1.42E-06	5.84691391
ABUW_RS0716	ABUW_2619	NZ_CP008706.1	261733	261980	+	WP_000217666.1		serine hydrolase	411.014839	1.229195612	0.148852694	8.370106419	5.76E-17	4.50E-16	5.34057243
ABUW_RS0160	ABUW_2497	NZ_CP008706.1	249332	2494349	-	WP_001210565.1		LLM class flavin-dependent oxidoreductase	82.0183624	1.228388045	0.240318268	5.11050071	3.20E-07	1.01E-06	5.997402882
ABUW_RS0425	ABUW_2939	NZ_CP008706.1	2952819	2954117	+	WP_000371878.1		MFS transporter	282.8430433	1.226632245	0.236227392	5.92591062	2.07E-07	6.65E-07	6.17700054
ABUW_RS0465	ABUW_0951	NZ_CP008706.1	959594	961000	+	WP_000107081.1		amino acid permease	5173.800192	1.225621643	0.162090248	7.561052744	3.99E-14	2.50E-13	12.60210093
ABUW_RS0840	ABUW_070	NZ_CP008706.1	710372	714207	+	WP_000100207.1		molibdopter molibdoxyltransferase MoeA	838.2678515	1.22361184	0.110604328	11.06323069	1.89E-28	3.34E-27	26.47591003
ABUW_RS0650	ABUW_0559	NZ_CP008706.1	856269	856628	+	WP_000387550.1		hythopetial protein	559.554375	1.220629984	0.15715621	2.360291833	0.01260564	0.03023913	15.9430664
ABUW_RS0240	ABUW_0485	NZ_CP008706.1	496585	497496	+	WP_001051938.1		SDR family oxidoreductase	34.9988263	1.220598472	0.351490166	3.472639237	0.000516388	0.01099631	2.960065591
ABUW_RS0465	ABUW_0663	NZ_CP008706.1	656820	655993	+	WP_001139332.1		hythopetial protein	37.2054944	1.220299233	0.430274633	2.777887029	0.00546968	0.01021529	1.99906063
ABUW_RS0740	ABUW_0968	NZ_CP008706.1	976340	977419	-	WP_000215801.1		ABC transporter permease	484.5023319	1.21996661	0.17782781	6.863555673	6.72E-12	3.44E-11	10.46381938
ABUW_RS0191	no	NZ_CP008706.1	256702	267188	-			RimM-like type II domain-containing protein	552.319222	1.215862823	0.13506656	6.53019475	1.44E-17	12.1E-16	9.51643632
ABUW_RS0675	ABUW_159	NZ_CP008706.1	118650	1187407	+	WP_000217886.1		TeR/AuR family transcriptional regulator	167.4533435	1.21542419	0.342354542	3.55019133	0.000394951	0.00028938	3.08190268
ABUW_RS0970	ABUW_431	NZ_CP008706.1	121357	1213880	+	WP_000673007.1		hythopetial protein	2.16141204	1.213443829	0.220740899	5.497140911	3.86E-08	1.35E-07	6.87042319
ABUW_RS0715	ABUW_3450														

ABLUW_RS0095	ABLUW_2079	NZ_CP008706.1	2060094	2060879	-	WP_000253153.1	modA	molybdate ABC transporter substrate-binding protein	243.529599	146943187	0.181228959	6.328697306	2.47E-10	1.08E-09	8.964999701
ABLUW_RS1400	ABLUW_2986	NZ_CP008706.1	3004830	3005846	-	WP_001420504.1		FecR domain-containing protein	37.8729989	14636573	0.46623536	2.45458992	0.0104849	0.02827438	16.22922661
ABLUW_RS02360	ABLUW_0480	NZ_CP008706.1	492078	492461	+	WP_000898414.1		DUF4256 domain-containing protein	222.22939.5	144287466	0.29412184	3.890384966	0.000100085	0.00023458	3.629708249
ABLUW_RS04215	ABLUW_0859	NZ_CP008706.1	838466	839999	-	WP_000626045.1		hypothetical protein	2200.79021	143222187	0.10360682	7.63379301	2.89E-4	1.82E-10	12.73887783
ABLUW_RS07195	ABLUW_822	NZ_CP008706.1	916569	917959	+	WP_004934374.1		transcriptional regulator	784.18877.5	143150997	0.139883555	8.96512306	3.7E-16	2.33E-10	14.63350575
ABLUW_RS04195	ABLUW_0369	NZ_CP008706.1	392186	393378	+	WP_001823776.1		putative DNA modification/repair codal SAM protein	430.429333	110978687	0.1846597	7.98790675	6.54E-13	3.66E-12	11.6377203
ABLUW_RS04580	ABLUW_0927	NZ_CP008706.1	936373	936956	+	WP_001019719.1		SCP2 steric-binding domain-containing protein	4098.045421	1108768224	0.18771807	7.04186644	1.9E-12	1.03E-11	10.98770064
ABLUW_RS18790	ABLUW_2219	NZ_CP008706.1	2204612	2204980	+	WP_000978740.1		hypothetical protein	67.64746433	1108677768	0.30098912	3.793077795	0.000148792	0.000339265	3.484840763
ABLUW_RS05200	ABLUW_1019	NZ_CP008706.1	1068477	1069179	-	WP_000885360.1		VIT family protein	5154338777	1108488774	0.27620854	4.075577157	4.55E-05	0.00018604	3.952320596
ABLUW_RS04750	ABLUW_0968	NZ_CP008706.1	978617	980104	-	WP_001042047.1		Tox family protein	997.006678	1108297164	0.172064384	6.05530075	3.70E-11	1.75E-10	9.755758609
ABLUW_RS02945	ABLUW_0599	NZ_CP008706.1	597328	598952	-	WP_001186846.1		DUF4184 family protein	225.2289896	1106214027	0.181219795	7.051645194	1.77E-12	9.58E-12	11.0854526
ABLUW_RS18250	ABLUW_3749	NZ_CP008706.1	3805847	3806515	-	WP_000626445.1		glutathione S-transferase	939.016993	1105154385	0.151604523	7.487602232	7.0E-14	4.33E-11	12.36373019
rRNA8		no	no	no	no	no	no		377.831004	1103821969	0.266026338	4.26209324	2.03E-05	5.20E-05	4.28395887
ABLUW_RS18405	ABLUW_3780	NZ_CP008706.1	3840088	3841195	-	WP_001160766.1		acyl-CoA dehydrogenase family protein	643.9599498	1103238559	0.312565616	3.625602111	0.000288289	0.000633229	3.99088389
ABLUW_RS02195	ABLUW_0439	NZ_CP008706.1	451386	451952	+	WP_000651536.1	mtA	thombosase	466.7476473	110180434	0.24718642	8.78329241	4.69E-06	1.30E-05	4.885870173
ABLUW_RS10770	ABLUW_3288	NZ_CP008706.1	3320447	3321067	-	WP_000566579.1		glutathione S-transferase N-terminal domain-containing protein	630.7528837	1102787968	0.95249998	6.825205149	8.77E-12	4.42E-11	10.35402848
ABLUW_RS16915	ABLUW_2318	NZ_CP008706.1	2302706	2304121	+	WP_000378386.1		cytosine permease	585.107479	11027319402	0.251958406	4.47778801	7.54E-06	2.04E-05	4.690480809
ABLUW_RS02150	ABLUW_0438	NZ_CP008706.1	452223	453108	+	WP_000406196.1		hypothetical protein	2001.025999	11027295102	0.238045096	4.73563686	2.8E-06	6.31E-06	5.200187378
ABLUW_RS04745	ABLUW_0967	NZ_CP008706.1	977483	978604	-	WP_001870874.1		HgO family secretion protein	93.97011975	1102543657	0.10076049	9.93720022	1.17E-20	1.25E-19	8.90432791
rRNA40		no	no	no	no	no	no		2.421947124	110055945	1.080552638	1.04188742	0.291787959	0.367018789	4.03531058
ABLUW_RS05590	ABLUW_1142	NZ_CP008706.1	166889	166895	+	WP_000380475.1		carbon starvation protein A	4232.63448	1104688485	0.302204512	3.721817471	0.000187954	0.000443579	3.535028874
ABLUW_RS07300			184160	184282	-			ADP-ribosyl phosphatase	29.4702157	11825018	0.520414576	2.80689289	0.031000713	0.0490813	1301828704
ABLUW_RS08830	ABLUW_1815	NZ_CP008706.1	181086	181228	+	WP_001886163.1		YnfA family protein	695.407039	118288253	0.206461004	5.164478192	6.08E-08	2.06E-07	6.8853878
ABLUW_RS04320	ABLUW_0882	NZ_CP008706.1	863355	864278	+	WP_000146247.1		DUF808 domain-containing protein	4600.802344	117800477	0.10008996	6.918933066	2.9E-12	1.54E-11	10.1160573
ABLUW_RS02440	ABLUW_0778	NZ_CP008706.1	764737	764889	+	WP_001291449.1		hypothetical protein	3.937277258	1107516325	0.996925642	1.1202275	0.262278179	0.30327847	0.481058144
ABLUW_RS05805	ABLUW_1889	NZ_CP008706.1	192702	192749	-	WP_000498089.1		nuvren L.D. transpeptidase	6105.047398	118603891	0.10843317	6.888907472	4.65E-23	5.82E-22	21.23539631
ABLUW_RS18710	ABLUW_2080	NZ_CP008706.1	2061070	2061240	-	WP_000664114.1		LyfR family transcriptional regulator	30.40782222	1105180291	0.384787212	2.888173693	0.000375423	0.000778941	2.499973471
ABLUW_RS14205	ABLUW_2941	NZ_CP008706.1	295532	295712	-	WP_000140226.1		thiamine pyrophosphate-binding protein	102.9680037	110518305	0.272782578	4.082072959	4.46E-05	0.00019959	3.960227636
ABLUW_RS09195	ABLUW_1876	NZ_CP008706.1	1876085	1876378	+	WP_000897235.1	calC	muconolactone Delta-isomerase	23.0267429	110208925	0.402248277	2.764981202	0.006565068	0.0138276	19.883789
ABLUW_RS09075	ABLUW_1854	NZ_CP008706.1	1859762	1860705	+	WP_000216290.1		conduricinase	306.7263758	110262869	0.375432094	2.954677771	0.00329595	0.00579421	2.233420842
ABLUW_RS02300	ABLUW_1830	NZ_CP008706.1	185764	1857437	-	WP_000107581.1		FMN-binding glutamyl synthase family protein	9257.23301	1106660602	0.174564139	6.36562846	1.94E-10	8.63E-10	9.063387476
ABLUW_RS03100	ABLUW_0630	NZ_CP008706.1	633179	633261	+	WP_000757319.1		hypothetical protein	822.01962	1108220253	0.25631833	4.323642644	1.53E-05	4.00E-05	4.397698995
ABLUW_RS03890	ABLUW_0793	NZ_CP008706.1	773502	773801	+	WP_000333588.1		DUF4256 domain-containing protein	2287.631594	1103968557	0.176164575	6.266888736	3.89E-10	1.58E-09	8.801694009
ABLUW_RS00495	ABLUW_0191	NZ_CP008706.1	217224	217701	+	WP_001256573.1		zinc-binding dehydrogenase	914.048944	1102567185	0.21836917	5.049097189	4.44E-07	1.37E-06	5.861972073
ABLUW_RS07400	ABLUW_1516	NZ_CP008706.1	1502706	1503200	-	WP_001350280.1		chalcone isomerase family protein	37.6342894	110161534	0.462205748	2.38310601	0.01784704	0.02852576	15.48441706
ABLUW_RS08170	ABLUW_1788	NZ_CP008706.1	1783706	1784032	-	WP_000955082.1		hypothetical protein	1195.63958	1100401958	0.177008878	6.216554333	5.08E-10	2.14E-09	8.689987848
ABLUW_RS18920	ABLUW_2865	NZ_CP008706.1	2873297	2875726	+	WP_000122274.1	lon	endopeptidase La	56429.76005	1107731635	0.209386474	5.242610058	1.58E-07	5.12E-07	6.280433839
ABLUW_RS05620	ABLUW_1296	NZ_CP008706.1	1314234	1314476	+	WP_000004363.1		AlpA family phage regulatory protein	65.42528158	110781079	0.262738329	4.17849439	2.94E-05	7.44E-05	4.12853275
ABLUW_RS08200	ABLUW_1833	NZ_CP008706.1	182812	1828923	+	WP_000172919.1	pcrF	3-oxoadipyl-CoA thioesterase	94.45037377	11096187403	0.329021876	3.331658705	0.000863301	0.00179108	2.74711493
ABLUW_RS03010	ABLUW_0733	NZ_CP008706.1	738688	738688	-	WP_001291625.1		AlpA family phage regulatory protein	51.4862411	11094572925	0.264924572	4.151839874	3.60E-05	9.02E-05	4.04433864
ABLUW_RS01505	ABLUW_2325	NZ_CP008706.1	2308990	2309550	+	WP_000037165.1		TeR/Acr family transcriptional regulator	124.0720834	1103186219	0.426252654	2.564643781	0.010328178	0.01705832	1.748437739
ABLUW_RS03895	ABLUW_0794	NZ_CP008706.1	773810	774288	+	WP_000271493.1		helic-tumor-helic domain-containing protein	2209.486995	1109278743	0.930886856	6.559576176	1.52E-08	5.52E-08	7.258221674
ABLUW_RS18180	ABLUW_3054	NZ_CP008706.1	3076771	3077391	+	WP_000959265.1	rhcC	threonine export protein RHC	776.0220489	1109240589	0.180413485	6.055261901	1.40E-09	5.65E-09	8.247602402
ABLUW_RS06500	ABLUW_0332	NZ_CP008706.1	943532	943761	+	WP_000178287.1		alpha-beta fold hydrolase	284.0192371	1108941291	0.207548395	5.249577002	1.52E-07	4.95E-07	6.305801932
ABLUW_RS08935	ABLUW_2028	NZ_CP008706.1	201064	2010888	-	WP_000050492.1		DUF5233 domain-containing protein	19.7398286	11088652376	0.49768327	2.87348862	0.028710566	0.048368268	13.38759919
ABLUW_RS08245	ABLUW_1833	NZ_CP008706.1	1890447	1891118	+	WP_000037356.1		iron-containing redox enzyme family protein	593.608021	11084749026	0.192220616	5.643250177	1.67E-08	6.03E-08	7.21700391
ABLUW_RS04055	ABLUW_0628	NZ_CP008706.1	605183	605827	+	WP_000165105.1		DNA-binding response regulator PmaA	583.515783	11082969516	0.128376371	4.435884495	3.29E-17	2.68E-16	15.5719747
ABLUW_RS08070	ABLUW_1823	NZ_CP008706.1	1818802	1819647	-	WP_000841963.1		metal-dependent hydrolase	164.2458559	1108282829	0.250371847	4.324808388	1.53E-05	3.98E-05	4.39985381
ABLUW_RS14085	ABLUW_2901	NZ_CP008706.1	2900451	2900888	-	WP_000444905.1		SRPBCC domain-containing protein	833.2830379	11080736846	0.217702569	4.964281564	6.90E-07	2.09E-06	5.678192427
ABLUW_RS04335	ABLUW_0986	NZ_CP008706.1	1000626	1000915	+	WP_000225971.1		DUF3106 domain-containing protein	712.1590786	11079206639	0.218165079	4.948702447	7.55E-07	2.28E-06	5.642231168
ABLUW_RS18230	ABLUW_2600	NZ_CP008706.1	2592795	2594145	+	WP_000041478.1		hypothetical protein	1115733008	11077004225	0.364382353	2.955606610	0.00319638	0.005962534	2.24565911
ABLUW_RS18330	ABLUW_2644	NZ_CP008706.1	2643212	2644768	-	WP_000927323.1		Tox family protein	318.187316	11076522402	0.187977185	6.40871807	1.47E-10	6.58E-10	9.18205844
ABLUW_RS18305	ABLUW_2121	NZ_CP008706.1	210534	2105925	+	WP_000925566.1		sulfite exporter TasE/SafE family protein	88.9635887	1107650597	0.297400809	3.619726524	0.000294915	0.000644649	3.89540257
ABLUW_RS03490	ABLUW_0709	NZ_CP008706.1	716374	716441	+	WP_000798875.1		DUF1176 domain-containing protein	528.0564702	11078291855	0.956672368	4.496709185	8.21E-11	3.79E-10	4.920997649
ABLUW_RS04325	ABLUW_0883	NZ_CP008706.1	864508	865207	+	WP_000128756.1		neutral zinc metalloproteinase	3882.693478	1107721242	0.148091676	7.243507468	4.37E-13	2.48E-12	11.60503017
ABLUW_RS01390	ABLUW_0079	NZ_CP008706.1	85188	86930	+	WP_0001081467.1		amino acid permease	2574.018251	11072027037	0.333289865	3.220312876	0.00205008	0.002191243	2.586491836
ABLUW_RS01905	ABLUW_1306	NZ_CP008706.1	133012	1330676	-	WP_000678123.1	bfr	bacterioferritin	5792.399381	1107378221	0.401554205	2.86586377	0.00768373	0.01018669	1.869592325
ABLUW_RS05290	ABLUW_1182	NZ_CP008706.1	122488	1224738	+	WP_000914201.1		DUF3015 family protein	179.0105204	11069846	0.206656001	5.176882992	2.28E-07	7.16E-07	8.143397935
ABLUW_RS18280	ABLUW_3149	NZ_CP008706.1	316728												

ABUW_RS04870	ABUW_0993	NZ_CP008706.1	1004810	1006090	-	WP_000858386.1	toIB	Tol-Pal system beta propeller repeat protein TolB	5569.546643	1.009064799	0.190424315	5.299033356	1.16E-07	3.82E-07	6.14729522
ABUW_RS06075	ABUW_1243	NZ_CP008706.1	1284655	1285656	-	WP_000951088.1	mtbB	lytic murein transglycosylase B	1049.730951	1.007725736	0.190033229	5.30289225	1.14E-07	3.75E-07	6.425747096
ABUW_RS14495	ABUW_2985	NZ_CP008706.1	3001517	3004621	-	WP_085920715.1		TonB-dependent receptor	65.87468086	1.006349242	0.267443502	3.762847982	0.000167969	0.000380455	3.419697
ABUW_RS05710	ABUW_1988	NZ_CP008706.1	1194101	1194961	-	WP_000160888.1	baufF	acinetobactin utilization protein BauF	152.351509	1.003804755	0.435443612	2.305246254	0.021527876	0.034700559	1459663525
ABUW_RS15310	ABUW_3153	NZ_CP008706.1	3179687	3180820	+	WP_001278637.1		HydY family secretion protein	484.4322916	1.003235628	0.280023891	3.582679409	0.000340088	0.000739457	3.131086986
ABUW_RS08330	ABUW_1711	NZ_CP008706.1	1711540	1712025	+	WP_001204147.1		molybdenum cofactor biosynthesis protein MoaE	560.9555076	1.00279547	0.196271545	5.10922493	3.23E-07	1.02E-06	5.992839209
ABUW_RS08930	ABUW_1835	NZ_CP008706.1	1831178	1831963	+	WP_000814773.1	pcaD	3-oxoadipate enol-lactonase	96.919347	1.001944433	0.283940102	3.528717596	0.000419758	0.000897293	3.047065885
ABUW_RS09140	ABUW_1877	NZ_CP008706.1	1876399	1877505	-	WP_001896121.1		mucronate cycloisomerase	128.5684332	1.001459325	0.247053286	4.0536167	5.04E-05	0.000122699	3.911158393

Table S20. RNA-seq data: Absolute and relative expression (TS/AT > 2-fold down)

ABUW_RS15125	ABUW_3116	NZ_CP008706.1	3135808	3186404	+	WP_000093856.1	scpB	SMC-Scp complex subunit ScpB	1880.248169	-1.001281623	0.130389758	-7.679142428	1.60E-14	1.04E-13	12.9847446
ABUW_RS01965	ABUW_0278	NZ_CP008706.1	295193	296701	-	WP_000868422.1		glutamate-1-RNA ligase	3986.287169	-1.0032276795	0.123402194	-8.130107434	4.29E-16	3.10E-15	14.508339911
rRNA1	no	no	no	no	no	no	no	no	420.2230604	-1.003925095	0.199730445	-5.02639994	5.00E-07	1.54E-06	5.819669539
ABUW_RS03865	ABUW_0788	NZ_CP008706.1	769640	769858	+	WP_001277691.1		hypothetical protein	86.3579141	-1.003942029	0.242846925	-4.137466314	3.51E-05	8.80E-05	4.055669969
ABUW_RS0355	ABUW_2751	NZ_CP008706.1	2741866	2742432	-	WP_000498534.1	mhB	ribonuclease HI	925.097271	-1.004025741	0.198765669	-5.13899928	1.04E-07	3.45E-07	6.46217816
ABUW_RS07860	ABUW_3668	NZ_CP008706.1	3726089	3726409	+	WP_000372102.1		metallorepressor AnrS/RnfB family transcription factor	341.7627471	-1.00502968	0.197463928	-5.36189705	8.27E-08	2.76E-07	6.559132445
ABUW_RS0975	ABUW_3897	NZ_CP008706.1	3964832	3965359	+	WP_000214980.1	hpt	hypoxanthine phosphoribosyltransferase	2927.398254	-1.006631326	0.160980681	-6.25318823	4.02E-10	1.72E-09	8.765645878
ABUW_RS0295	ABUW_219	NZ_CP008706.1	2103070	2103987	+	WP_001023749.1		EamA family transporter	360.071949	-1.007055356	0.236319168	-4.261420533	2.03E-05	5.21E-05	4.82320146
ABUW_RS19660	no	NZ_CP008706.1	3104611	310915	-		mpB	Rhase P RNA component class A	20781.41966	-1.007256206	0.270348682	-3.725767028	0.000194722	0.000437067	3.359451737
ABUW_RS04310	ABUW_0879	NZ_CP008706.1	860607	861538	+	WP_000270944.1		hypothetical protein	814.7530093	-1.007547973	0.124032304	-8.123270648	4.54E-16	3.28E-15	14.48458599
ABUW_RS01995	ABUW_0324	NZ_CP008706.1	346371	347312	-	WP_085916581.1		tiacylglycerol lipase	406.5285106	-1.009778777	0.25245456	-3.999843674	6.34E-05	0.0001952281	3.81735383
ABUW_RS05855	ABUW_189	NZ_CP008706.1	1237378	1234453	-	WP_000066126.1		SmeMstS family protein	1092.767785	-1.011027072	0.19579755	-6.448615246	1.10E-10	5.10E-10	9.292563229
ABUW_RS01010	ABUW_0231	NZ_CP008706.1	250130	250219	-			IRNA-Ser	922.9454877	-1.012663973	0.262912969	-3.85107949	0.000107297	0.000272072	3.565317612
ABUW_RS16945	ABUW_3283	NZ_CP008706.1	3317225	3317933	+	WP_000383959.1		hypothetical protein	1000.834856	-1.01323328	0.1818332	-5.592772592	2.23E-08	8.01E-08	7.096134109
ABUW_RS01340	ABUW_0273	NZ_CP008706.1	292197	292272	-			IRNA-Glu	1442.869217	-1.01371842	0.140989864	-2.42486832	0.0193257	0.022566389	1.590678048
ABUW_RS04445	ABUW_0906	NZ_CP008706.1	901178	901251	-			IRNA-Cys	152.543464	-1.013829736	0.265971427	-3.181199442	0.000197959	0.000315995	3.500319176
rRNA4	no	no	no	no	no	no	no	no	679.4626037	-1.015195851	0.200420961	-5.065317744	4.08E-07	1.27E-06	5.8963715312
ABUW_RS0985	ABUW_2259	NZ_CP008706.1	2244205	2245932	-	WP_001070729.1	mbA	lipid A export permease/ATP-binding protein MbA	5249.734235	-1.016280204	0.100784396	-7.770653359	7.81E-15	5.16E-14	13.8751979
ABUW_RS14050	ABUW_2893	NZ_CP008706.1	2901203	2901715	-	WP_000462919.1		hypothetical protein	623.873973	-1.01826385	0.16694857	-6.108669878	1.00E-09	4.10E-09	8.38710058
ABUW_RS07490	ABUW_1634	NZ_CP008706.1	1620409	1621251	-	WP_001003277.1		zinc-ribbon and DUF3426 domain-containing protein	115.590553	-1.018358362	0.195862621	-8.515681022	1.66E-17	1.39E-16	15.88002963
ABUW_RS06085	ABUW_1245	NZ_CP008706.1	1288947	1287597	-	WP_001157401.1		hypothetical protein	863.622666	-1.01841974	0.148724314	-6.847691205	7.51E-12	3.82E-11	10.74919814
ABUW_RS0260	ABUW_2732	NZ_CP008706.1	2719637	2720653	+	WP_000546643.1		aspartate carboxyltransferase catalytic subunit	2349.023415	-1.018965349	0.15867227	-6.143259005	8.08E-10	3.33E-09	8.477042793
ABUW_RS04425	ABUW_0902	NZ_CP008706.1	886516	888660	-	WP_032068126.1		hypothetical protein	453.788756	-1.021930328	0.240471137	-4.243686364	2.20E-05	6.62E-05	4.250192717
ABUW_RS1705	ABUW_3436	NZ_CP008706.1	3479863	3480102	-	WP_000203891.1		RNA-binding protein	440.173254	-1.021817227	0.191352751	-6.33281566	2.41E-10	1.06E-09	8.978100405
ABUW_RS17030	ABUW_3501	NZ_CP008706.1	3548268	3548879	-	WP_000248028.1		DUF1285 domain-containing protein	1007.778379	-1.021891716	0.158090061	-6.463984599	1.02E-10	4.63E-10	9.334205996
ABUW_RS0430	ABUW_2146	NZ_CP008706.1	2131186	2132310	-	WP_000486131.1		HREDC domain-containing protein	1667.638478	-1.022386051	0.185306235	-5.517278194	3.44E-08	1.21E-07	6.917062886
ABUW_RS01325	ABUW_0270	NZ_CP008706.1	290441	290779	-	WP_001200011.1		hypothetical protein	1534.960123	-1.022592242	0.154798305	-6.805665371	3.95E-11	1.87E-10	9.728778478
ABUW_RS17615	ABUW_3618	NZ_CP008706.1	3676627	3676896	+	WP_000089961.1		oxidative damage protection protein	797.0002336	-1.022863097	0.140336962	-9.803458677	1.09E-22	1.33E-21	20.87538884
ABUW_RS18515	ABUW_3805	NZ_CP008706.1	3864106	3865044	-	WP_001212195.1		hypothetical protein	782.2597383	-1.023793597	0.265184678	-3.860972758	0.00012936	0.000262866	3.580265149
ABUW_RS04455	ABUW_0908	NZ_CP008706.1	902493	903161	+	WP_001278001.1		methyltransferase	1072.794836	-1.025434592	0.198949182	-6.843118967	7.75E-12	3.94E-11	10.40483562
ABUW_RS02960	ABUW_0602	NZ_CP008706.1	602037	602483	-	WP_001290065.1		hypothetical protein	845.574442	-1.025995578	0.109743492	-10.52959836	6.31E-26	9.78E-25	24.00972508
ABUW_RS03900	ABUW_0796	NZ_CP008706.1	774559	774882	+	WP_000523931.1		DUF4238 domain-containing protein	271.9089848	-1.025993551	0.232760293	-4.407940628	1.04E-05	2.78E-05	4.556115621
ABUW_RS18435	ABUW_3057	NZ_CP008706.1	3083959	3083974	-	WP_000621543.1	rml	ribosomal protein S18-alanine N-acetyltransferase	344.2318445	-1.029933422	0.154822199	-6.652362685	2.88E-11	1.39E-10	8.854410266
ABUW_RS02030	no	NZ_CP008706.1	3378498	3378620	+	WP_001984446.1		hypothetical protein	12.31869254	-1.030626074	0.500930901	-2.057421634	0.039645686	0.061970428	1.209571607
ABUW_RS02610	ABUW_0531	NZ_CP008706.1	530609	540970	-	WP_001027022.1	secD	protein translocase subunit SecD	25153.85116	-1.032364036	0.240391857	-4.198024031	7.07E-05	3.53E-05	10.591322899
ABUW_RS07495	ABUW_1635	NZ_CP008706.1	1621205	1622170	-	WP_000871703.1	pmA	50S ribosomal protein L11methyltransferase	2958.381955	-1.033176586	0.13200701	-7.826679735	5.91E-15	3.36E-14	13.47390624
ABUW_RS05880	ABUW_1204	NZ_CP008706.1	1242291	1242875	-	WP_000925669.1		aminodeoxychromatolanthranilate synthase component	1040.84241	-1.033223354	0.191013785	-10.22853194	1.48E-24	2.04E-23	22.69070947
ABUW_RS14730	ABUW_3035	NZ_CP008706.1	3062107	3062430	-	WP_000442585.1		RnfH family protein	2366.651029	-1.033327372	0.148628894	-6.952492535	3.59E-12	1.69E-11	10.74263936
ABUW_RS01605	ABUW_0326	NZ_CP008706.1	348612	349519	+	WP_000208895.1	tsuB	IRNA pseudouridine(S5) synthase TsuB	865.4788899	-1.034408095	0.190437934	-5.431713344	5.58E-08	1.91E-07	6.91241951
ABUW_RS0270	ABUW_2114	NZ_CP008706.1	2198535	2199278	-	WP_000808191.1		GnRf family transcriptional regulator	16.0237919	-1.035461349	0.50614622	-2.552810565	0.0085453	0.008374601	1.738782086
ABUW_RS17870	ABUW_3451	NZ_CP008706.1	347362	3484840	+	WP_000862762.1	asd	aspartate-semialdehyde dehydrogenase	959.966197	-1.036263788	0.23380657	-4.432101874	9.33E-06	2.50E-05	4.602008941
ABUW_RS1905	ABUW_2385	NZ_CP008706.1	2373057	2374448	-	WP_001986580.1		LLM class family-dependent oxidoreductase	809.691487	-1.037319541	0.212806517	-4.874467199	1.09E-06	3.25E-06	5.488267368
ABUW_RS0980	ABUW_2258	NZ_CP008706.1	2243192	2244202	-	WP_000504791.1		tetraacyldisaccharide 4'-kinase	973.5209333	-1.03737013	0.132885787	-7.806479199	5.88E-15	3.92E-14	13.40640557
ABUW_RS16110	ABUW_0327	NZ_CP008706.1	349537	350313	+	WP_000525222.1		TSP family transporter	490.371832	-1.044862351	0.151378703	-6.90296804	5.09E-12	2.64E-11	10.57827488
ABUW_RS16055	ABUW_3305	NZ_CP008706.1	3338002	3338916	-	WP_000724041.1	cysM	lysine synthase CysM	1062.487223	-1.045050689	0.204494769	-5.10249457	3.21E-07	1.01E-06	5.995268081
ABUW_RS08880	ABUW_1825	NZ_CP008706.1	1820595	1822332	+	WP_000148658.1		CTP synthase	18781.20598	-1.046884859	0.150202019	-6.969712313	3.18E-12	1.87E-11	10.7702961
ABUW_RS1995	ABUW_2383	NZ_CP008706.1	2370150	2371034	+	WP_000472481.1		hypothetical protein	175.801632	-1.048533874	0.175873873	-5.961858048	2.49E-09	9.78E-09	8.000951335
ABUW_RS06515	ABUW_1335	NZ_CP008706.1	1346762	1349641	-	WP_001027069.1	adeG	multidrug efflux RND transporter permease subunit AdeG	137.5027374	-1.048663825	0.23679196	-4.428644204	9.48E-08	2.54E-05	4.595405816
ABUW_RS17260	ABUW_3547	NZ_CP008706.1	3604440	3604769	-	WP_000555701.1	secG	preprotein translocase subunit SecG	3223.024936	-1.049183297	0.207347527	-5.060022302	4.19E-07	1.30E-06	5.884645565
ABUW_RS1490	ABUW_2571	NZ_CP008706.1	2561045	2561812	-	WP_001072410.1		OmpA family protein	253.9073497	-1.054781947	0.19269954	-6.907400981	4.94E-12	2.56E-11	10.59102443
ABUW_RS16540	ABUW_3222	NZ_CP008706.1	3251156	3252200	-	WP_001278262.1	nadA	quinolinate synthase NadA	934.96696	-1.055792795	0.14523446	-8.47805191	2.29E-17	1.89E-16	9.72250159
ABUW_RS17945	ABUW_3886	NZ_CP008706.1	3742627	3744794	-	WP_001022443.1	ppa	inorganic diphosphatase	9635.390436	-1.052651845	0.19279421	-5.67790957	7.62E-11	5.35E-10	4.522336884
ABUW_RS00265	ABUW_0054	NZ_CP008706.1	58977	59435	+	WP_001001208.1		YcgN family cysteine cluster protein	505.2437464	-1.057404032	0.19989326	-5.50736068	3.64E-08	1.28E-07	6.893340916
ABUW_RS00070	ABUW_0014	NZ_CP008706.1	1610	17392	+	WP_000303558.1		tyrosine-1-RNA ligase	3545.526666	-1.058616146	0.148835158	-7.122477018	1.06E-12	5.86E-12	11.62207487
ABUW_RS13325	ABUW_2745	NZ_CP008706.1	2731932	2734511	-	WP_000517922.1		adenosine nucleotide synthase	30452.30006	-1.060044622	0.192390786	-5.833978951	4.09E-12	2.4E-11	10.29914466
ABUW_RS01660	ABUW_0337	NZ_CP008706.1	358322	359551	+	WP_000709181.1		MFS transporter	341.8131756	-1.063663209	0.393475577	-2.702509001	0.00686489	0.00284674	1.09836367
ABUW_RS16700	ABUW_3435	NZ_CP008706.1	3479496	3479845	-	WP_001083874.1		ASCH domain-containing protein	982.9694159	-1.06388459	0.143507685	-7.910886259	5.00E-14	1.77E-13	17.70074343
ABUW_RS04095	ABUW_010	NZ_CP008706.1	11721	12184	-	WP_001022027.1		D-tyrosyl-TRNA(Ty)deacylase	504.6645882	-1.06586809	0.12866531	-8.174807701	4.05E-17	3.27E-16	15.4856147
ABUW_RS1955	ABUW_2873	NZ_CP008706.1	2882101	2882784	-	WP_001022044.1	adk	adenylate kinase	1						

ABUW_RS17475	ABUW_3590	NZ_CP008706.1	365275	3655363	-	WP_00033899.1	poB	DNA-directed RNA polymerase subunit beta	15085.9078	-1.088738919	0.8058368	-6.03247981	163E-09	6.50E-09	8.8688028
ABUW_RS1790	ABUW_2636	NZ_CP008706.1	2635492	2639185	+	WP_00044889.1		femdomon family protein	939.22218	-1.088828341	0.82190044	-5.976660884	2.28E-09	8.87E-09	8.04720545
ABUW_RS20280	no	NZ_CP008706.1	2181956	2882114	-			hypothetical protein	55.44343002	-1.000225305	0.22581623	-4.827944536	138E-06	4.05E-06	5.933099335
ABUW_RS06695	ABUW_0172	NZ_CP008706.1	1387449	1388634	-	WP_00165436.1		thiazole synthase	2794.09684	-1.090274021	0.13799865	-7.940823709	2.01E-15	1.37E-14	13.8635336
ABUW_RS0860	ABUW_2851	NZ_CP008706.1	2883597	2884238	-	WP_000896578.1		cation transporter	480.2622055	-1.090387356	0.202652388	-5.380579859	7.42E-08	2.49E-07	6.80294741
ABUW_RS1120	ABUW_0199	NZ_CP008706.1	2278559	2272147	-	WP_00101423.1		LipA/C ligand binding domain-containing protein	212.5627097	-1.09185693	0.193327765	-5.952193121	2.65E-09	1.04E-08	9.98485689
ABUW_RS08085	ABUW_0178	NZ_CP008706.1	197620	198357	-	WP_00045860.1	msuE	FMN reductase	53.4222782	-1.092398055	0.21471032	-5.08771921	3.62E-07	1.04E-06	5.94484435
ABUW_RS0218	ABUW_1866	NZ_CP008706.1	1682008	1825111	-	WP_000388070.1		low molecular weight phosphotyrosine protein phosphatase	8000.224796	-1.095536637	0.19700522	-6.558984589	5.38E-11	2.52E-10	9.586863825
ABUW_RS02930	ABUW_0596	NZ_CP008706.1	59490	594963	-	WP_00198590.1		hypothetical protein	106.355826	-1.09718104	0.242567371	-4.52318170	6.09E-06	1.67E-05	4.777252965
ABUW_RS1070	ABUW_2203	NZ_CP008706.1	219520	2195966	+	WP_000331712.1	lscU	Fe-S cluster assembly scaffold lscU	9280.838752	-1.098221243	0.27860244	-4.61708612	3.89E-06	1.09E-05	4.963934487
ABUW_RS10720	ABUW_2205	NZ_CP008706.1	2190032	2190550	+	WP_001016254.1	hscB	Fe-S protein assembly-co-chaperone HscB	3694.936268	-1.098854	0.195554327	-5.922006887	3.9E-09	1.24E-08	7.907685795
ABUW_RS02250	ABUW_0458	NZ_CP008706.1	470499	471074	-	WP_000543071.1		xanthine phosphoribosyltransferase	2387.203375	-1.099109383	0.19200611	-5.778684827	7.63E-09	2.82E-08	7.54908891
ABUW_RS17840	ABUW_3664	NZ_CP008706.1	3723375	3742721	-	WP_000041016.1		cation transporter	432.966502	-1.10031437	0.208457155	-3.686674462	0.000272704	0.000505469	3.296305786
ABUW_RS1955	ABUW_3893	NZ_CP008706.1	3960729	3961889	+	WP_000822396.1		glutathionylperoxidase synthase family protein	394.686072	-1.100369954	0.219812455	-5.005949077	5.56E-07	1.7E-06	5.768090687
ABUW_RS1340	ABUW_2748	NZ_CP008706.1	2737313	2739949	+	WP_000189457.1	alaS	alanine- :RNA ligase	9488.8599	-1.100404668	0.195609283	-5.9328607931	3.06E-09	1.9E-08	7.924712571
ABUW_RS1225	ABUW_2105	NZ_CP008706.1	2088018	2090222	-	WP_001986280.1		TonB-dependent siderophore receptor	674.8258896	-1.102295582	0.104594787	-10.53876217	5.72E-26	8.9E-25	24.05034659
ABUW_RS1000	ABUW_2262	NZ_CP008706.1	2247058	2247145	+	WP_0000023429.1		PaB/RepB/SpO1 family partition protein	2035.05231	-1.102556619	0.180005444	-7.989225574	136E-15	9.32E-15	14.03076176
ABUW_RS0470	ABUW_1425	NZ_CP008706.1	1415063	1415623	+	WP_000203946.1		hypothetical protein	14.26584385	-1.108862964	0.565815857	-1.958759432	0.050023915	0.076227819	1.17885006
ABUW_RS00770	ABUW_0133	NZ_CP008706.1	104107	1045129	+	WP_001985518.1	ema	GTPase Gta	7341.1334810	-1.111968482	0.153594483	-7.23442966	4.67E-13	2.65E-12	15.76900442
ABUW_RS10380	ABUW_2706	NZ_CP008706.1	212912	2124003	-	WP_000191844.1	arcC	chitinase	3097.526888	-1.11690196	0.177840586	-6.250856531	4.08E-10	1.74E-09	8.75912841
ABUW_RS10710	ABUW_2876	NZ_CP008706.1	2885001	2887019	+	WP_000198154.1	ntfA	penicillin-binding protein 2	977.5536938	-1.110207079	0.162503354	-6.84839191	1.747E-12	3.80E-11	10.49196943
ABUW_RS05100	ABUW_0139	NZ_CP008706.1	1048696	1048711	-			RNA- Asn	34.29558737	-1.121028906	0.443316682	-2.511959522	0.01003353	0.020098832	1.068769252
ABUW_RS10385	ABUW_2107	NZ_CP008706.1	212406	2125020	-	WP_000441010.1	prnB	15S ribosomal protein L3 N55: glutamine methyltransferase	9885.635922	-1.110433293	0.168355575	-6.01581377	3.75E-11	1.78E-10	9.574048615
ABUW_RS07480	ABUW_0697	NZ_CP008706.1	109880	112003	+	WP_001026799.1	sefB	phosphoserine phosphatase SefB	3787.788393	-1.110771075	0.289608	-8.654271024	4.96E-18	4.32E-17	16.36483891
ABUW_RS00125	ABUW_0582	NZ_CP008706.1	1695758	167197	+	WP_012300567.1	kdpB	potassium-transporting ATPase subunit KdpB	246.7248029	-1.116013851	0.19121702	-6.147243061	7.88E-10	3.26E-09	8.646680095
ABUW_RS10715	ABUW_2204	NZ_CP008706.1	2196927	2196947	+	WP_000505197.1	lscA	iron-sulfur cluster assembly protein lscA	16559.28945	-1.116491547	0.21177524	-5.712751255	131E-07	4.27E-07	6.936961274
ABUW_RS04395	ABUW_0806	NZ_CP008706.1	893329	893865	-	WP_000197936.1		DOMON-like domain-containing protein	886.3264542	-1.116782579	0.169791857	-6.976475497	3.03E-12	1.60E-11	10.79534771
ABUW_RS02435	ABUW_0496	NZ_CP008706.1	507167	507979	+	WP_000284347.1	smA	adenine(5'G)-N6(adenine(5'G)-N6(5'-dimethyltrans	4622.731277	-1.116122887	0.151374024	-7.373278838	1.66E-13	9.91E-13	12.00402472
ABUW_RS10130	ABUW_1116	NZ_CP008706.1	316646	3137369	+	WP_001029149.1	ruB	23S rRNA pseudouridine(2005) synthase RuB	3305.748487	-1.118386538	0.116808288	-9.91045826	3.62E-23	4.57E-22	21.94249249
ABUW_RS05035	ABUW_3300	NZ_CP008706.1	1615432	1621599	-	WP_001023216.1	surE	5'3'-nucleotidase SurE	823.5952353	-1.120679667	0.1765049	-6.349283359	2.16E-10	9.07E-09	9.10224561
ABUW_RS19685	no	NZ_CP008706.1	674650	675740	-	WP_085940648.1		64 family transposase tSAbA1	463.7118897	-1.12232878	0.237919719	-4.838047017	131E-08	3.86E-06	5.413503516
ABUW_RS08655	ABUW_0777	NZ_CP008706.1	1775572	1776873	+	WP_001186668.1	bmC	anchored-chain amino acid transport system E carrier protein	4073.025376	-1.10631293	0.220038601	-5.188072763	3.08E-07	9.70E-07	6.03238463
ABUW_RS19195	ABUW_3885	NZ_CP008706.1	3953022	3954143	+	WP_000306194.1		5-(carboxymethyl)imidazole ribonucleotide synthase	4977.399784	-1.127970292	0.197808333	-6.005974676	1.90E-09	7.45E-09	8.933712246
ABUW_RS01780	ABUW_1445	NZ_CP008706.1	144415	1445525	+	WP_000836263.1	naaD	7-(3'-N6)-thiouracil-acyltransferase complex transfer	670.179368	-1.129141817	0.179620339	-6.286268604	3.25E-10	1.50E-09	8.85251941
ABUW_RS16260	ABUW_4048	NZ_CP008707.1	28186	29005	-	WP_000259031.1	suI1	sulfonamide-resistant dihydropteroate synthase SuI1	2743.621145	-1.103468193	0.251864584	-4.488043279	7.9E-06	1.05E-05	4.70962658
ABUW_RS18445	ABUW_3263	NZ_CP008706.1	3293552	3293929	+	WP_000268123.1		DUF4951 domain-containing protein	3915.262085	-1.110330201	0.193596023	-6.172802616	6.71E-10	2.79E-09	8.554469044
ABUW_RS18335	ABUW_3402	NZ_CP008706.1	3447176	3448510	-	WP_001198423.1		trigger factor	29049.37583	-1.114223459	0.154272485	-11.7320458817	2.29E-13	1.34E-12	11.724499261
ABUW_RS12860	ABUW_2630	NZ_CP008706.1	2648551	2649572	+	WP_001182272.1		cysteine- :RNA ligase	8987.478586	-1.114351024	0.18863194	-8.802754906	133E-18	1.20E-17	16.9027466
ABUW_RS08470	ABUW_0759	NZ_CP008706.1	1736031	1737227	+	WP_000184643.1		1-deoxy-D-xylulose-5-phosphate reductoisomerase	5527.045313	-1.115465294	0.154688742	-7.340322765	2.01E-10	1.26E-12	11.96838430
ABUW_RS10705	ABUW_0795	NZ_CP008706.1	774374	774550	+	WP_001863384.1		hypothetical protein	324.5175629	-1.119751036	0.19334185	-5.883418104	4.02E-09	1.55E-08	7.8322861
ABUW_RS0440	ABUW_0487	NZ_CP008706.1	507980	508191	+	WP_000167234.1		symmetrical(NH ₂ -nucleosyl)tetraphosphatase	3176.031575	-1.119462266	0.16062643	-7.093865337	130E-12	7.12E-12	11.47572461
ABUW_RS02445	ABUW_0498	NZ_CP008706.1	508862	509305	-	WP_000151366.1		DUF2147 domain-containing protein	977.7760011	-1.119466857	0.159879653	-7.135955256	9.61E-13	5.33E-12	11.27335569
ABUW_RS02925	ABUW_0595	NZ_CP008706.1	593951	594188	+	WP_0005058629.1	weeB	UDP-N-acetylglucosamine-2-epimerase (non-hydrolyzing)	970.862239	-1.122333546	0.172586253	-6.618334475	3.63E-11	1.73E-10	9.762458573
ABUW_RS04085	ABUW_0162	NZ_CP008706.1	119993	181459	+	WP_000956023.1		MP dehydrogenase	5935.60974	-1.143091847	0.142506649	-8.02122917	1.05E-15	7.23E-15	14.1048884
ABUW_RS18225	ABUW_3106	NZ_CP008706.1	3159391	3160335	+	WP_001984191.1		RNA-diphydrolase synthase	586.1595888	-1.146823028	0.214847413	-4.694256515	2.68E-06	7.62E-06	5.18218804
ABUW_RS14335	ABUW_2993	NZ_CP008706.1	3012642	3010259	+	WP_000624780.1		hypothetical protein	95.37577849	-1.145781197	0.284136349	-0.402401081	5.52E-05	0.00013678	3.873993437
ABUW_RS04190	ABUW_0854	NZ_CP008706.1	835009	835482	+	WP_000582210.1		RNA (NADPH(24'-2'-O)-methyltransferase	988.8231698	-1.147319622	0.19984123	-8.201542509	2.38E-16	1.78E-15	14.76033004
ABUW_RS12805	ABUW_3148	NZ_CP008706.1	3174093	317456	+	WP_001026776.1	metG	methionine- :RNA ligase	576.314914	-1.145066373	0.166652237	-6.859006673	5.62E-12	2.90E-11	9.03729006
ABUW_RS19975	ABUW_2257	NZ_CP008706.1	2242421	2242182	+	WP_000608092.1	kdsB	3-deoxy-manno-oxalotransferase	2396.503528	-1.148126205	0.184658365	-13.56207087	6.72E-42	2.17E-40	39.8642899
ABUW_RS17285	ABUW_3552	NZ_CP008706.1	3609987	3612933	+	WP_000874125.1		dephospho-CoA kinase	110.649192	-1.149106311	0.193324481	-6.788416559	1.6E-11	5.70E-11	10.24383956
ABUW_RS01465	ABUW_0298	NZ_CP008706.1	318069	322244	+	WP_001103947.1	gIB	glutamate synthase large subunit	15107.44394	-1.149851338	0.214912777	-6.494855963	2.67E-06	7.06E-06	5.18677784
ABUW_RS17950	ABUW_2115	NZ_CP008706.1	2400886	2401827	+	WP_001985666.1		serine acetyltransferase	313.0845396	-1.150444003	0.389963475	-2.956197344	0.003119577	0.000595687	2.22068814
ABUW_RS16345	ABUW_0148	NZ_CP008706.1	1025500	1026231	-	WP_000108087.1	dapD	5-tetrahydrofolate-2,6-dicarboxylate N-succinyltransf	7006.66181	-1.150507357	0.172508268	-6.663781506	2.67E-11	1.29E-10	9.49018987
ABUW_RS16275	ABUW_2610	NZ_CP008706.1	2603566	2603883	+	WP_001038420.1		hypothetical protein	626.8208053	-1.150700939	0.205835779	-5.590383489	2.27E-08	8.1E-08	7.09141271
ABUW_RS180180	ABUW_0241	NZ_CP008706.1	258729	259679	+	WP_000118180.1		homoserine kinase	1992.207024	-1.15085211	0.154858826	-7.431573065	107E-19	6.48E-13	12.827341
ABUW_RS13360	ABUW_3183	NZ_CP008706.1	3188651	3188844	-	WP_000806837.1		cold shock domain-containing protein	1272.654885	-1.152712051	0.19672639	-6.345044964	2.22E-10	9.81E-10	9.00825883
ABUW_RS17975	ABUW_3692	NZ_CP008706.1	3759101	3752245	-	WP_000527792.1		trimeric intracellular cation channel family protein	80109.78972	-1.153776088	0.217474442	-5.30533604	1.02E-07	3.71E-07	6.430498825
ABU															

ABUW_RS0575	ABUW_1534	NZ_CP008706.1	845148	845348	+	WP_001885517.1		NF038 034 family lipoprotein	1673.609057	-1.234489093	0.17824131	-6.925942671	4.33E-12	2.26E-11	0.64628714
ABUW_RS1480	ABUW_1795	NZ_CP008706.1	385727	385812	-	WP_001103054.1		RuA family pyruvate decarboxylase synthase	264.6473166	-1.235153461	0.554478707	0.227594034	0.025907599	0.041936399	13.78448118
ABUW_RS0990	ABUW_2260	NZ_CP008706.1	2242692	2243637	-	WP_000696684.1		bisphosphoryl transporter BxbD	188.363632	-1.235181955	0.03961601	-9.220418	2.96E-20	3.06E-19	0.51465741
ABUW_RS1845	ABUW_2361	NZ_CP008706.1	2347619	2348458	+	WP_001478868.1		RNA methyltransferase	1384.045969	-1.238193031	0.174369446	-1.70877741	1.17E-12	6.40E-12	1.119353062
ABUW_RS1370	ABUW_1353	NZ_CP008706.1	319797	319923	-	WP_00119555.1	nuoN	NADH:quinone oxidoreductase subunit NuoN	9537.7839	-1.238449411	0.219730098	-5.876946023	4.18E-09	1.61E-08	7.794087075
ABUW_RS0270	no	NZ_CP008706.1	51986	52128	-	WP_002009485.1		hypothetical protein	61.7484575	-1.240238888	0.494197389	-2.509703835	0.02081246	0.020646055	1.68519239
ABUW_RS0770	ABUW_0745	NZ_CP008706.1	744709	744976	-	WP_000065162.1		N 6 DNA methylase	4542.627258	-1.240385937	0.11458235	-6.838266884	8.62E-12	4.05E-11	0.39231979
ABUW_RS1730	ABUW_2207	NZ_CP008706.1	2182467	2182805	+	WP_001017383.1	tdx	ISC system 2Fe-2S type ferredoxin	6107.057401	-1.242164241	0.172818899	-7.187606485	6.59E-13	3.68E-12	1.143360898
ABUW_RS0690	ABUW_0445	NZ_CP008706.1	1287621	1288433	-	WP_000110172.1	queF	2PH-dependent 7-cyano-7-deazaiguanylate reductase G	634.496764	-1.244654272	0.150119306	-8.219198893	1.12E-16	8.52E-16	5.06933422
ABUW_RS0720	ABUW_0550	NZ_CP008706.1	553705	553920	-	WP_000556351.1		hypothetical protein	296.424053	-1.244827167	0.119185005	-6.495042407	8.30E-11	3.83E-10	9.416686432
ABUW_RS1850	ABUW_3060	NZ_CP008706.1	3086280	3087470	-	WP_001023961.1	tuf	elongation factor Tu	23118.1247	-1.245796769	0.177795552	-6.298374548	3.01E-10	1.30E-09	8.885032376
ABUW_RS1725	ABUW_3548	NZ_CP008706.1	3604782	3605576	-	WP_000101693.1		triose-phosphate isomerase	3180.553632	-1.248592554	0.210118863	-6.21020354	5.25E-10	2.20E-09	8.65690357
ABUW_RS0960	ABUW_0960	NZ_CP008706.1	1002822	1003793	-	WP_000061797.1		class fructose-bisphosphatase	2627.275644	-1.249179037	0.158881168	-7.862348514	3.77E-15	2.55E-14	11.09371068
ABUW_RS1925	ABUW_2868	NZ_CP008706.1	2870628	2871507	+	WP_000702193.1	nmH	5-tRNA (pseudouridine(5)-tRNA)-methyltransferase Rb	238.086202	-1.250102763	0.136456754	-9.11011022	5.13E-20	5.19E-19	0.28441175
ABUW_RS20015	no	NZ_CP008707.1	26187	26574	+			Mutapropase C-terminal domain-containing protein	175.671793	-1.253053634	0.227359801	-5.51049593	3.58E-08	1.26E-07	6.90060658
ABUW_RS1305	ABUW_0710	NZ_CP008706.1	719781	719939	-	WP_000796650.1	galB	>-tRNA(Aaa)/Glu- tRNA(Gln) aminoacyltransferase subunit G	6890.18704	-1.254571272	0.224299617	-5.17144219	2.32E-07	7.38E-07	6.11883695
ABUW_RS1900	ABUW_3192	NZ_CP008706.1	3192055	3192630	-	WP_000290730.1	rpmF	50S ribosomal protein L32	27950.58897	-1.255473917	0.10954768	-7.404842805	13.1E-13	7.87E-13	0.13888772
rRNA-5S	no	no	no	no	no	no	no		7.596495144	-1.256058875	0.170587961	-1.759571293	0.074480522	0.18654502	0.940849929
ABUW_RS0195	ABUW_0365	NZ_CP008706.1	387343	389412	-	WP_000033906.1		glycine - tRNA ligase subunit beta	1809.34371	-1.25589193	0.226194268	-5.552519398	2.82E-08	9.98E-08	0.90919203
ABUW_RS01405	ABUW_0529	NZ_CP008706.1	514771	514749	-	WP_000514025.1		methionine ABC transporter ATP-binding protein	5552.750816	-1.256542979	0.172254474	-7.293942287	3.01E-13	1.73E-12	11.7610147
ABUW_RS0290	ABUW_1724	NZ_CP008706.1	1721879	1722340	-	WP_001081637.1		hypothetical protein	477.5584818	-1.257387017	0.230481876	-5.45547499	4.88E-08	1.68E-07	6.775306361
ABUW_RS13720	ABUW_2734	NZ_CP008706.1	2721559	2723563	+	WP_001058022.1	rmkK	69)-N(7)-methyltransferase RmkK/23S tRNA (guanine)P	2486.357841	-1.258718615	0.154800746	-9.338124851	9.15E-21	1.05E-19	0.197736315
ABUW_RS07100	ABUW_1461	NZ_CP008706.1	1450589	1450692	+			tRNA- Trp	660.3103261	-1.261332572	0.345177647	-3.655603379	0.000256578	0.000566006	3.24717913
ABUW_RS1010	ABUW_3092	NZ_CP008706.1	3102959	3102952	+	WP_000108866.1	kgpE	1-cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	7003.334137	-1.262164745	0.235086051	-5.368093591	7.92E-08	2.65E-07	6.576978855
ABUW_RS01045	ABUW_1919	NZ_CP008706.1	1917528	1917839	+	WP_001044232.1		hypothetical protein	272.675963	-1.262220959	0.304733022	-4.142018124	3.44E-05	8.84E-05	4.063657759
ABUW_RS01580	ABUW_1953	NZ_CP008706.1	1937893	1938495	-	WP_001050043.1	cyoA	ubiquinol oxidase subunit II	79095.44868	-1.267107641	0.220043323	-5.758533028	8.48E-09	3.9E-08	5.007893237
ABUW_RS1895	ABUW_3895	NZ_CP008706.1	3963292	3964617	+	WP_000505288.1	guaD	guanine deaminase	1980.433526	-1.267850251	0.11869255	-6.99043626	2.74E-12	1.44E-11	0.8306061
ABUW_RS01750	ABUW_1797	NZ_CP008706.1	1797078	1797136	+	WP_000753036.1		DUF1443 family protein	397.191551	-1.271028602	0.11168415	-9.004308082	2.16E-19	2.08E-18	0.782827165
ABUW_RS05105	ABUW_1950	NZ_CP008706.1	1950748	1950205	+	WP_0003031226.1		glyoxylate:hydroxy-3-phosphate dehydrogenase	47029.24908	-1.274575701	0.16385021	-7.574767919	3.60E-14	2.26E-13	0.124650079
ABUW_RS01710	ABUW_1459	NZ_CP008706.1	1450338	1450411	+				6075.735996	-1.276992676	0.230322774	-4.357998335	13.1E-05	3.46E-05	4.460518031
ABUW_RS010715	ABUW_0350	NZ_CP008706.1	371518	372729	+	WP_001051782.1		GluLys/Pro/Val dehydrogenase	50164.86063	-1.278377143	0.190348032	-6.75968724	1.87E-11	9.00E-11	0.140202125
ABUW_RS00960	ABUW_2051	NZ_CP008706.1	2030334	2030334	+			hypothetical protein	178.8009979	-1.279330524	0.460165946	-2.780341654	0.005430173	0.009199203	0.210190985
ABUW_RS07716	ABUW_1679	NZ_CP008706.1	1667343	1667780	+	WP_000993407.1		2-amino-4-hydroxy-6-hydroxymethylpyridoxal phosphate	779.552183	-1.280546338	0.102338569	-10.38529017	2.89E-25	4.25E-24	23.37022246
ABUW_RS10080	ABUW_3310	NZ_CP008706.1	3344551	3344952	+	WP_001047580.1	ntfS	ribosome silencing factor	91629.26628	-1.281197384	0.225819798	-5.873655566	1.40E-08	5.09E-08	7.293190709
ABUW_RS01380	ABUW_0786	NZ_CP008706.1	786228	786288	+	WP_000443392.1		hypothetical protein	384.7616428	-1.281378979	0.241930377	-5.192051131	1.06E-07	3.50E-07	6.456595715
ABUW_RS10740	ABUW_2626	NZ_CP008706.1	2621822	2621435	+	WP_001033905.1		exo-alpha-sialidase	59155.9567	-1.283720908	0.265347796	-4.837880427	1.13E-06	3.88E-06	5.143841761
ABUW_RS01045	ABUW_1919	NZ_CP008706.1	1917528	1917839	+	WP_001044232.1	ncr	ribonuclease II	2696.635998	-1.28416797	0.178535585	-7.30219298	2.83E-13	1.64E-12	11.7848247
ABUW_RS14250	ABUW_2355	NZ_CP008706.1	2348466	2350534	+	WP_001051531.1		helic-tum-helic transcriptional regulator	653.5758009	-1.284811941	0.162572661	-8.420980558	3.73E-17	3.02E-16	5.519502039
ABUW_RS01335	ABUW_0536	NZ_CP008706.1	545634	545634	+	WP_000524235.1	queA	D(34)-5-adenosylmethionine ribosyltransferase-isomerase	1256.05852	-1.285070887	0.18214147	-7.05852425	1.68E-12	9.10E-12	11.039517431
ABUW_RS01000	ABUW_0124	NZ_CP008706.1	271363	278667	-	WP_000084730.1	rmB	16S rRNA (cytosine(167)-C)-methyltransferase Rmb	175.498683	-1.287657032	0.144300603	-8.92434844	4.52E-19	4.26E-18	0.37160414
ABUW_RS00820	ABUW_0161	NZ_CP008706.1	1794927	179857	+	WP_000592249.1		YigA family cysteine cluster protein	148.253966	-1.289333556	0.219700807	-5.895422005	3.74E-09	1.44E-08	7.540915999
ABUW_RS14315	ABUW_3382	NZ_CP008706.1	3421882	3421382	-	WP_000554329.1	lecX	Fe-S cluster assembly protein lecX	657.0273215	-1.294707094	0.155197819	-8.342302095	7.29E-17	5.70E-16	5.254432394
ABUW_RS01235	ABUW_0048	NZ_CP008706.1	55164	55399	-	WP_0010287365.1		hypothetical protein	398.987744	-1.3003194304	0.140313325	-9.26778913	1.90E-20	2.00E-19	0.69801165
ABUW_RS01058	ABUW_0336	NZ_CP008706.1	940495	940610	+	WP_000719408.1	ptdJ	pyridoxal phosphate synthase	2201247449	-1.300507645	0.19992198	-9.3164368	1.20E-20	1.28E-19	0.193910036
ABUW_RS10900	ABUW_2342	NZ_CP008706.1	2330839	2332132	-	WP_0011610309.1	tpaA	30S ribosomal protein S1	206336.9575	-1.300828956	0.11654297	-8.587602142	8.88E-18	7.15E-17	0.10128285
ABUW_RS0425	ABUW_0088	NZ_CP008706.1	94238	95305	+	WP_000862934.1		DNA cytosine methyltransferase	665.75911	-1.304885688	0.15417319	-8.465185736	2.56E-17	2.10E-16	5.67807741
ABUW_RS11745	ABUW_2416	NZ_CP008706.1	2403358	2403867	+	WP_000592233.1		rodanase-like domain-containing protein	29.33491776	-1.308228949	0.327308459	-3.99629295	6.42E-05	0.000140575	3.819227341
ABUW_RS14250	ABUW_2355	NZ_CP008706.1	2348466	2350534	+	WP_000554329.1		glutaminase	2796.73827	-1.309560735	0.162514704	-6.58845561	8.97E-18	7.62E-17	0.18762036
ABUW_RS01765	ABUW_0563	NZ_CP008706.1	562998	563819	+	WP_001046004.1		carbamoyl-hydroxylating class D beta-lactamase OXA-2	33002.84624	-1.311455876	0.158588612	-8.269546339	1.94E-16	1.01E-15	14.99371954
ABUW_RS10965	ABUW_2255	NZ_CP008706.1	2241976	2241147	-	WP_0010183027.1		PilE domain-containing protein	353.9904428	-1.316637916	0.13832113	-6.03040169	9.72E-16	6.75E-15	14.7077066
ABUW_RS01705	ABUW_1637	NZ_CP008706.1	1627290	1624670	+	WP_000559187.1	mmG	dine-5-carboxymethylthionine(34)synthase enzyme	7237.390754	-1.319999904	0.18645231	-7.07955086	1.45E-12	7.88E-12	11.0322248
ABUW_RS02185	ABUW_0567	NZ_CP008706.1	566518	566793	-	WP_000693361.1		phage tail sheath protein	62.3907995	-1.320042616	0.29431926	-4.48517414	7.29E-06	1.98E-05	4.704323388
ABUW_RS01580	ABUW_1919	NZ_CP008706.1	1917528	1917839	+	WP_001044232.1	epmB	EF-2 beta-lysylase protein EpmB	1740.179242	-1.320801097	0.170728186	-12.33554371	5.83E-35	1.4E-33	32.8589467
ABUW_RS18885	ABUW_3838	NZ_CP008706.1	3906199	3907044	+	WP_000026926.1		carboxylating nicotinate-nucleotide diphosphorylase	957.783711	-1.322700587	0.186520041	-6.049340219	1.45E-09	5.85E-09	8.23255226
ABUW_RS19205	ABUW_3749	NZ_CP008706.1	3749249	3749268	-	WP_000490209.1		zinc ABC transporter substrate-binding protein	769.8475144	-1.324948192	0.143248826	-9.240284512	2.26E-20	2.36E-19	0.12728085
ABUW_RS01055	ABUW_0333	NZ_CP008706.1	3407008	3405240	+	WP_000457893.1		serine hydroxymethyltransferase	9066.1919	-1.325147505	0.175269213	-7.678043638	1.62E-14	1.04E-13	0.91871873
ABUW_RS19380	ABUW_3187	NZ_CP008706.1	3193896	3194785	-	WP_001011937.1	nuoL	NADH:quinone oxidoreductase subunit L	34396.29329	-1.328117428	0.240418943	-5.524404352	3.31E-08	1.9E-07	6.933918736
ABUW_RS11005	ABUW_2304	NZ_CP008706.1	228819												

ABUW_RS09850	ABUW_2029	NZ_CP008706.1	205665	2016589	-	WP_000367699.1		hypothetical protein	10.5	140101	-1430594929	0.234869581	-6.09	0.8347	1.02E-09	4.57E-09	8.34002678
ABUW_RS04810	ABUW_0981	NZ_CP008706.1	926991	979761	-	WP_000071984.1	purM	phosphoribosylcyclohydromethylamine cyclo-ligase	170	62391	-1433458622	0.7417688	-8.23175407	184E-16	1.39E-15	4.85799063	
ABUW_RS17515	ABUW_3598	NZ_CP008706.1	3655338	3660528	-	WP_000162360.0	tuf	elongation factor T	18723	8966	-1437236271	0.205959473	-6.97344054	2.99E-12	1.58E-11	0.8009507	
ABUW_RS16930	ABUW_3481	NZ_CP008706.1	3333664	3530739	+			tRNA-Lys	506	15531	-143786379	0.41061628	-3.476324286	0.000508337	0.001025	2.965571959	
ABUW_RS14765	ABUW_3042	NZ_CP008706.1	3068759	3069211	-	WP_000868162.1	dut	dUTP-diphosphatase	803	339808	-1438216039	0.92545538	-8.84802048	8.91E-19	8.9E-19	17.06840948	
ABUW_RS02770	no	NZ_CP008706.1	563824	564586	-			ATP-binding protein	4696	16362	-1438838855	0.9990788	-7.97509458	6.0E-10	3.44E-12	1146330676	
ABUW_RS1085	ABUW_2279	NZ_CP008706.1	2264979	2264716	+	WP_000240376.1		DUF2058 domain-containing protein	546	272617	-1441910204	0.234892376	-6.07329982	8.39E-10	3.45E-09	8.426095	
ABUW_RS08780	ABUW_1719	NZ_CP008706.1	179767	1792671	-	WP_000246661.1		adenosine kinase	2785	74939	-1442240402	0.12429106	-11.0030096	3.94E-31	7.97E-30	29.0984769	
ABUW_RS1075	ABUW_2271	NZ_CP008706.1	2262287	2263489	-	WP_000889009.1	satT	serine/threonine transporter SatT	4686	74791	-1443590967	0.17956453	-8.037599456	9.0E-16	6.37E-15	14.9603703	
ABUW_RS04970	ABUW_1015	NZ_CP008706.1	1024711	1025421	-	WP_0001657724.1	queE	7-carboxy-7-deazaguanine synthase QueE	536	125509	-1447026531	0.92052455	-7.534538071	4.90E-14	3.06E-13	12.5478022	
ABUW_RS17505	ABUW_3596	NZ_CP008706.1	3656866	3659126	-	WP_000063880.1	secE	preprotein translocase subunit SecE	8589	430001	-145182903	0.237339424	-6.114419917	9.69E-10	3.96E-09	8.402316343	
ABUW_RS08890	ABUW_1627	NZ_CP008706.1	162367	1624456	+	WP_000078452.1	eno	phosphorylpyruvate hydratase	24287	51993	-1452248158	0.14608969	-9.940893541	2.76E-23	3.51E-22	21.45481514	
ABUW_RS08455	ABUW_1736	NZ_CP008706.1	1733894	1734448	+	WP_000060428.1	fr	ribosome recycling factor	5586	980737	-1453376901	0.144410991	-10.06374587	7.99E-24	1.05E-22	21.9778921	
ABUW_RS02280	ABUW_0464	NZ_CP008706.1	475506	476957	-	WP_0002181411	malB	18-isopentenyladenosine(7T; C2)-methyltransferase	9619	805016	-1454472684	0.138532663	-10.49919178	8.72E-26	1.34E-24	23.87435035	
ABUW_RS17295	ABUW_3554	NZ_CP008706.1	361040	361899	-	WP_000118150.1	rnbB	3S rRNA (guanosine(225'5'-C)-2'-O)-methyltransferase Rnb	966	930679	-1456403391	0.150635676	-9.669386839	4.1E-22	4.80E-21	20.3989919	
ABUW_RS19475	ABUW_2399	NZ_CP008706.1	2342758	2343825	+	WP_000956445.1		type I RasGAPase	7550	64452	-148010688	0.251698884	-5.803431471	6.50E-09	2.45E-08	7.61164868	
ABUW_RS00965	ABUW_0195	NZ_CP008706.1	219250	220582	+	WP_000080219.1		DUF475 domain-containing protein	5334	950811	-1462999005	0.81929333	-8.081957739	6.39E-16	4.54E-15	14.34258505	
ABUW_RS00400	ABUW_0093	NZ_CP008706.1	95317	95766	-	WP_000084198.1	nusB	transcription antitermination factor NusB	9063	9994	-147120561	0.175683779	-8.37459937	5.54E-17	4.41E-16	15.3553367	
ABUW_RS00480	ABUW_1737	NZ_CP008706.1	1733631	1733206	+	WP_000102222.1	uppG	6'-trans-glyco-5'-deoxyriboyltransferase	3190	332732	-1471604761	0.165554763	-8.82357096	6.55E-19	6.06E-18	17.2197272	
ABUW_RS16760	ABUW_2046	NZ_CP008706.1	2072721	2077076	+	WP_000107587.1		c-histone-binding protein	301	8039641	-1471920595	0.98554232	-7.43234562	1.23E-10	7.41E-10	12.0007083	
ABUW_RS05100	ABUW_0143	NZ_CP008706.1	105034	105179	-	WP_0001383202.1		pyridoxal phosphate-dependent aminotransferase	6116	936386	-1473060101	0.193197673	-7.62021653	2.44E-14	1.55E-13	12.80951556	
ABUW_RS16430	ABUW_3381	NZ_CP008706.1	3420637	3421068	-	WP_000963851.1	ndk	nucleoside-diphosphate kinase	13627	97567	-1477983379	0.197408172	-7.486941212	7.05E-14	12.36220825		
ABUW_RS09800	ABUW_2018	NZ_CP008706.1	2009188	2009382	-	WP_000367699.1		hypothetical protein	10.8	378993	-1479245887	0.24000433	-6.037631915	1.56E-09	6.27E-09	8.20275266	
ABUW_RS05380	ABUW_1160	NZ_CP008706.1	116011	116649	+	WP_0001279312.1		RuaA family pseudouridine synthase	169	852472	-1480044879	0.269597875	-5.498921941	4.02E-08	1.40E-07	15.839319014	
ABUW_RS16325	ABUW_3198	NZ_CP008706.1	3226052	3227638	-	WP_000031555.1		DUF852 domain-containing protein	3257	508537	-1480473703	0.389637244	-3.799620611	0.000144918	0.00033182	3.74933401	
ABUW_RS02100	ABUW_1212	NZ_CP008706.1	1250361	1252504	-	WP_000046148.1		DUF2726 domain-containing protein	300	722539	-1484782408	0.280332888	-5.26467385	1.1E-07	3.87E-07	6.85933398	
ABUW_RS04385	ABUW_0894	NZ_CP008706.1	891229	892368	-	WP_000160445.1	carA	16e-hydrolyzing carbamoyl-phosphate synthase small	8564	727879	-1487708248	0.248930636	-5.976396768	2.28E-09	8.96E-09	8.04692002	
ABUW_RS16255	ABUW_4047	NZ_CP008707.1	27538	28038	-	WP_0003716623.1		GNAT family N ₆ -acetyltransferase	814	7079071	-1490502125	0.233758276	-6.37623294	1.81E-10	8.06E-10	9.036300505	
ABUW_RS00380	ABUW_0167	NZ_CP008706.1	16619	167614	+	WP_0966410204.1	phB	peptide chain release factor 2	8124	137348	-1491230871	0.100792573	-11.40149055	4.1E-30	7.50E-29	28.010753	
ABUW_RS10045	ABUW_2271	NZ_CP008706.1	2256682	2257869	-	WP_000101093.1		phosphoglycolate kinase	4507	690302	-14946931	0.1645496	-9.10397764	8.60E-20	8.55E-19	18.06801741	
ABUW_RS16095	ABUW_3718	NZ_CP008706.1	3776743	3776549	-	WP_000182542.1		hypothetical protein	99	0048923	-150100907	0.267566004	-5.60965213	0.02E-08	7.26E-06	17.0759504	
ABUW_RS02185	ABUW_0415	NZ_CP008706.1	460043	460193	+			tRNA-Ser	81	3373258	-1501850753	0.236977239	-6.33731866	2.33E-10	1.03E-09	8.98993146	
ABUW_RS17245	ABUW_3544	NZ_CP008706.1	3604014	3604090	-			tRNA-Met	1235	294708	-1502207782	0.283252367	-5.30342163	1.14E-07	3.74E-07	8.426891989	
ABUW_RS10170	ABUW_2276	NZ_CP008706.1	2261567	2261965	-	WP_000651464.1		helic-turn-helix transcriptional regulator	492	607339	-150299677	0.310593008	-4.839074731	1.30E-06	3.84E-06	5.4564191	
ABUW_RS16390	ABUW_3169	NZ_CP008706.1	3195900	3195608	-	WP_012378792.1	nuoJ	NADH-quinone oxidoreductase subunit J	1111	80451	-1505195978	0.244525624	-6.155576663	7.48E-10	3.10E-09	8.503601697	
ABUW_RS07116	ABUW_160	NZ_CP008706.1	1650439	1650523	+			tRNA-Leu	793	7242603	-150909186	0.392714781	-3.842702789	0.000121687	0.00028021	3.550968973	
ABUW_RS16425	ABUW_3176	NZ_CP008706.1	3203608	3204285	-	WP_000878003.1		NADH-quinone oxidoreductase subunit B	8017	1788965	-1510191076	0.270410962	-5.58955008	2.1E-08	7.77E-08	10.9661504	
ABUW_RS05060	ABUW_1031	NZ_CP008706.1	1043057	1043431	-	WP_001024039.1		DUF4845 domain-containing protein	1440	244316	-1511729429	0.146064362	-10.38784731	2.82E-25	4.9E-24	23.3872474	
ABUW_RS10170	ABUW_2296	NZ_CP008706.1	2288363	2284819	+	WP_001026545.1		methionine adenosyltransferase	1022	90254	-1518005739	0.13852374	-10.95882677	6.03E-28	1.04E-26	25.98387638	
ABUW_RS08465	ABUW_1738	NZ_CP008706.1	1732026	1730300	-	WP_000893489.1		phosphatidate-cytidyltransferase	5468	340164	-1518779654	0.174699988	-6.69364865	3.5E-18	3.06E-17	16.5145446	
ABUW_RS02100	no	NZ_CP008706.1	241145	241158	+	WP_0002017921.1		hypothetical protein	7.89	997162	-152142197	0.6253438	-2.437228902	0.00400307	0.024866738	160438181	
ABUW_RS17445	ABUW_3584	NZ_CP008706.1	3642842	3644266	-	WP_000949434.1		TRAP transporter large permease subunit	3010	95145	-1527382659	0.21418397	-7.16528399	8.29E-10	4.61E-12	11.33621703	
ABUW_RS17255	ABUW_3546	NZ_CP008706.1	3604299	3604383	-			tRNA-Leu	1530	895283	-1528067981	0.319696105	-4.779841274	1.75E-06	5.1E-06	5.291820943	
ABUW_RS04380	ABUW_0893	NZ_CP008706.1	887894	891214	-	WP_001106293.1	carB	carbamoyl-phosphate synthase large subunit	59623	59425	-1529718985	0.23691496	-6.459558688	1.08E-10	4.87E-10	9.31931001	
ABUW_RS05130	ABUW_1397	NZ_CP008706.1	1325867	1326630	-	WP_000173536.1		methionine synthase	7548	28191	-1531916799	0.36183161	-4.20466377	2.62E-05	6.87E-05	4.175971646	
ABUW_RS16325	ABUW_2727	NZ_CP008706.1	2714369	2715085	+	WP_000202080.1	trnB	tRNA (guanosine(40)-T ₇)-methyltransferase TrnB	806	9630589	-1536262194	0.341422806	-6.363371462	1.97E-10	8.75E-10	9.058077974	
ABUW_RS05935	ABUW_1216	NZ_CP008706.1	1252902	1252977	-	WP_000162360.0		tRNA-Ala	14	8801538	-153971562	0.39871616	-3.86483339	0.00011185	0.000259493	3.58587473	
ABUW_RS02265	ABUW_0461	NZ_CP008706.1	472920	473804	+	WP_000914774.1		energy transducer TonB	681	2046210	-1541971636	0.155419496	-9.920318592	3.40E-23	4.30E-22	21.36167238	
ABUW_RS04440	ABUW_0905	NZ_CP008706.1	901081	901186	-			tRNA-Leu	70	2023016	-154414238	0.304483259	-5.071033963	3.95E-07	1.23E-06	5.908809314	
ABUW_RS16660	ABUW_3427	NZ_CP008706.1	3472862	3473725	-	WP_0010517006.1	putI	fomyltetrahydrofolate deformylase	3650	483239	-1545657407	0.15096361	-11.136816564	6.02E-30	1.1E-28	27.93921973	
ABUW_RS16050	ABUW_1300	NZ_CP008706.1	132446	134256	-	WP_000952665.1		aspartate-1-decarboxylase	3019	399988	-155221162	0.16248587	-9.592006664	1.26E-21	1.42E-20	19.84794609	
ABUW_RS04915	ABUW_1002	NZ_CP008706.1	101220	1018053	+	WP_000471070.1	putL	phosphoribosylcyclohydromethylaminimidase synthase	2034	41958	-1556259727	0.16079973	-9.678719277	3.71E-22	4.37E-21	10.39034194	
ABUW_RS18170	ABUW_2378	NZ_CP008706.1	2365305	2366039	-	WP_000694032.1		aspartate/glutamate racemase family protein	57	5891943	-1557980755	0.3398177648	-4.583945912	4.56E-06	1.27E-05	4.897235511	
tRNA ^{Arg}	no	no	no	no	no	no	no	no	625	635609	-1561634185	0.301098324	-5.8192514	2.21E-07	7.04E-07	6.32119234	
ABUW_RS16470	ABUW_2165	NZ_CP008706.1	218312	218435	-	WP_000826151.1		hypothetical protein	102	873221	-1562771628	0.240259378	-6.269680363	3.62E-10	1.55E-09	8.80091762	
ABUW_RS16325	ABUW_3397	NZ_CP008706.1	3441852	3443378	-	WP_0002017467.1		formate lyase	8764	720097	-1564010362	0.176420279	-8.865258427	7.63E-19	7.04E-18	17.62069094	
ABUW_RS16380	ABUW_3755	NZ_CP008706.1	381907	381675	-	WP_000210750.1	guaA	glutamine-hydrolyzing GMP synthase	1269	38414	-1569232166	0.210237237	-7.358397439	1.86E-10	1.10E-10	11	

ABLUW_RS4360	ABLUW_2958	NZ_CP008706.1	2970802	2971221	-	WP_000856365.1	pgsD	beta-1,6-N-acetyl-D-glucosamine biosynthesis protein	802.9848679	-1.68610697	0.178738439	-9.4335444231	3.96E-21	4.36E-20	9.36008321
ABLUW_RS4465	ABLUW_2854	NZ_CP008706.1	2107568	2108032	-	WP_000800305.1		cell envelope integrity protein ToA	641.0228225	-1.690708716	0.240396282	-7.033004693	2.02E-12	1.00E-11	9.06364826
ABLUW_RS4505	ABLUW_3903	NZ_CP008706.1	3960443	3971003	-	WP_00188090.1	yhcC	membrane protein insertase YhcC	33583.20947	-1.691906853	0.202890975	-8.337360077	7.56E-17	5.89E-16	9.22966868
ABLUW_RS4545	ABLUW_2969	NZ_CP008706.1	2982649	2984271	-	WP_000243371.1		BCCT family transporter	7253.254778	-1.695345844	0.31481997	-5.38519664	7.24E-08	2.43E-07	6.01372752
ABLUW_RS4540	ABLUW_4048	NZ_CP008707.1	26377	27569	+	WP_0018192.1		Tnfr family NTP-binding protein	580.78151	-1.696621972	0.232915006	-7.28428483	3.23E-13	1.88E-12	11.7310923
ABLUW_RS4503	ABLUW_3209	NZ_CP008706.1	321433	320404	+	WP_000605584.1	pth	aminoacyl tRNA hydrolase	5600.845586	-1.697832769	0.484331519	-9.3290163	5.21E-25	7.47E-24	23.087316
ABLUW_RS0755	ABLUW_9102	NZ_CP008706.1	87724	16026	+	WP_00024070.1		LDP-3; O-acetyl-N-acetylglucosamine deacetylase	2634.371161	-1.697579212	0.107037275	-14.92084691	2.11E-50	9.65E-49	48.015911
ABLUW_RS0185	ABLUW_0262	NZ_CP008706.1	279723	281084	+	WP_000090022.1	etfA	energy-dependent translocation thiolase protein EtfA	27249.05219	-1.699980094	0.16615282	-9.11627299	4.94E-24	8.61E-23	22.17996273
ABLUW_RS0930	ABLUW_0294	NZ_CP008706.1	025218	0252893	+			tRNA-Ans	78.80741006	-1.700186802	0.429657168	-3.957077801	7.59E-05	0.000180241	3.74414576
ABLUW_RS08765	ABLUW_0600	NZ_CP008706.1	1792099	1795008	+	WP_000819236.1		TonB-dependent siderophore receptor	1957.479374	-1.700319364	0.249326261	-6.816657532	9.10E-12	4.59E-11	9.03836258
ABLUW_RS1800	ABLUW_3719	NZ_CP008706.1	3777003	3778197	+	WP_001020674.1		TonB-dependent copper receptor	212164189	-1.706205507	0.263760796	-6.468176842	9.88E-11	4.52E-10	9.344978461
ABLUW_RS1375	ABLUW_2755	NZ_CP008706.1	2744837	2748156	-	WP_000729980.1		NCS2 family permease	1374.321945	-1.7107277004	0.17691641	-9.680099573	3.63E-22	4.29E-21	20.3674579
ABLUW_RS0750	ABLUW_2007	NZ_CP008706.1	2002712	2002906	+	WP_000367699.1		hypothetical protein	109.6806405	-1.713735837	0.254665062	-6.729371613	1.70E-11	8.31E-11	9.08031992
ABLUW_RS04545	ABLUW_0928	NZ_CP008706.1	934561	935466	+	WP_000271249.1	ticA	tRNA-2-thiocytylidine(32) synthetase TicA	3018.347183	-1.714688245	0.158421423	-9.82339885	2.67E-27	4.40E-26	25.35617005
ABLUW_RS1855	ABLUW_3732	NZ_CP008706.1	3789350	3790744	+	WP_000094481.1	atpD	FOF1 ATP synthase subunit beta	166844.2032	-1.725761778	0.227603852	-7.582304781	3.39E-14	2.14E-13	92.6695263
ABLUW_RS8070	ABLUW_3710	NZ_CP008706.1	3772479	3772554	+			tRNA-Ala	3600.466472	-1.72624996	0.256350117	-6.733954248	1.65E-11	8.00E-11	9.0347151
ABLUW_RS0340	ABLUW_0691	NZ_CP008706.1	698433	698508	+			tRNA-Val	1556.04106	-1.729283324	0.28568405	-6.053675635	1.42E-09	5.70E-09	8.243808337
ABLUW_RS1120	ABLUW_3519	NZ_CP008706.1	3565597	3565866	-	WP_001229357.1	ipaD	SOS ribosomal protein S15	36383.46633	-1.729665627	0.179501902	-9.634402315	5.72E-22	5.65E-21	20.185229
ABLUW_RS1840	ABLUW_3889	NZ_CP008706.1	3932449	3938333	+			tRNA-Ala	3588.094699	-1.72993915	0.252896305	-6.840724497	7.88E-12	3.99E-11	9.39922452
ABLUW_RS1649	ABLUW_3173	NZ_CP008706.1	3198855	3201216	-	WP_001091998.1	nuoF	NADH-quinone oxidoreductase subunit NuoF	22232.86764	-1.732346209	0.3062804	-5.61928955	1.92E-08	6.91E-08	7.16073555
ABLUW_RS09745	ABLUW_2006	NZ_CP008706.1	2002482	2002700	-	WP_001053107.1		phage coat protein	160.3457185	-1.732408565	0.216406999	-8.042489684	8.80E-16	6.91E-16	14.20907751
ABLUW_RS02805	ABLUW_2897	NZ_CP008706.1	2905084	2905215	+			hypothetical protein	1798.95203	-1.734914619	0.21099946	-8.107098191	5.18E-16	3.71E-15	14.3062098
ABLUW_RS1625	ABLUW_3219	NZ_CP008706.1	3250675	3250750	-			tRNA-His	7252.01828	-1.736405260	0.306232723	-5.688791911	1.28E-08	4.68E-08	7.329974453
ABLUW_RS03215	ABLUW_0653	NZ_CP008706.1	658534	659547	-	WP_000371932.1		methyltransferase	2401.281788	-1.737182864	0.235189466	-7.386122751	1.51E-13	9.02E-13	9.04643445
ABLUW_RS0640	ABLUW_0236	NZ_CP008706.1	0276220	0280095	+	WP_000253781.1		elongation factor Ts	41843.25274	-1.745281686	0.203477581	-6.577267179	9.72E-18	8.24E-17	9.08403874
ABLUW_RS0190	ABLUW_3737	NZ_CP008706.1	3794371	3794416	-	WP_000044060.1	atpE	FOF1 ATP synthase subunit C	45828.50365	-1.75144307	0.25381948	-6.900539614	5.18E-12	2.68E-11	9.0740075
ABLUW_RS1810	ABLUW_3256	NZ_CP008706.1	3287705	3287780	+			tRNA-Ala	3602.73212	-1.753242884	0.253169371	-6.912888297	4.75E-12	2.47E-11	9.06065626
ABLUW_RS8070	ABLUW_9143	NZ_CP008706.1	165698	165787	-	WP_001058816		TonB-dependent siderophore receptor	669.020509	-1.757018964	0.356023851	-4.93515884	8.01E-07	2.42E-06	5.61895941
ABLUW_RS01940	ABLUW_1022	NZ_CP008706.1	1041431	1041919	+	WP_000930084.1	puhB	adenylylsuccinate lyase	9530.79736	-1.757210726	0.143326994	-2.59666443	1.49E-34	3.53E-33	32.45972706
ABLUW_RS03220	ABLUW_0654	NZ_CP008706.1	659810	660568	-	WP_000700851.1		uacK/xanthine permease	1750.287403	-1.757685756	0.219588218	-6.027871877	1.66E-09	6.63E-09	8.17852592
ABLUW_RS0185	ABLUW_0643	NZ_CP008706.1	648574	650517	+	WP_000251974.1		nifH/nifS/nifE reductase	3884.623421	-1.76075514	0.228440032	-7.707047894	1.29E-14	6.37E-14	9.07704641
ABLUW_RS1860	ABLUW_3731	NZ_CP008706.1	378919	3789332	-	WP_000224542.1		FOF1 ATP synthase subunit epsilon	31716.2131	-1.762320236	0.22966567	-7.673773899	1.67E-14	1.07E-13	92.9602932
ABLUW_RS1920	ABLUW_3278	NZ_CP008706.1	3319128	3319128	+	WP_000897689.1		hypothetical protein	20722.67108	-1.763887652	0.318633385	-5.535790455	3.16E-08	1.09E-07	6.960607874
ABLUW_RS1820	ABLUW_3739	NZ_CP008706.1	3795681	3796079	-	WP_000042371.1		ATP synthase subunit I	7626.102559	-1.764716021	0.330144758	-5.854285196	4.79E-09	1.83E-08	7.16423182
ABLUW_RS1805	ABLUW_2896	NZ_CP008706.1	2904183	2905091	-	WP_001040400.1	cydD	sulfate adenylyltransferase subunit CydD	7826.503791	-1.780275082	0.198444078	-8.94864071	3.60E-19	3.41E-18	17.46702629
ABLUW_RS1875	ABLUW_3734	NZ_CP008706.1	379122	3791266	+	WP_001186631.1		FOF1 ATP synthase subunit alpha	92342.9981	-1.780892566	0.263885991	-6.177916039	1.21E-11	5.98E-11	9.02308771
ABLUW_RS07070	ABLUW_1451	NZ_CP008706.1	1443681	1444127	-	WP_000209410.1		GaIIb/VicQ domain-containing protein	20557.99746	-1.795328331	0.171537696	-9.14660863	1.24E-25	1.87E-24	23.72861003
ABLUW_RS01625	ABLUW_1029	NZ_CP008706.1	1016958	1016129	-	WP_000844623.1		hypothetical protein	175.7478276	-1.798486293	0.241505784	-7.448666193	9.43E-14	5.72E-13	9.24251162
ABLUW_RS01820	ABLUW_3906	NZ_CP008706.1	3971862	3971206	+	WP_000081929.1	rpmH	SOS ribosomal protein L34	22591.97003	-1.805807497	0.198872246	-9.56099975	1.17E-21	1.32E-20	9.88068081
ABLUW_RS00445	ABLUW_018	NZ_CP008706.1	1251036	1254111	+	WP_000106804.1		hypothetical protein	17919651703	-1.806780245	0.241527877	-7.473668716	7.80E-14	4.80E-13	92.9300882
ABLUW_RS1855	ABLUW_3738	NZ_CP008706.1	3794701	3795576	+	WP_000718561.1	atpB	FOF1 ATP synthase subunit A	81916.58938	-1.806803381	0.256030875	-7.05974609	1.70E-12	9.23E-12	11.03491696
ABLUW_RS1635	ABLUW_3221	NZ_CP008706.1	3250917	3250993	-			tRNA-Pro	1654.140052	-1.811899647	0.319453702	-5.833912221	5.41E-09	2.06E-08	7.68574917
ABLUW_RS17535	ABLUW_3602	NZ_CP008706.1	3661033	3661168	+			tRNA-Thr	4673.477769	-1.815899489	0.252462784	-7.182742143	6.35E-13	3.56E-12	11.44873882
ABLUW_RS02340	ABLUW_0475	NZ_CP008706.1	487891	487966	+			tRNA-Ala	2861241041	-1.820647156	0.287735533	-6.799207302	1.05E-11	5.25E-11	9.2802194
ABLUW_RS16035	ABLUW_3078	NZ_CP008706.1	3120266	3120336	+	WP_001193287.1		ribose-phosphate pyrophosphokinase	3143.10057	-1.82447111	0.126378806	-8.47166601	2.43E-17	2.01E-16	9.61978785
ABLUW_RS17530	ABLUW_3601	NZ_CP008706.1	3660893	3660976	-			tRNA-Tyr	91836.97438	-1.827837364	0.300575997	-6.081107593	1.18E-09	4.85E-09	8.314062263
ABLUW_RS10175	ABLUW_0289	NZ_CP008706.1	297154	298915	+	WP_001085598.1		sulfate ABC transporter substrate-binding protein	290.2902415	-1.837236368	0.19144542	-9.571719789	1.05E-21	1.20E-20	9.12203
ABLUW_RS1870	ABLUW_3733	NZ_CP008706.1	3790775	3791644	+	WP_001248971.1	atpG	FOF1 ATP synthase subunit gamma	55467.57216	-1.839037364	0.251954027	-7.299089804	2.90E-13	1.67E-12	11.77608504
ABLUW_RS01070	ABLUW_0644	NZ_CP008706.1	650510	650995	+	WP_000392547.1		DUF1934 domain-containing protein	1821.350918	-1.839089377	0.20566984	-8.940708221	3.87E-19	3.66E-18	17.436856
ABLUW_RS00410	ABLUW_0194	NZ_CP008706.1	1250162	1250167	+	WP_000722131.1		DUF4468 domain-containing protein	3641.237914	-1.843335484	0.162653707	-8.523948593	1.54E-17	1.30E-16	15.88704235
ABLUW_RS00085	ABLUW_0017	NZ_CP008706.1	94660	20035	+			tRNA-Ala	2865.374788	-1.848041513	0.271897316	-6.806814423	9.98E-12	4.99E-11	9.0353984
ABLUW_RS10875	ABLUW_1452	NZ_CP008706.1	1441365	1441369	+	WP_001138722.1	ipaU	SOS ribosomal protein S21	30163.00110	-1.848508752	0.17906431	-9.42182694	7.67E-36	1.88E-34	33.72473888
ABLUW_RS01865	ABLUW_0389	NZ_CP008706.1	409111	409641	+	WP_000433618.1		inositol monophosphatase	7645.493775	-1.858084111	0.161542339	-11.45729924	2.16E-30	4.25E-29	28.3780092
ABLUW_RS02905	ABLUW_0187	NZ_CP008706.1	1905273	1912054	+	WP_000733010.1	omp33-36	protein Omp33-36	43762.53578	-1.868035489	0.319639907	-6.01585704	1.81E-09	7.21E-09	9.82005095
ABLUW_RS0210	no	NZ_CP008706.1	708740	708880	+	WP_000409037.1		hypothetical protein	1007.587211	-1.871954078	0.217105935	-8.621986034	6.61E-18	5.68E-17	9.24545558
ABLUW_RS01625	ABLUW_3903	NZ_CP008706.1	3909512	3909886	+	WP_000246374.1	qpsL	SOS ribosomal protein S12	39230.13657	-1.87305733	0.206565084	-9.05488076	1.37E-19	1.34E-18	17.87387843
ABLUW_RS09890	ABLUW_0234	NZ_CP008706.1	026444	0265926	-	WP_000914842.1		adenosylhomocysteine	02414.91652	-1.873910218	0.177736074	-9.541321175	5.48E-26	8.52E-25	24.06930877
ABLUW_RS02425	ABLUW_0494	NZ_CP008706.1	505559	505987	-	WP_000854895.1	ripM	SOS ribosomal protein L13	44508.47449	-1.874320626	0.203167442	-9.225951081	2.81E-20	2.91E-19	9.58596041
ABLUW_RS01235	ABLUW_0533	NZ_CP008706.1	541450	542563	+	WP_000667229.1	tgt	tRNA-guanosine(24) transglycosylase Tgt	50						

ABUW_RS18185	ABUW_3736	NZ_CP008706.1	3737632	3794332	-	WP_001624691.1		F0F1ATP synthase subunit B	36085.43341	-2.005735015	0.274365234	-7.3045693	2.66E-10	1.55E-12	118.6276675
ABUW_RS19225	ABUW_2999	NZ_CP008706.1	2999483	2950254	+	WP_000720612.1		hypothetical protein	970.3792777	-2.006910304	0.200802524	-9.99447589	1.6E-23	2.07E-22	2.168302675
ABUW_RS19230	ABUW_2998	NZ_CP008706.1	2999006	2959727	+	WP_000024256.1		hypothetical protein	9104.058063	-2.007682185	0.204378328	-9.82357737	8.9E-23	1.0E-21	20.95802987
ABUW_RS19415	ABUW_3257	NZ_CP008706.1	3287936	3287912	-			rRNA-1e	95988.93776	-2.010350006	0.317282373	-6.339195543	2.3E-10	1.02E-09	8.992197217
ABUW_RS19740	ABUW_3543	NZ_CP008706.1	3603274	3603788	-	WP_000777730.1	rmP	ribosome maturation factor RmP	90556.93193	-2.018818166	0.228584159	-8.836194838	9.90E-9	9.59E-9	17.04148293
ABUW_RS19840	ABUW_3098	NZ_CP008706.1	3123116	312414	-	WP_0019273422.1	rmY	50S ribosomal protein L25	9014.32645	-2.022781628	0.24716326	-8.185976299	2.70E-6	1.99E-6	10.74042629
ABUW_RS19841	ABUW_3848	NZ_CP008706.1	829662	829973	+	WP_000271409.1	rmU	50S ribosomal protein L21	54542.30376	-2.022947621	0.20539298	-8.849636166	8.88E-23	8.53E-22	21.06914465
ABUW_RS19848	ABUW_3991	NZ_CP008706.1	3655669	3656040	-	WP_001525580.1	rmL	50S ribosomal protein L7L12	125996.0769	-2.053785	0.194714184	-10.54758807	5.21E-26	8.17E-25	24.08774967
ABUW_RS19855	ABUW_0316	NZ_CP008706.1	343087	343569	+	WP_001646489.1		preP ₁ -type N-terminal cleavage/methylation domain-containing	325.648921	-2.061659029	0.159261174	-16.2003007	3.52E-62	1.75E-50	49.76674318
ABUW_RS19855	ABUW_3600	NZ_CP008706.1	3660780	3660855	-			rRNA-Gly	3504.761008	-2.063710708	0.265088013	-7.785001994	6.97E-15	4.63E-14	13.3396714
ABUW_RS19855	ABUW_0235	NZ_CP008706.1	1278330	1279082	-	WP_001088218.1	rsB	30S ribosomal protein S2	102238.9676	-2.066916034	0.205748395	-10.04583793	9.58E-24	1.25E-22	21.90466416
ABUW_RS19855	ABUW_0424	NZ_CP008706.1	440667	440843	+	WP_000849088.1	rmD	50S ribosomal protein L30	58027.68502	-2.069406641	0.240693929	-8.342049667	7.30E-17	5.70E-16	15.24044728
ABUW_RS19855	ABUW_0427	NZ_CP008706.1	442673	442789	+	WP_000867807.1	rmJ	50S ribosomal protein L36	9327.933958	-2.069717619	0.21404343	-10.669616251	4.06E-22	4.75E-21	20.32294087
ABUW_RS19855	ABUW_0425	NZ_CP008706.1	440847	441287	+	WP_0010715340.1	rmO	50S ribosomal protein L15	81988.17951	-2.073100404	0.24767019	-8.370528568	5.74E-17	4.56E-16	15.34188887
ABUW_RS19855	ABUW_2754	NZ_CP008706.1	2743727	2744725	+	WP_0010717412.1		adenosine deaminase	33552.053443	-2.075867721	0.193573638	-11.308109275	1.20E-29	2.24E-28	27.64923863
ABUW_RS19855	ABUW_3541	NZ_CP008706.1	3599042	3601741	-	WP_001030326.1	infB	translation initiation factor IF-2	12708.377	-2.078050258	0.185727148	-11.18184842	4.64E-29	8.58E-28	27.06645775
ABUW_RS19855	ABUW_0511	NZ_CP008706.1	163763	165520	+	WP_001020191.1	tdaA	Flp plus assembly complex ATPase component TsdA	494.7243398	-2.08693657	0.186689562	-12.36936245	3.83E-35	9.35E-34	33.02926018
ABUW_RS19855	ABUW_3592	NZ_CP008706.1	3560583	3565589	-	WP_001186213.1	rmU	50S ribosomal protein L10	88989.34102	-2.057183364	0.216242626	-9.857175263	6.38E-23	7.54E-22	21.0030402
rRNA-9	no	no	no	no	no	no	no	no							
ABUW_RS19855	ABUW_3595	NZ_CP008706.1	312799	312863	+			rRNA-Gln	297.1666871	-2.10887819	0.19719807	-10.9339552	8.60E-27	1.55E-25	24.8303222
ABUW_RS20055	ABUW_0418	NZ_CP008706.1	437390	438526	+	WP_001010197.1	rmE	50S ribosomal protein L5	24190.0444	-2.121625249	0.246768736	-8.598841611	8.05E-18	6.90E-17	16.70071994
ABUW_RS19855	ABUW_3599	NZ_CP008706.1	3660692	3660766	-			rRNA-Thr	2945.731904	-2.122738456	0.284637162	-7.457701008	8.80E-14	5.38E-13	12.6897768
ABUW_RS20075	ABUW_0422	NZ_CP008706.1	439180	441680	+	WP_001001384.1	rmR	50S ribosomal protein L18	42395.98474	-2.108924441	0.264107559	-8.09114284	5.91E-16	4.22E-15	14.37519884
ABUW_RS20075	ABUW_0421	NZ_CP008706.1	439180	441680	+	WP_000091932.1	rmF	50S ribosomal protein L6	77599.17305	-2.145488351	0.243561097	-8.08819353	1.26E-18	1.91E-17	16.9421473
ABUW_RS19855	ABUW_0322	NZ_CP008706.1	345003	345743	+	WP_000464595.1	tmD	rRNA (guanosine(37)-N1-methyltransferase TmD)	131.73.18309	-2.148454264	0.237443941	-10.048259614	1.45E-19	1.41E-18	17.8496149
ABUW_RS19855	ABUW_0843	NZ_CP008706.1	828993	830249	-	WP_000201832.1	rmA	50S ribosomal protein L27	30326.02303	-2.149586971	0.196406109	-8.04459953	7.05E-28	1.20E-26	25.93936455
ABUW_RS19855	ABUW_3641	NZ_CP008706.1	370109	3702430	-	WP_000840548.1		sigma-54-dependent Fis family transcriptional regulator	238.1890296	-2.14955721	0.21647938	-10.9591969	4.99E-24	6.66E-23	22.17647538
ABUW_RS20065	ABUW_0420	NZ_CP008706.1	438853	439248	+	WP_000062616.1	rsH	30S ribosomal protein S8	14162.66771	-2.162296978	0.237256699	-10.11674672	7.96E-20	8.09E-20	16.09928587
ABUW_RS19855	ABUW_0423	NZ_CP008706.1	440183	440660	+	WP_001014102.1	rsE	30S ribosomal protein S5	127117.7193	-2.165572465	0.260846819	-8.302085019	1.02E-16	7.84E-16	15.0591003
ABUW_RS19855	ABUW_2842	NZ_CP008706.1	2855958	2857601	+			hypothetical protein	1774.622033	-2.17381719	0.187059367	-11.62100435	3.22E-31	6.56E-30	29.18371449
ABUW_RS20075	ABUW_0431	NZ_CP008706.1	444316	445323	+	WP_000189631.1	rmA	DNA-directed RNA polymerase subunit alpha	317291.15397	-2.17398285	0.266337761	-8.162523693	3.28E-16	2.39E-16	14.62074602
ABUW_RS20075	ABUW_0417	NZ_CP008706.1	437557	437974	+	WP_001095365.1	rmK	50S ribosomal protein L24	44858.95409	-2.181066479	0.218452147	-8.9334878	3.18E-24	4.33E-23	22.36336562
ABUW_RS19855	ABUW_0428	NZ_CP008706.1	442897	443253	+	WP_000090908.1	rmM	30S ribosomal protein S10	81939.95891	-2.181035358	0.261710494	-8.335586668	7.71E-17	5.96E-16	15.22450015
ABUW_RS19855	ABUW_0321	NZ_CP008706.1	344409	344857	+	WP_001016236.1	rmM	ribosome maturation factor RmM	50620.40753	-2.184602753	0.245441008	-8.899594798	5.66E-19	5.26E-18	17.28782568
ABUW_RS19855	ABUW_3285	NZ_CP008706.1	331823	331827	-	WP_001093639.1	rmI	50S ribosomal protein L35	12405.93484	-2.18753583	0.225591902	-10.69672131	3.18E-22	3.68E-21	20.43363455
ABUW_RS19855	ABUW_3540	NZ_CP008706.1	3598461	3599042	-	WP_000891704.1		ribosome-binding factor A	14401.45414	-2.18801823	0.186872648	-11.07894329	1.16E-31	2.39E-30	29.62075586
ABUW_RS20025	ABUW_0514	NZ_CP008706.1	525402	525595	-	WP_000779317.1		hypothetical protein	1923.448781	-2.190660283	0.177895922	-12.51428007	7.59E-35	1.82E-33	32.73993110
ABUW_RS20025	ABUW_0430	NZ_CP008706.1	443672	444298	+	WP_001030204.1	rsD	30S ribosomal protein S4	143627.8764	-2.203206160	0.254830451	-8.645968395	5.34E-18	4.62E-17	16.33511914
ABUW_RS20025	ABUW_0429	NZ_CP008706.1	442973	443569	+	WP_001040166.1	rsK	30S ribosomal protein S11	59266.30441	-2.203621056	0.2604116	-8.462073983	2.63E-17	2.16E-16	16.66738733
ABUW_RS19855	ABUW_3284	NZ_CP008706.1	331762	331821	-	WP_001024588.1	rmT	50S ribosomal protein L20	33645.3677	-2.2110373	0.240226386	-9.204250084	3.44E-20	3.55E-19	16.45033689
ABUW_RS19855	ABUW_3604	NZ_CP008706.1	397109	3971629	+	WP_000251652.1	ymD	membrane protein insertion efficiency factor YelD	5043.093825	-2.214340972	0.220337299	-10.0459778	9.21E-24	1.20E-22	19.12974624
ABUW_RS19855	ABUW_2380	NZ_CP008706.1	236697	2367866	+	WP_001093556.1	tauC	taurine ABC transporter permease TauC	527.3526298	-2.22022881	0.287437784	-7.724005525	1.01E-14	7.35E-14	13.93731739
ABUW_RS20025	ABUW_0432	NZ_CP008706.1	445342	445719	+	WP_001021630.1	rmQ	50S ribosomal protein L17	87978.97395	-2.222935348	0.23860878	-9.19330564	1.20E-20	1.28E-19	16.89261006
ABUW_RS20040	ABUW_0725	NZ_CP008706.1	723653	723234	+	WP_000491967.1		hypothetical protein	661323879	-2.226095806	0.1922611	-11.57847031	5.30E-31	1.07E-29	28.97895864
ABUW_RS20070	ABUW_0397	NZ_CP008706.1	694365	694793	+	WP_001028338.1		membrane protein	618.4320409	-2.227463621	0.208061889	-10.7087743	9.86E-27	1.55E-25	24.8941975
ABUW_RS20060	ABUW_0416	NZ_CP008706.1	438536	438841	+	WP_0010714824.1	rsN	30S ribosomal protein S14	45389.78961	-2.230233623	0.229783772	-10.705879609	2.85E-22	3.39E-21	20.48946821
ABUW_RS19855	ABUW_0605	NZ_CP008706.1	661167	662882	+	WP_001028092.1	typA	translational GTPase TypA	37234.49062	-2.236623995	0.218399962	-10.33198985	5.05E-25	7.30E-24	23.06687
ABUW_RS19855	ABUW_3403	NZ_CP008706.1	344925	345195	+	WP_000052885.1		TonB-dependent histidine receptor	7747.738344	-2.277341745	0.197442264	-12.574099194	4.69E-06	1.30E-05	8.85659134
ABUW_RS19855	ABUW_2189	NZ_CP008706.1	2150091	2150978	+	WP_000011876.1		salicylate exporter TauE/SalE family protein	667.46087	-2.283535564	0.353463741	-6.46610379	1.01E-10	4.58E-10	9.338839933
ABUW_RS19855	ABUW_2973	NZ_CP008706.1	2988890	2990530	+	WP_000714073.1	mqo	malate dehydrogenase (quinone)	13528.92757	-2.298241661	0.216450543	-8.782212844	1.60E-18	1.44E-17	16.54314015
ABUW_RS19855	ABUW_0405	NZ_CP008706.1	432180	432471	+	WP_000077092.1	rsJ	30S ribosomal protein S10	89528.80339	-2.299327214	0.223180652	-10.30253789	6.86E-25	9.70E-24	20.0195957
ABUW_RS19855	ABUW_2422	NZ_CP008706.1	240932	241063	-	WP_001010359.1		amino acid ABC transporter ATP-binding protein	163.9656982	-2.306827198	0.344365647	-6.69873635	2.10E-11	1.02E-10	9.91820909
ABUW_RS19855	ABUW_2423	NZ_CP008706.1	241066	2410731	+	WP_000418072.1		amino acid ABC transporter permease	168.884193	-2.310430823	0.436706135	-5.290584764	1.22E-07	3.99E-07	6.39861882
ABUW_RS19855	ABUW_0677	NZ_CP008706.1	682476	681114	-	WP_000859411.1		hypothetical protein	135.5588234	-2.310431764	0.225604984	-12.5419076	1.01E-24	1.09E-23	22.79770425
ABUW_RS20075	ABUW_0547	NZ_CP008706.1	533248	5334375	+	WP_000090661.1	rsR	30S ribosomal protein S18	42249.38501	-2.314162263	0.225254692	-10.27326999	9.30E-25	1.31E-23	22.88421847
ABUW_RS20049	ABUW_018	NZ_CP008706.1	9282913	9303397	+	WP_001648811.1	cysW	sulfate ABC transporter permease subunit CysW	95.90065251	-2.323217623	0.210809951	-10.9188805	9.57E-28	1.61E-26	25.78219093
ABUW_RS19775	ABUW_2276	NZ_CP008706.1	2202330	2202596	+	WP_000106562.1	rmT	30S ribosomal protein S20	5845.673991	-2.327871631	0.205692424	-11.93273305	1.09E-29	2.05E-28	27.88715658
ABUW_RS19870	ABUW_0319	NZ_CP008706.1	343566	343991	+	WP_000778336.1		preP ₁ -type N-terminal cleavage/methylation domain-containing	305.5428715	-2.328234992	0.				

ABUW_RS16790	ABUW_3453	NZ_CP008706.1	3500053	3501315	+	WP_000967566.1		hypothetical protein	1224.585304	-3.31561477	0.199581657	-1.659251422	7.89E-62	6.12E-60	59.21348034
ABUW_RS01290	ABUW_0263	NZ_CP008706.1	281563	282156	+	WP_000721434.1		hypothetical protein	4441.725076	-3.400976089	0.239447927	-1.120340588	8.73E-46	3.32E-44	43.47926394
ABUW_RS01550	ABUW_0315	NZ_CP008706.1	337394	338395	+	WP_000079197.1		PIIW family protein	353.5946306	-3.469025738	0.256383361	-1.353061964	1.03E-41	3.25E-40	39.48854141
ABUW_RS03355	ABUW_0682	NZ_CP008706.1	687035	691555	+	WP_000658892.1		Hpt domain-containing protein	6681.029179	-3.475769435	0.190502096	-1.24530807	2.25E-74	3.24E-72	71.48886692
ABUW_RS03345	ABUW_0680	NZ_CP008706.1	684227	684763	+	WP_000729762.1		purine-binding chemotaxis protein CheW	2158.743622	-3.505907759	0.245779532	-1.126444148	3.64E-46	1.40E-44	43.85429638
ABUW_RS03350	ABUW_0681	NZ_CP008706.1	684810	686888	+	WP_000505931.1		methyle-accepting chemotaxis protein	8701.720525	-3.579959992	0.216424791	-1.1654135817	1.85E-61	1.40E-59	58.85235731
ABUW_RS01555	ABUW_0316	NZ_CP008706.1	338392	339210	+	WP_000149374.1		hypothetical protein	436.9271152	-3.721182112	0.232440968	-1.1600914913	1.10E-57	6.84E-56	55.16510908
ABUW_RS11280	ABUW_2319	NZ_CP008706.1	2304179	2304616	-	WP_001161759.1		PACE efflux transporter	486.7408237	-3.725851103	0.501425192	-7.43052243	1.08E-13	6.52E-13	12.18547401
ABUW_RS17270	ABUW_3549	NZ_CP008706.1	3605867	3607579	+	WP_001274987.1	pilB	type IV pilus assembly ATPase PilB	1238.801225	-3.728915009	0.198948797	-1.174308905	2.20E-78	4.23E-76	75.37371194
ABUW_RS17275	ABUW_3550	NZ_CP008706.1	3607609	3608835	+	WP_000279216.1		type II secretion system F family protein	1140.985159	-3.763011912	0.1919395862	-1.187206623	1.94E-79	4.33E-77	76.36321598
ABUW_RS01545	ABUW_0314	NZ_CP008706.1	336833	337393	+	WP_002194578.1	pilV	type IV pilus modification protein PilV	167.2603096	-3.810621622	0.312849759	-1.1218035659	3.96E-34	9.27E-33	32.0331313
ABUW_RS08615	ABUW_1769	NZ_CP008706.1	1766667	1767173	+	WP_000734811.1		PEGA domain-containing protein	206.5046345	-4.025464655	0.276444599	-1.1415616015	4.93E-48	2.05E-46	45.68855812
ABUW_RS01435	ABUW_0292	NZ_CP008706.1	311519	312259	+	WP_000076101.1		type 4a pilus biogenesis protein PilQ	1434.943211	-4.071936728	0.254596322	-1.15199369815	1.41E-57	8.63E-56	55.06394962
ABUW_RS01440	ABUW_0293	NZ_CP008706.1	312270	312797	+	WP_000695059.1		pilus assembly protein PilP	402.4531548	-4.095078663	0.224116505	-1.1827209765	1.38E-74	2.06E-72	71.6861582
ABUW_RS01870	ABUW_0381	NZ_CP008706.1	407351	409198	+	WP_000047395.1		DEAD/IDEAH box helicase	81860.12305	-4.235870058	0.376622872	-1.1124698038	2.40E-29	4.45E-28	27.35167267
ABUW_RS01430	ABUW_0291	NZ_CP008706.1	310881	311522	+	WP_000201229.1		PIN domain-containing protein	1512.438045	-4.334229374	0.247187862	-1.1753415129	7.86E-69	9.60E-67	66.01781347
ABUW_RS08010	ABUW_1641	NZ_CP008706.1	1637480	1637818	+	WP_001243508.1		hypothetical protein	261.4524357	-4.868052522	0.315206803	-1.1644399576	8.28E-54	4.45E-52	51.35179525
ABUW_RS01495	ABUW_0304	NZ_CP008706.1	327823	328296	+	WP_000993729.1		pilin	11795.64268	-5.078891355	0.314764571	-1.1613552421	1.44E-58	9.48E-57	56.02302861

Appendix II

Table S 21. sRNAs expression TPM values (EEP)

locus_tag	*old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	EEP_1	EEP_2	EEP_3	EEP_Mean	EEP_Mean_10
newcandsRNA1	no	no	no	no	no	no	no	no	0.88954009	0.73827304	0.17870617	0.6021731	10
sRNA1	no	no	no	no	no	no	no	no	276.535776	245.014367	181.56547	234.371871	234.371871
sRNA10	no	no	no	no	no	no	no	no	1.5927576	1.32190782	0.63996129	1.18487557	10
sRNA100	no	no	no	no	no	no	no	no	361.825338	229.807842	124.312481	238.648554	238.648554
sRNA101	no	no	no	no	no	no	no	no	99.5641158	97.3063301	94.2157747	97.0287402	97.0287402
sRNA102	no	no	no	no	no	no	no	no	130.700742	154.47798	90.0254456	125.068723	125.068723
sRNA103	no	no	no	no	no	no	no	no	3.80206653	2.89256173	7.12903114	4.60788646	10
sRNA104	no	no	no	no	no	no	no	no	15.7152083	7.13279426	8.6821415	10.510048	10.510048
sRNA105	no	no	no	no	no	no	no	no	13.4154217	6.76000014	5.77526042	8.65022743	10
sRNA106	no	no	no	no	no	no	no	no	2.31755179	2.19822873	0.53210265	1.68262772	10
sRNA109	no	no	no	no	no	no	no	no	27.199399	17.3068239	14.9357119	19.8139783	19.8139783
sRNA110	no	no	no	no	no	no	no	no	27.199399	17.3068239	14.9357119	19.8139783	19.8139783
sRNA13	no	no	no	no	no	no	no	no	28.8323378	18.9331313	34.1175062	27.2943251	27.2943251
sRNA14	no	no	no	no	no	no	no	no	4.32168228	2.60856476	0.63142847	2.5205585	10
sRNA15	no	no	no	no	no	no	no	no	1404.29808	922.49086	399.838093	908.875679	908.875679
sRNA17	no	no	no	no	no	no	no	no	37.9203998	31.1624429	29.9728705	33.0185711	33.0185711
sRNA18	no	no	no	no	no	no	no	no	42.0109529	26.0291502	23.4441265	30.4947432	30.4947432
sRNA19	no	no	no	no	no	no	no	no	48.7091278	28.6975396	28.6720072	35.3595582	35.3595582
sRNA2	no	no	no	no	no	no	no	no	32390.283	35130.1086	24392.2428	30637.5448	30637.5448
sRNA20	no	no	no	no	no	no	no	no	32.3762393	20.5303708	26.3095197	26.4053766	26.4053766
sRNA21	no	no	no	no	no	no	no	no	3.71901167	2.84916054	3.2184461	3.2622061	10
sRNA22	no	no	no	no	no	no	no	no	0.21508041	0.1785058	0.34567252	0.24641958	10
sRNA24	no	no	no	no	no	no	no	no	231.299706	171.045702	106.211379	169.518929	169.518929
sRNA25	no	no	no	no	no	no	no	no	3.25677014	3.47522608	1.24624041	2.65941221	10
sRNA26	no	no	no	no	no	no	no	no	347.760371	282.38223	224.699742	284.947448	284.947448
sRNA27	no	no	no	no	no	no	no	no	4.8877277	4.40427107	4.0399452	4.44398132	10
sRNA28	no	no	no	no	no	no	no	no	7.56035926	4.1831425	5.91964193	5.88771456	10
sRNA29	no	no	no	no	no	no	no	no	6.28608332	3.26070595	1.26285694	3.60321541	10
sRNA3	no	no	no	no	no	no	no	no	574.199593	671.233481	639.944449	628.459174	628.459174
sRNA30	no	no	no	no	no	no	no	no	2.41085582	0	0	0.80361861	10
sRNA31	no	no	no	no	no	no	no	no	10.6247652	5.64352952	4.55357071	6.94062182	10
sRNA32	no	no	no	no	no	no	no	no	4.32168228	5.86927071	10.734284	6.97507901	10
sRNA37	no	no	no	no	no	no	no	no	911.217961	776.609734	1267.10184	984.976512	984.976512
sRNA38	no	no	no	no	no	no	no	no	22.1787214	11.5702469	14.7672788	16.1720824	16.1720824
sRNA39	no	no	no	no	no	no	no	no	0.76535105	0	0	0.25511702	10
sRNA4	no	no	no	no	no	no	no	no	2.1047154	5.89547281	1.69132627	3.23050482	10
sRNA40	no	no	no	no	no	no	no	no	1.22775065	0	0.49330349	0.57368471	10
sRNA42	no	no	no	no	no	no	no	no	31.9362205	32.3629947	22.6860529	28.9950893	28.9950893
sRNA43_truncated	no	no	no	no	no	no	no	no	4.81077805	0.99817529	2.89941646	2.90278993	10
sRNA44	no	no	no	no	no	no	no	no	0.33484109	0.55580215	0	0.29688108	10
sRNA46	no	no	no	no	no	no	no	no	334.740274	313.579987	258.427379	302.249213	302.249213
sRNA48	no	no	no	no	no	no	no	no	112.869822	62.1744778	97.1222608	90.722187	90.722187
sRNA49	no	no	no	no	no	no	no	no	16.5539413	10.9911436	6.91733439	11.4874731	11.4874731
sRNA5	no	no	no	no	no	no	no	no	1.73329503	0	2.08928539	1.27419347	10
sRNA50	no	no	no	no	no	no	no	no	8.03618607	4.56992879	8.37121081	6.99244189	10
sRNA53	no	no	no	no	no	no	no	no	170.016302	84.1868106	157.158635	137.120583	137.120583
sRNA54	no	no	no	no	no	no	no	no	153.426495	80.4494864	144.031012	125.968998	125.968998
sRNA55	no	no	no	no	no	no	no	no	4.01809303	5.83592258	6.99594046	5.61665202	10
sRNA56	no	no	no	no	no	no	no	no	2.85154589	0.78888047	0.50921651	1.38321563	10
sRNA57	no	no	no	no	no	no	no	no	5.68019577	2.06249473	2.2827159	3.34165403	10
sRNA58	no	no	no	no	no	no	no	no	34.0635499	29.1382234	26.8692967	30.02369	30.02369
sRNA59	no	no	no	no	no	no	no	no	1.91790634	2.60470593	1.12087895	1.88116374	10
sRNA6	no	no	no	no	no	no	no	no	13.8400982	13.4627632	15.3073569	14.2034061	14.2034061
sRNA60	no	no	no	no	no	no	no	no	7.15841056	5.38845474	3.21065325	5.2520619	10
sRNA61	no	no	no	no	no	no	no	no	13.2332405	8.93277228	16.730964	12.9656589	12.9656589
sRNA62	no	no	no	no	no	no	no	no	118.656159	96.6378577	93.4412296	102.911749	102.911749
sRNA63	no	no	no	no	no	no	no	no	5.08034751	5.39703053	4.57241308	5.01659704	10
sRNA64	no	no	no	no	no	no	no	no	9.92539472	6.43560384	8.47443476	8.27847778	10
sRNA65	no	no	no	no	no	no	no	no	17.3329503	15.6441958	8.35714155	13.7780959	13.7780959
sRNA69	no	no	no	no	no	no	no	no	17.8346936	9.56146857	14.7768505	14.0576709	14.0576709
sRNA7	no	no	no	no	no	no	no	no	567.7119	305.487388	297.166025	390.121771	390.121771
sRNA70	no	no	no	no	no	no	no	no	267.756402	245.61622	245.021701	252.798108	252.798108
sRNA71	no	no	no	no	no	no	no	no	18.3500935	14.4974501	12.4773291	15.1082909	15.1082909
sRNA72	no	no	no	no	no	no	no	no	26.8415122	18.2177093	15.3383435	20.1325217	20.1325217
sRNA73	no	no	no	no	no	no	no	no	4.65252878	3.00328179	8.30826937	5.32135998	10
sRNA74	no	no	no	no	no	no	no	no	6.9867872	5.7986781	3.41752524	5.40099685	10
sRNA75	no	no	no	no	no	no	no	no	4.86467238	1.73032745	5.13780243	3.91093409	10
sRNA76	no	no	no	no	no	no	no	no	815.159157	514.901203	841.724428	723.928263	723.928263
sRNA77	no	no	no	no	no	no	no	no	10.2490489	5.46826463	5.29458657	7.0039667	10
sRNA8	no	no	no	no	no	no	no	no	26.7249909	17.0618334	18.7225884	20.8364709	20.8364709
sRNA81	no	no	no	no	no	no	no	no	83.6904584	61.0658836	76.499988	73.75211	73.75211
sRNA84	no	no	no	no	no	no	no	no	808.514727	735.832642	788.496305	777.614558	777.614558
sRNA85	no	no	no	no	no	no	no	no	32.5677014	14.5873687	13.293231	20.1494337	20.1494337
sRNA86	no	no	no	no	no	no	no	no	9.68169083	7.68594973	9.47142709	8.94635588	10
sRNA87	no	no	no	no	no	no	no	no	204.817697	105.25367	166.21426	158.761875	158.761875
sRNA88	no	no	no	no	no	no	no	no	75.3781794	56.5315415	59.912283	63.9406679	63.9406679
sRNA89	no	no	no	no	no	no	no	no	18792.9123	18557.6513	14591.4161	17313.9932	17313.9932
sRNA9	no	no	no	no	no	no	no	no	404.701382	279.612749	133.899157	272.737763	272.737763
sRNA90	no	no	no	no	no	no	no	no	632.849653	433.664628	227.906214	431.473498	431.473498
sRNA91	no	no	no	no	no	no	no	no	37.5454069	27.2163763	25.5881296	30.1166376	30.1166376
sRNA92	no	no	no	no	no	no	no	no	149.063373	96.6441856	73.6947936	106.467451	106.467451
sRNA93	no	no	no	no	no	no	no	no	82.4173208	50.7265764	24.6163328	52.5867433	52.5867433
sRNA94	no	no	no	no	no	no	no	no	95.2100826	80.0713678	109.990766	95.0907389	95.0907389
sRNA95	no	no	no	no	no	no	no	no	82.194675	51.8066109	53.5883375	62.5298745	62.5298745
sRNA96	no	no	no	no	no	no	no	no	257.046855	281.743025	225.655659	254.81518	254.81518
sRNA97	no	no	no	no	no	no	no	no	1647.83026	1175.44591	560.159253	1127.8118	1127.8118
sRNA98	no	no	no	no	no	no	no	no	5.42795024	2.25246135	1.24624041	2.97555066	10
sRNA99	no	no	no	no	no	no	no	no	3404.80799	1564.64647	2469.24554	2479.56666	2479.56666

Table S 22. sRNAs expression TPM values (MEP)

locus_tag	'old_locus_tag'	chrom	start	stop	strand	refseq_id	symbol	name	MEP_1	MEP_2	MEP_3	MEP_Mean	MEP_Mean_10
newcandsRNA1	no	no	no	no	no	no	no	no	0.67499224	0.69214324	0.82381082	0.73031543	10
sRNA1	no	no	no	no	no	no	no	no	155.248216	187.224746	235.060689	192.511217	192.511217
sRNA10	no	no	no	no	no	no	no	no	1.38125825	3.71793158	0.98337779	2.02752254	10
sRNA100	no	no	no	no	no	no	no	no	229.603716	137.563469	151.158181	172.775122	172.775122
sRNA101	no	no	no	no	no	no	no	no	104.364966	92.1916579	101.111939	99.2228542	99.2228542
sRNA102	no	no	no	no	no	no	no	no	101.707105	88.98495	122.484085	104.392047	104.392047
sRNA103	no	no	no	no	no	no	no	no	7.41869353	1.97223611	2.73865426	4.04319463	10
sRNA104	no	no	no	no	no	no	no	no	7.66598331	3.43908671	3.63849781	4.91452261	10
sRNA105	no	no	no	no	no	no	no	no	7.47900811	7.08321383	4.43719245	6.33313813	10
sRNA106	no	no	no	no	no	no	no	no	2.00980836	0.51521898	2.24850988	1.59117907	10
sRNA109	no	no	no	no	no	no	no	no	16.1182213	10.2290784	12.0350312	12.7941103	12.7941103
sRNA110	no	no	no	no	no	no	no	no	16.1182213	10.2290784	12.0350312	12.7941103	12.7941103
sRNA13	no	no	no	no	no	no	no	no	29.6747741	22.1876562	27.3865426	26.4163243	26.4163243
sRNA14	no	no	no	no	no	no	no	no	3.74781406	0.61139319	0.97026608	1.77649111	10
sRNA15	no	no	no	no	no	no	no	no	354.511296	464.929698	693.156861	504.199285	504.199285
sRNA17	no	no	no	no	no	no	no	no	36.2274317	29.6022654	38.3807786	34.7368252	34.7368252
sRNA18	no	no	no	no	no	no	no	no	26.0592832	38.1364071	22.1552094	28.7836333	28.7836333
sRNA19	no	no	no	no	no	no	no	no	40.4158984	31.8174009	30.8158488	34.349716	34.349716
sRNA2	no	no	no	no	no	no	no	no	24481.8304	16992.4471	22407.3527	21293.8767	21293.8767
sRNA20	no	no	no	no	no	no	no	no	19.2438264	46.4205943	25.1550466	30.2731558	30.2731558
sRNA21	no	no	no	no	no	no	no	no	2.48090075	3.11632453	2.4727655	2.68999693	10
sRNA22	no	no	no	no	no	no	no	no	0.7460811	0	0	0.2486937	10
sRNA24	no	no	no	no	no	no	no	no	81.386451	105.491831	160.472476	115.783586	115.783586
sRNA25	no	no	no	no	no	no	no	no	1.74838216	1.20669709	0.38299977	1.11269301	10
sRNA26	no	no	no	no	no	no	no	no	139.877577	193.448628	284.447146	205.92445	205.92445
sRNA27	no	no	no	no	no	no	no	no	5.32864559	3.04247798	3.7936944	4.05493932	10
sRNA28	no	no	no	no	no	no	no	no	5.54775108	4.22343982	5.50562168	5.09227086	10
sRNA29	no	no	no	no	no	no	no	no	4.08852443	2.44557277	1.69796564	2.74402095	10
sRNA3	no	no	no	no	no	no	no	no	543.007151	704.107753	611.363382	619.492762	619.492762
sRNA30	no	no	no	no	no	no	no	no	0.23230252	0.416859	0.99231758	0.5471597	10
sRNA31	no	no	no	no	no	no	no	no	7.00258091	5.95226547	3.3236278	5.42615806	10
sRNA32	no	no	no	no	no	no	no	no	5.45136591	3.66835916	5.33646345	4.81872951	10
sRNA37	no	no	no	no	no	no	no	no	858.504238	1745.55326	1619.59016	1407.88255	1407.88255
sRNA38	no	no	no	no	no	no	no	no	11.2654235	6.90282638	21.1267615	13.0983371	13.0983371
sRNA39	no	no	no	no	no	no	no	no	0.33186075	0	0	0.11062025	10
sRNA4	no	no	no	no	no	no	no	no	2.28154265	3.27532068	6.82218339	4.12634891	10
sRNA40	no	no	no	no	no	no	no	no	0	0	1.13703056	0.37901019	10
sRNA42	no	no	no	no	no	no	no	no	37.1823143	31.5764449	25.9270203	31.5619265	31.5619265
sRNA43_truncated	no	no	no	no	no	no	no	no	5.7364501	9.35805908	0.74255057	5.27901992	10
sRNA44	no	no	no	no	no	no	no	no	0.29037816	0	0	0.09679272	10
sRNA46	no	no	no	no	no	no	no	no	209.509401	177.008191	212.83256	199.783384	199.783384
sRNA48	no	no	no	no	no	no	no	no	61.5011091	142.226637	64.7529271	89.4935577	89.4935577
sRNA49	no	no	no	no	no	no	no	no	8.90057988	14.4261315	8.17639957	10.501037	10.501037
sRNA5	no	no	no	no	no	no	no	no	0	0	0	0	10
sRNA50	no	no	no	no	no	no	no	no	7.0981327	11.8110049	6.43168804	8.44694187	10
sRNA53	no	no	no	no	no	no	no	no	93.393838	112.404368	188.042719	131.280308	131.280308
sRNA54	no	no	no	no	no	no	no	no	91.6393407	120.486624	170.633001	127.586322	127.586322
sRNA55	no	no	no	no	no	no	no	no	2.32302525	5.73181119	4.1346566	4.06316435	10
sRNA56	no	no	no	no	no	no	no	no	0.54953285	0.49305903	0.78247265	0.60835484	10
sRNA57	no	no	no	no	no	no	no	no	1.84722489	8.28695594	5.26047876	5.1315532	10
sRNA58	no	no	no	no	no	no	no	no	28.8153983	30.8948688	22.4503056	27.3868576	27.3868576
sRNA59	no	no	no	no	no	no	no	no	2.72165088	2.17062672	3.0141402	2.6354726	10
sRNA6	no	no	no	no	no	no	no	no	17.4226893	22.0008914	25.3592271	21.5942693	21.5942693
sRNA60	no	no	no	no	no	no	no	no	7.65154643	5.44036316	2.05564848	5.04918602	10
sRNA61	no	no	no	no	no	no	no	no	11.6290366	9.33564457	19.3907967	13.4518259	13.4518259
sRNA62	no	no	no	no	no	no	no	no	69.2411396	79.1359738	92.1361542	80.1710892	80.1710892
sRNA63	no	no	no	no	no	no	no	no	3.87704903	2.21366501	4.01489413	3.36853606	10
sRNA64	no	no	no	no	no	no	no	no	8.33843799	6.27482488	5.36199677	6.65841988	10
sRNA65	no	no	no	no	no	no	no	no	14.2797728	17.5325989	12.0391472	14.617173	14.617173
sRNA69	no	no	no	no	no	no	no	no	15.3703926	11.549815	12.1739212	13.0313763	13.0313763
sRNA7	no	no	no	no	no	no	no	no	346.246913	377.153176	281.377164	334.925751	334.925751
sRNA70	no	no	no	no	no	no	no	no	211.092294	222.626869	325.882847	253.20067	253.20067
sRNA71	no	no	no	no	no	no	no	no	15.9134185	14.0034669	13.9439437	14.6202763	14.6202763
sRNA72	no	no	no	no	no	no	no	no	17.4838216	15.9655308	21.2122949	18.2205491	18.2205491
sRNA73	no	no	no	no	no	no	no	no	2.68981871	0	0.63833295	1.10938388	10
sRNA74	no	no	no	no	no	no	no	no	9.74712655	3.30908687	3.00082293	5.35234545	10
sRNA75	no	no	no	no	no	no	no	no	2.89282389	1.73035809	1.37301804	1.99873334	10
sRNA76	no	no	no	no	no	no	no	no	595.426375	784.865543	887.444568	755.912162	755.912162
sRNA77	no	no	no	no	no	no	no	no	6.66607245	4.5569679	2.03394287	4.41899441	10
sRNA8	no	no	no	no	no	no	no	no	19.0163927	8.53106782	12.4103801	13.3192802	13.3192802
sRNA81	no	no	no	no	no	no	no	no	56.5498572	64.576145	75.5688006	65.5649343	65.5649343
sRNA84	no	no	no	no	no	no	no	no	568.844354	623.36631	629.055843	607.088836	607.088836
sRNA85	no	no	no	no	no	no	no	no	21.0702465	12.8714357	14.6816578	16.20778	16.20778
sRNA86	no	no	no	no	no	no	no	no	8.03103014	7.53323756	10.9154934	8.82658704	10
sRNA87	no	no	no	no	no	no	no	no	121.002286	188.812604	186.918907	165.577932	165.577932
sRNA88	no	no	no	no	no	no	no	no	47.5409818	46.0677662	59.739057	51.115935	51.115935
sRNA89	no	no	no	no	no	no	no	no	15508.5591	15220.2278	16764.899	15831.2286	15831.2286
sRNA9	no	no	no	no	no	no	no	no	81.7478751	146.896683	212.19204	146.945533	146.945533
sRNA90	no	no	no	no	no	no	no	no	487.544924	183.157421	283.844176	318.182173	318.182173
sRNA91	no	no	no	no	no	no	no	no	30.0869238	39.9377812	34.6244146	34.8830399	34.8830399
sRNA92	no	no	no	no	no	no	no	no	48.236936	68.1687063	92.2271637	69.5442687	69.5442687
sRNA93	no	no	no	no	no	no	no	no	20.4932227	25.4242714	39.9874512	28.6349818	28.6349818
sRNA94	no	no	no	no	no	no	no	no	75.0112346	86.0388002	99.178408	86.7428143	86.7428143
sRNA95	no	no	no	no	no	no	no	no	45.3906907	81.4520537	68.4612087	65.1013177	65.1013177
sRNA96	no	no	no	no	no	no	no	no	274.491661	265.19532	314.721677	284.802886	284.802886
sRNA97	no	no	no	no	no	no	no	no	1211.58825	442.265195	584.743198	746.198881	746.198881
sRNA98	no	no	no	no	no	no	no	no	3.36227338	3.01674273	2.39374856	2.92425489	10
sRNA99	no	no	no	no	no	no	no	no	1697.66373	1731.08392	1924.25253	1784.33339	1784.33339

Table S 23. sRNAs expression TPM values (LEP)

locus_tag	*old_locus_tag*	chrom	start	stop	strand	refseq_id	symbol	name	LEP_1	LEP_2	LEP_3	LEP_Mean	LEP_Mean_10
newcwndsRNA1	no	no	no	no	no	no	no	no	9.083142255	26.60994423	39.66214552	25.11841067	25.11841067
sRNA1	no	no	no	no	no	no	no	no	376.7113735	568.7660982	556.4810952	500.6528556	500.6528556
sRNA10	no	no	no	no	no	no	no	no	0.427993012	3.688736819	2.168448229	2.095059353	10
sRNA100	no	no	no	no	no	no	no	no	754.2936249	695.7970236	984.3240233	811.4715573	811.4715573
sRNA101	no	no	no	no	no	no	no	no	312.0474522	362.0398116	514.333094	396.1401193	396.1401193
sRNA102	no	no	no	no	no	no	no	no	63.9701238	100.4480775	119.9516857	94.78996234	94.78996234
sRNA103	no	no	no	no	no	no	no	no	58.9157692	91.47802887	140.1913438	96.86171396	96.86171396
sRNA104	no	no	no	no	no	no	no	no	17.6832446	26.53841212	26.40989238	23.5438497	23.5438497
sRNA105	no	no	no	no	no	no	no	no	6.179801534	3.328860057	6.849123063	5.452594885	10
sRNA106	no	no	no	no	no	no	no	no	4.448241975	4.34497277	2.253724282	3.682313009	10
sRNA109	no	no	no	no	no	no	no	no	31.18422928	51.44369118	51.53400617	44.72064221	44.72064221
sRNA110	no	no	no	no	no	no	no	no	31.18422928	51.44369118	51.53400617	44.72064221	44.72064221
sRNA13	no	no	no	no	no	no	no	no	67.0890551	55.7673545	60.39011733	61.08217564	61.08217564
sRNA14	no	no	no	no	no	no	no	no	6.756583011	11.52525326	12.83721351	10.3730166	10.3730166
sRNA15	no	no	no	no	no	no	no	no	3189.598958	2480.885629	2608.066796	2759.517128	2759.517128
sRNA17	no	no	no	no	no	no	no	no	83.12093815	79.0873475	72.784834	78.33103988	78.33103988
sRNA18	no	no	no	no	no	no	no	no	261.5249179	250.445342	158.8764049	223.6152856	223.6152856
sRNA19	no	no	no	no	no	no	no	no	25.20791493	34.5076729	39.70694231	33.14084338	33.14084338
sRNA2	no	no	no	no	no	no	no	no	28956.40969	28214.94431	38474.59046	31881.98149	31881.98149
sRNA20	no	no	no	no	no	no	no	no	11.33917288	9.548211767	13.86736028	11.58491497	11.58491497
sRNA21	no	no	no	no	no	no	no	no	13.22207537	20.75959006	26.48454244	20.15540262	20.15540262
sRNA22	no	no	no	no	no	no	no	no	1.155893535	1.66038032	0.585639303	1.133971053	10
sRNA24	no	no	no	no	no	no	no	no	297.3091802	326.3501513	331.1333254	318.264219	318.264219
sRNA25	no	no	no	no	no	no	no	no	12.00182508	9.577772794	10.97919577	10.85293122	10.85293122
sRNA26	no	no	no	no	no	no	no	no	800.3647648	937.374628	929.987587	889.2423266	889.2423266
sRNA27	no	no	no	no	no	no	no	no	210.442744	125.0557538	120.1587521	151.8857499	151.8857499
sRNA28	no	no	no	no	no	no	no	no	8.751330791	13.46874299	12.66830281	11.62945886	11.62945886
sRNA29	no	no	no	no	no	no	no	no	13.09087958	39.12520187	41.18606002	31.13404716	31.13404716
sRNA3	no	no	no	no	no	no	no	no	275.0418249	298.706789	275.0077401	282.9187847	282.9187847
sRNA30	no	no	no	no	no	no	no	no	2.303380572	2.067928217	4.011629223	2.794312671	10
sRNA31	no	no	no	no	no	no	no	no	16.90160864	27.7778435	19.47954574	21.38633261	21.38633261
sRNA32	no	no	no	no	no	no	no	no	8.868015202	14.55821465	14.4418652	12.62269835	12.62269835
sRNA37	no	no	no	no	no	no	no	no	1421.490672	3599.411526	4340.31313	3120.405109	3120.405109
sRNA38	no	no	no	no	no	no	no	no	21.11432191	54.29979254	59.09604339	44.83671928	44.83671928
sRNA39	no	no	no	no	no	no	no	no	0	2.363346534	1.041981616	1.135109383	10
sRNA4	no	no	no	no	no	no	no	no	2.82781097	4.874402226	3.223630625	3.64194794	10
sRNA40	no	no	no	no	no	no	no	no	0.32991128	2.843401298	0	1.057770859	10
sRNA42	no	no	no	no	no	no	no	no	20.48215658	31.60091503	31.46846875	27.85051345	27.85051345
sRNA43_truncated	no	no	no	no	no	no	no	no	9.695351897	13.9268635	9.005698255	10.87597122	10.87597122
sRNA44	no	no	no	no	no	no	no	no	1.439612857	2.067928217	4.558669571	2.688736882	10
sRNA46	no	no	no	no	no	no	no	no	626.9591393	733.7809802	753.1510347	704.6303847	704.6303847
sRNA48	no	no	no	no	no	no	no	no	68.71101367	91.75993342	75.47302436	78.64799048	78.64799048
sRNA49	no	no	no	no	no	no	no	no	32.38320158	43.4497277	41.01778194	38.95023707	38.95023707
sRNA5	no	no	no	no	no	no	no	no	1.397271303	1.338071199	0.589945474	1.108429325	10
sRNA50	no	no	no	no	no	no	no	no	71.34081493	77.43242324	57.7431479	68.83879536	68.83879536
sRNA53	no	no	no	no	no	no	no	no	216.9356437	400.1898606	374.5370646	330.5541896	330.5541896
sRNA54	no	no	no	no	no	no	no	no	200.2948261	371.7992318	361.3232941	311.1391174	311.1391174
sRNA55	no	no	no	no	no	no	no	no	14.75603179	26.36608477	30.54308613	23.88840089	23.88840089
sRNA56	no	no	no	no	no	no	no	no	1.362214317	2.445936601	3.019505867	2.275885595	10
sRNA57	no	no	no	no	no	no	no	no	2.289504785	4.933129963	3.383301754	3.535312168	10
sRNA58	no	no	no	no	no	no	no	no	22.68666503	44.52645437	51.49680066	39.56997335	39.56997335
sRNA59	no	no	no	no	no	no	no	no	8.433235082	7.806734926	6.409111776	7.549693928	10
sRNA6	no	no	no	no	no	no	no	no	80.13844906	47.56234899	22.08422148	49.92833984	49.92833984
sRNA60	no	no	no	no	no	no	no	no	6.083787669	6.425765646	3.85297722	5.454176845	10
sRNA61	no	no	no	no	no	no	no	no	21.05110538	30.23880662	45.40107324	32.23032841	32.23032841
sRNA62	no	no	no	no	no	no	no	no	224.2545319	228.2058848	264.6381213	239.032846	239.032846
sRNA63	no	no	no	no	no	no	no	no	21.84240197	16.31524055	25.45309576	21.20357943	21.20357943
sRNA64	no	no	no	no	no	no	no	no	105.3493535	104.8766121	71.78704925	94.0043829	94.0043829
sRNA65	no	no	no	no	no	no	no	no	233.111429	470.6665443	755.7201521	486.4993751	486.4993751
sRNA69	no	no	no	no	no	no	no	no	24.28940791	39.3728112	35.44108524	33.02259142	33.02259142
sRNA7	no	no	no	no	no	no	no	no	169.9702914	493.2353452	410.8576929	358.0211098	358.0211098
sRNA70	no	no	no	no	no	no	no	no	475.5312499	466.1529781	523.8373811	488.507203	488.507203
sRNA71	no	no	no	no	no	no	no	no	21.80970377	32.14575839	26.18368774	26.71304997	26.71304997
sRNA72	no	no	no	no	no	no	no	no	22.56753435	46.96792428	40.11629223	36.55058362	36.55058362
sRNA73	no	no	no	no	no	no	no	no	7.223320653	9.57772794	14.07589201	10.29232849	10.29232849
sRNA74	no	no	no	no	no	no	no	no	37.87517538	46.43245007	61.62193342	48.64318629	48.64318629
sRNA75	no	no	no	no	no	no	no	no	271.4485111	181.338941	172.3865199	208.3896417	208.3896417
sRNA76	no	no	no	no	no	no	no	no	3822.27074	4671.591481	6353.486474	4949.116232	4949.116232
sRNA77	no	no	no	no	no	no	no	no	50.35962492	75.44726923	71.26248184	65.689792	65.689792
sRNA8	no	no	no	no	no	no	no	no	46.15688975	67.35995634	101.6901361	71.73566073	71.73566073
sRNA81	no	no	no	no	no	no	no	no	67.65328588	108.4866957	111.0912708	95.74375078	95.74375078
sRNA84	no	no	no	no	no	no	no	no	1186.800844	1135.338545	1544.477251	1288.872213	1288.872213
sRNA85	no	no	no	no	no	no	no	no	52.78580477	94.97958021	129.4982065	92.42119716	92.42119716
sRNA86	no	no	no	no	no	no	no	no	51.80549697	79.9401965	87.39620807	73.04730051	73.04730051
sRNA87	no	no	no	no	no	no	no	no	167.6725563	406.3276208	424.3674442	332.7892071	332.7892071
sRNA88	no	no	no	no	no	no	no	no	84.99742145	86.33359849	102.0633109	91.13144362	91.13144362
sRNA89	no	no	no	no	no	no	no	no	40956.95285	33311.07735	29132.5065	34466.84557	34466.84557
sRNA9	no	no	no	no	no	no	no	no	779.8752307	603.7069376	634.4054355	672.6625346	672.6625346
sRNA90	no	no	no	no	no	no	no	no	1289.173314	1350.098635	2019.946487	1553.072812	1553.072812
sRNA91	no	no	no	no	no	no	no	no	43.16516616	65.67339773	43.35147708	50.73001366	50.73001366
sRNA92	no	no	no	no	no	no	no	no	235.9271424	200.2241085	207.0172299	214.3894936	214.3894936
sRNA93	no	no	no	no	no	no	no	no	215.8991678	177.473285	150.7339891	181.368814	181.368814
sRNA94	no	no	no	no	no	no	no	no	102.8471809	128.1670779	155.0731941	128.6958176	128.6958176
sRNA95	no	no	no	no	no	no	no	no	44.17338399	45.49442077	54.36813289	48.01197922	48.01197922
sRNA96	no	no	no	no	no	no	no	no	281.540509	246.5504094	274.5285436	267.5398206	267.5398206
sRNA97	no	no	no	no	no	no	no	no	4233.671416	4123.30203	6387.74807	4914.907172	4914.907172
sRNA98	no	no	no	no	no	no	no	no	6.667680603	5.986107997	5.278459504	5.977416034	10
sRNA99	no	no	no	no									

Table S 24. sRNAs expression TPM values (ESP)

locus_tag	*old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	ESP_1	ESP_2	ESP_3	ESP_Mean	ESP_Mean_10
newcandsRNA1	no	no	no	no	no	no	no	no	67.89759084	75.5336063	72.68770475	72.03963396	72.03963396
sRNA1	no	no	no	no	no	no	no	no	454.3915695	546.9453834	460.5552921	487.297415	487.297415
sRNA10	no	no	no	no	no	no	no	no	1.402769873	1.836957341	0	1.079909071	10
sRNA100	no	no	no	no	no	no	no	no	888.194001	869.8330686	948.8026603	902.2765766	902.2765766
sRNA101	no	no	no	no	no	no	no	no	311.4149118	454.6662783	302.6774397	356.2528766	356.2528766
sRNA102	no	no	no	no	no	no	no	no	153.138026	135.2618985	135.2702085	141.2233777	141.2233777
sRNA103	no	no	no	no	no	no	no	no	81.10926019	118.3948635	87.11888524	95.54100297	95.54100297
sRNA104	no	no	no	no	no	no	no	no	25.66289551	30.30214214	22.17474567	26.04659444	26.04659444
sRNA105	no	no	no	no	no	no	no	no	3.375771402	4.144354977	1.937364019	3.152496799	10
sRNA106	no	no	no	no	no	no	no	no	0.583173992	1.527357789	2.008110458	1.372880746	10
sRNA109	no	no	no	no	no	no	no	no	49.77315258	65.09187686	51.3252437	55.39675771	55.39675771
sRNA110	no	no	no	no	no	no	no	no	49.77315258	65.09187686	51.3252437	55.39675771	55.39675771
sRNA13	no	no	no	no	no	no	no	no	37.20608266	39.09953825	32.02900192	36.11154094	36.11154094
sRNA14	no	no	no	no	no	no	no	no	2.76813255	3.624929153	2.118184661	2.837082121	10
sRNA15	no	no	no	no	no	no	no	no	1849.217662	2912.705138	2392.00695	2384.64325	2384.64325
sRNA17	no	no	no	no	no	no	no	no	48.61751788	61.22803594	66.02569274	58.62374885	58.62374885
sRNA18	no	no	no	no	no	no	no	no	71.94403904	70.32272831	71.37076409	71.21251048	71.21251048
sRNA19	no	no	no	no	no	no	no	no	13.5346617	15.0268109	13.77900736	14.11349332	14.11349332
sRNA2	no	no	no	no	no	no	no	no	21345.03483	24516.97455	20310.03485	22057.34808	22057.34808
sRNA20	no	no	no	no	no	no	no	no	7.689257082	8.810591692	9.806410466	8.76875308	10
sRNA21	no	no	no	no	no	no	no	no	12.76565982	19.13645852	15.03808285	15.64673373	15.64673373
sRNA22	no	no	no	no	no	no	no	no	0.252566838	0	0.579795071	0.27745397	10
sRNA24	no	no	no	no	no	no	no	no	207.2099221	296.2279532	202.4825366	235.3068039	235.3068039
sRNA25	no	no	no	no	no	no	no	no	6.19187544	7.154465434	7.316098334	6.887479736	10
sRNA26	no	no	no	no	no	no	no	no	704.1076739	790.2982749	649.3146142	714.573521	714.573521
sRNA27	no	no	no	no	no	no	no	no	125.2875159	109.682024	121.0301603	118.6665667	118.6665667
sRNA28	no	no	no	no	no	no	no	no	4.097564629	5.58942612	5.487073751	5.0580215	10
sRNA29	no	no	no	no	no	no	no	no	24.68251523	30.35878166	29.12503908	28.05544533	28.05544533
sRNA3	no	no	no	no	no	no	no	no	342.829574	376.0565894	319.2954345	346.0605326	346.0605326
sRNA30	no	no	no	no	no	no	no	no	0.629121034	4.634142383	1.083162611	2.115475343	10
sRNA31	no	no	no	no	no	no	no	no	15.63728724	16.82847218	12.60218037	15.0226466	15.0226466
sRNA32	no	no	no	no	no	no	no	no	8.304397649	4.078045297	5.295461652	5.892634866	10
sRNA37	no	no	no	no	no	no	no	no	2649.207527	2996.278099	2369.60784	2671.697822	2671.697822
sRNA38	no	no	no	no	no	no	no	no	39.43844762	32.52204583	40.14301575	37.3678364	37.3678364
sRNA39	no	no	no	no	no	no	no	no	0.449372167	0	1.031583439	0.493651869	10
sRNA4	no	no	no	no	no	no	no	no	2.162603554	2.427407915	0.709213614	1.766408361	10
sRNA40	no	no	no	no	no	no	no	no	1.441735703	1.41598795	1.241123825	1.366282493	10
sRNA42	no	no	no	no	no	no	no	no	30.45774587	32.76273917	32.1057181	31.77540104	31.77540104
sRNA43_truncated	no	no	no	no	no	no	no	no	2.118468788	9.709631661	5.673708912	5.833936454	10
sRNA44	no	no	no	no	no	no	no	no	4.325207109	1.158535596	3.610542035	3.031428247	10
sRNA46	no	no	no	no	no	no	no	no	469.1687023	625.4099038	477.2321287	523.9369116	523.9369116
sRNA48	no	no	no	no	no	no	no	no	310.8284431	187.198407	280.7043443	259.5770648	259.5770648
sRNA49	no	no	no	no	no	no	no	no	22.54939437	22.52852739	13.83364982	19.63719053	19.63719053
sRNA5	no	no	no	no	no	no	no	no	0.508847895	1.499281359	0	0.669376418	10
sRNA50	no	no	no	no	no	no	no	no	44.21322822	43.59526538	53.15520218	46.9878986	46.9878986
sRNA53	no	no	no	no	no	no	no	no	210.6720348	251.7200527	247.7854291	236.7258388	236.7258388
sRNA54	no	no	no	no	no	no	no	no	198.0646566	228.7455293	231.4481946	219.4194602	219.4194602
sRNA55	no	no	no	no	no	no	no	no	20.44643361	20.85364073	20.30929895	20.53645776	20.53645776
sRNA56	no	no	no	no	no	no	no	no	0	1.096248736	1.708213436	0.934820724	10
sRNA57	no	no	no	no	no	no	no	no	2.084437161	0.409442299	0.478505571	0.99079501	10
sRNA58	no	no	no	no	no	no	no	no	15.95111842	15.42523044	18.02710349	16.46781745	16.46781745
sRNA59	no	no	no	no	no	no	no	no	5.73281889	6.032611387	5.405130976	5.732520417	10
sRNA6	no	no	no	no	no	no	no	no	5.067919441	7.551935736	8.424598082	7.014817753	10
sRNA60	no	no	no	no	no	no	no	no	5.278218845	6.911941182	6.50713508	6.232431702	10
sRNA61	no	no	no	no	no	no	no	no	25.27785711	29.09982423	27.34931542	27.24233225	27.24233225
sRNA62	no	no	no	no	no	no	no	no	177.1009534	249.9447118	187.0493712	204.6983455	204.6983455
sRNA63	no	no	no	no	no	no	no	no	25.77226857	29.99941368	27.93812527	27.90326917	27.90326917
sRNA64	no	no	no	no	no	no	no	no	26.22441363	31.12192464	22.15732638	26.50122155	26.50122155
sRNA65	no	no	no	no	no	no	no	no	1406.201158	1404.826634	1195.27525	1335.434347	1335.434347
sRNA69	no	no	no	no	no	no	no	no	18.47156119	18.52495514	27.47269579	21.48973737	21.48973737
sRNA7	no	no	no	no	no	no	no	no	142.1551403	192.0079661	125.7672142	153.3101069	153.3101069
sRNA70	no	no	no	no	no	no	no	no	318.4355379	460.9964249	412.125059	397.1856739	397.1856739
sRNA71	no	no	no	no	no	no	no	no	11.81014636	14.2446692	9.512805362	11.85587364	11.85587364
sRNA72	no	no	no	no	no	no	no	no	15.8299078	18.43650708	15.59695689	16.62112392	16.62112392
sRNA73	no	no	no	no	no	no	no	no	7.891605953	10.73169815	5.57417016	8.065824755	10
sRNA74	no	no	no	no	no	no	no	no	53.86443492	50.45004492	59.77866504	54.69771496	54.69771496
sRNA75	no	no	no	no	no	no	no	no	68.22402157	130.324325	78.12054866	92.22296506	92.22296506
sRNA76	no	no	no	no	no	no	no	no	5443.125023	5002.355678	5187.557553	5211.012751	5211.012751
sRNA77	no	no	no	no	no	no	no	no	35.03149112	56.78023732	40.45601138	44.0892466	44.0892466
sRNA8	no	no	no	no	no	no	no	no	105.41435	121.4456642	100.9832222	109.2810788	109.2810788
sRNA81	no	no	no	no	no	no	no	no	62.44677719	79.22829621	57.57639518	66.41715619	66.41715619
sRNA84	no	no	no	no	no	no	no	no	2209.12356	2291.068504	2424.438859	2308.210308	2308.210308
sRNA85	no	no	no	no	no	no	no	no	71.02445358	76.31429796	68.98035572	72.10636909	72.10636909
sRNA86	no	no	no	no	no	no	no	no	103.8049706	110.4470601	82.83615012	99.02939362	99.02939362
sRNA87	no	no	no	no	no	no	no	no	313.7895353	359.4943526	319.67456	330.9861493	330.9861493
sRNA88	no	no	no	no	no	no	no	no	95.43619779	99.4221121	85.897314	93.58520796	93.58520796
sRNA89	no	no	no	no	no	no	no	no	77170.64216	77982.58451	63637.33186	72930.18618	72930.18618
sRNA9	no	no	no	no	no	no	no	no	459.7733433	639.9764302	515.0773706	538.2757147	538.2757147
sRNA90	no	no	no	no	no	no	no	no	1435.575559	1506.868632	1426.841081	1456.428424	1456.428424
sRNA91	no	no	no	no	no	no	no	no	32.09024629	34.80589736	25.30291152	30.73301839	30.73301839
sRNA92	no	no	no	no	no	no	no	no	175.5987827	241.157135	205.1637415	207.3065531	207.3065531
sRNA93	no	no	no	no	no	no	no	no	64.06445381	153.263171	81.79128888	99.70630457	99.70630457
sRNA94	no	no	no	no	no	no	no	no	91.15490251	111.0865386	84.3430384	95.52815983	95.52815983
sRNA95	no	no	no	no	no	no	no	no	36.42279671	39.79671398	44.41916846	40.21289305	40.21289305
sRNA96	no	no	no	no	no	no	no	no	146.0604502	181.1942553	173.1396333	166.7981129	166.7981129
sRNA97	no	no	no	no	no	no	no	no	8884.231331	7737.427365	7644.030228	8088.562975	8088.562975
sRNA98	no	no	no	no	no	no	no	no	6.373989424	3.130078627	3.658049167	4.387372406	10
sRNA99	no	no	no	no	no	no	no	no	8211.042843	6361.79628	7465.534728	7346.124617	7346.124617

Table S 25. sRNAs expression TPM values (LSP)

locus_tag	*old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	LSP_1	LSP_2	LSP_3	LSP_Mean	LSP_Mean_10
newcandnsRNA1	no	no	no	no	no	no	no	no	199.3013632	173.0543275	177.1470677	183.1675861	183.1675861
sRNA1	no	no	no	no	no	no	no	no	476.1315172	312.6926643	410.7815946	399.86861	399.86861
sRNA10	no	no	no	no	no	no	no	no	0.366759682	0	2.501772444	0.956177375	10
sRNA100	no	no	no	no	no	no	no	no	4437.225832	5103.008205	4222.429512	4587.554517	4587.554517
sRNA101	no	no	no	no	no	no	no	no	119.4169525	101.6869382	67.37103898	96.15830987	96.15830987
sRNA102	no	no	no	no	no	no	no	no	4428.692155	5634.354105	3901.894523	4654.980261	4654.980261
sRNA103	no	no	no	no	no	no	no	no	138.3275549	109.0674417	81.33258372	109.5758601	109.5758601
sRNA104	no	no	no	no	no	no	no	no	1110.034854	1132.844276	1114.092879	1118.990669	1118.990669
sRNA105	no	no	no	no	no	no	no	no	7.060869325	3.926934603	4.085356627	5.024386852	10
sRNA106	no	no	no	no	no	no	no	no	18.6017214	16.73359493	10.40062701	15.24531445	15.24531445
sRNA109	no	no	no	no	no	no	no	no	716.5017148	562.2766208	474.0171481	584.2651612	584.2651612
sRNA110	no	no	no	no	no	no	no	no	716.5017148	562.2766208	474.0171481	584.2651612	584.2651612
sRNA13	no	no	no	no	no	no	no	no	122.2768893	111.6642856	122.2832552	118.7414767	118.7414767
sRNA14	no	no	no	no	no	no	no	no	7.961130164	5.366810625	3.878938608	5.735626466	10
sRNA15	no	no	no	no	no	no	no	no	1240.548376	1224.176297	987.5893752	1150.771349	1150.771349
sRNA17	no	no	no	no	no	no	no	no	51.87560363	59.21607504	43.4092957	51.50032479	51.50032479
sRNA18	no	no	no	no	no	no	no	no	69.05975874	58.71609644	55.90594461	61.2272666	61.2272666
sRNA19	no	no	no	no	no	no	no	no	30.6481356	25.19115191	25.6376972	27.15899491	27.15899491
sRNA2	no	no	no	no	no	no	no	no	14121.03734	13309.86127	12023.4182	13151.43894	13151.43894
sRNA20	no	no	no	no	no	no	no	no	19.09867085	17.22679954	14.03992931	16.78846656	16.78846656
sRNA21	no	no	no	no	no	no	no	no	113.5673136	106.0335886	80.36900602	99.98996938	99.98996938
sRNA22	no	no	no	no	no	no	no	no	0.792415079	0.195869001	0.193046049	0.39377671	10
sRNA24	no	no	no	no	no	no	no	no	187.7851972	181.4788564	172.1368184	180.4669573	180.4669573
sRNA25	no	no	no	no	no	no	no	no	12.14167579	9.886230098	9.604548946	10.54415161	10.54415161
sRNA26	no	no	no	no	no	no	no	no	515.0986917	398.5974974	472.3324037	462.0095309	462.0095309
sRNA27	no	no	no	no	no	no	no	no	30.35588193	26.96122873	22.31099975	26.54270347	26.54270347
sRNA28	no	no	no	no	no	no	no	no	9.820473064	4.236955756	10.96171347	8.339714097	10
sRNA29	no	no	no	no	no	no	no	no	8.68486927	1.073362125	1.939469304	3.899233566	10
sRNA3	no	no	no	no	no	no	no	no	217.835948	168.4189913	176.0833973	187.4461122	187.4461122
sRNA30	no	no	no	no	no	no	no	no	15.29721292	10.00178344	17.79182585	14.3636074	14.3636074
sRNA31	no	no	no	no	no	no	no	no	18.26745339	23.09276687	28.7360181	23.36541279	23.36541279
sRNA32	no	no	no	no	no	no	no	no	14.47478212	8.944684375	6.347354086	9.22273526	10
sRNA37	no	no	no	no	no	no	no	no	4147.66367	4275.634296	4480.485237	4301.261068	4301.261068
sRNA38	no	no	no	no	no	no	no	no	211.5769563	128.1109633	207.8815339	182.5231512	182.5231512
sRNA39	no	no	no	no	no	no	no	no	4.934584812	1.393976786	3.091243873	3.139935157	10
sRNA4	no	no	no	no	no	no	no	no	22.29374924	13.1774368	10.39001413	15.28706672	15.28706672
sRNA40	no	no	no	no	no	no	no	no	0.848131765	0.83856416	2.203942391	1.296879439	10
sRNA42	no	no	no	no	no	no	no	no	39.49145271	41.13483593	41.49218489	40.70615784	40.70615784
sRNA43_truncated	no	no	no	no	no	no	no	no	8.308229531	4.381068988	5.937150931	6.208816787	10
sRNA44	no	no	no	no	no	no	no	no	4.317761711	4.573986328	2.103763191	3.66517041	10
sRNA46	no	no	no	no	no	no	no	no	514.6427069	539.2779063	444.4854138	499.4686757	499.4686757
sRNA48	no	no	no	no	no	no	no	no	191.3615263	150.5435862	179.7520472	173.8857199	173.8857199
sRNA49	no	no	no	no	no	no	no	no	159.48689	159.1952815	168.4901576	162.3907764	162.3907764
sRNA5	no	no	no	no	no	no	no	no	4.390329135	1.183855285	1.944655051	2.506279823	10
sRNA50	no	no	no	no	no	no	no	no	14.80375444	9.351260937	11.08649809	11.74717115	11.74717115
sRNA53	no	no	no	no	no	no	no	no	427.9988119	133.2203876	323.2188788	294.8126928	294.8126928
sRNA54	no	no	no	no	no	no	no	no	416.0875945	148.790198	302.5936905	289.157161	289.157161
sRNA55	no	no	no	no	no	no	no	no	73.71036064	37.81162031	48.0860158	53.20266558	53.20266558
sRNA56	no	no	no	no	no	no	no	no	9.630399392	3.462458468	4.26569495	5.78618427	10
sRNA57	no	no	no	no	no	no	no	no	5.558839518	1.939811069	2.549138187	3.349262925	10
sRNA58	no	no	no	no	no	no	no	no	20.59576711	11.41874601	12.9423	14.98560437	14.98560437
sRNA59	no	no	no	no	no	no	no	no	10.2779518	11.74982208	8.763605247	10.26379304	10.26379304
sRNA6	no	no	no	no	no	no	no	no	9.457954224	7.996005729	7.079330104	8.177763352	10
sRNA60	no	no	no	no	no	no	no	no	22.54017978	10.91554703	9.712288503	14.38933844	14.38933844
sRNA61	no	no	no	no	no	no	no	no	47.45474975	36.31434734	59.2293021	47.66613306	47.66613306
sRNA62	no	no	no	no	no	no	no	no	329.0386459	293.299086	283.810904	302.0495453	302.0495453
sRNA63	no	no	no	no	no	no	no	no	102.0097791	105.3005257	109.9843251	105.7648767	105.7648767
sRNA64	no	no	no	no	no	no	no	no	64.85083304	28.81129914	24.77695235	39.47969484	39.47969484
sRNA65	no	no	no	no	no	no	no	no	6365.378564	5458.756719	6973.338547	6265.82461	6265.82461
sRNA69	no	no	no	no	no	no	no	no	30.09911225	19.97421999	17.0018413	22.35839118	22.35839118
sRNA7	no	no	no	no	no	no	no	no	1159.33958	794.2879725	1412.947467	1122.191673	1122.191673
sRNA70	no	no	no	no	no	no	no	no	1237.436536	925.5803831	940.604283	1034.540401	1034.540401
sRNA71	no	no	no	no	no	no	no	no	13.81388263	10.92644079	8.551824367	11.0973826	11.0973826
sRNA72	no	no	no	no	no	no	no	no	80.32185522	47.69291223	69.49110664	65.83529136	65.83529136
sRNA73	no	no	no	no	no	no	no	no	25.71178402	8.944684375	8.815769564	14.49074599	14.49074599
sRNA74	no	no	no	no	no	no	no	no	44.20777528	30.1537298	31.3550567	35.23885392	35.23885392
sRNA75	no	no	no	no	no	no	no	no	330.5473534	304.5411878	324.2290344	319.7725252	319.7725252
sRNA76	no	no	no	no	no	no	no	no	7030.8032	3541.543628	7397.276012	5989.87428	5989.87428
sRNA77	no	no	no	no	no	no	no	no	272.7507469	268.007189	263.9802799	268.2460719	268.2460719
sRNA8	no	no	no	no	no	no	no	no	2314.492414	2025.658987	1991.338832	2110.496744	2110.496744
sRNA81	no	no	no	no	no	no	no	no	127.0290605	93.99857662	107.5106572	109.5127648	109.5127648
sRNA84	no	no	no	no	no	no	no	no	10241.20991	12099.47455	12845.45783	11728.7141	11728.7141
sRNA85	no	no	no	no	no	no	no	no	186.1723621	105.453121	109.9651256	133.8635363	133.8635363
sRNA86	no	no	no	no	no	no	no	no	601.3496535	711.4857514	638.7025049	650.5126366	650.5126366
sRNA87	no	no	no	no	no	no	no	no	282.3114674	290.9653211	272.2517071	281.8428319	281.8428319
sRNA88	no	no	no	no	no	no	no	no	152.8688472	90.98616152	158.9298736	134.2616274	134.2616274
sRNA89	no	no	no	no	no	no	no	no	87703.57846	118501.819	99587.12906	101930.8422	101930.8422
sRNA9	no	no	no	no	no	no	no	no	232.1329134	164.4476264	207.2486004	201.2763801	201.2763801
sRNA90	no	no	no	no	no	no	no	no	9785.435889	8702.466387	8286.572942	8924.825073	8924.825073
sRNA91	no	no	no	no	no	no	no	no	462.6969162	307.9424	402.4683186	391.0358783	391.0358783
sRNA92	no	no	no	no	no	no	no	no	115.6724734	88.96851838	96.31346106	100.3181509	100.3181509
sRNA93	no	no	no	no	no	no	no	no	20.55669861	18.06649121	19.11538153	19.24619045	19.24619045
sRNA94	no	no	no	no	no	no	no	no	236.6743608	223.4728403	234.3288426	231.4920146	231.4920146
sRNA95	no	no	no	no	no	no	no	no	45.70983826	29.65869029	26.7952996	34.05460938	34.05460938
sRNA96	no	no	no	no	no	no	no	no	183.2277287	167.4345988	123.2176456	157.959991	157.959991
sRNA97	no	no	no	no	no	no	no	no	49842.28488	54647.62858	49150.52353	51213.479	51213.479
sRNA98	no	no	no	no	no	no	no	no	1.071324334	1.765398232	2.435936327	1.75752964	10
sRNA99	no	no	no	no	no	no	no	no	17363.54547	12857.13333	28957.67303	19726.11061	19726.11061

Table S 26. sRNAs expression TPM values (NaCl)

locus_tag	old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	NaCl_1	NaCl_2	NaCl_3	NaCl_Mean	NaCl_Mean_10
newcandsRNA1	no	no	no	no	no	no	no	no	0.945030241	0.856257798	1.197477024	0.99588354	10
sRNA1	no	no	no	no	no	no	no	no	513.2695499	464.412823	436.3606276	471.3476668	471.3476668
sRNA10	no	no	no	no	no	no	no	no	2.961201179	3.449619675	7.290045938	4.566955597	10
sRNA100	no	no	no	no	no	no	no	no	240.0750309	255.4804114	176.1655597	223.907014	223.907014
sRNA101	no	no	no	no	no	no	no	no	226.3782639	195.8577047	150.9829452	191.0729713	191.0729713
sRNA102	no	no	no	no	no	no	no	no	97.63168243	162.8797321	160.2366533	140.2493559	140.2493559
sRNA103	no	no	no	no	no	no	no	no	4.375845674	6.404670221	5.459465143	5.413327013	10
sRNA104	no	no	no	no	no	no	no	no	3.65214812	4.490893762	4.231085486	4.124709123	10
sRNA105	no	no	no	no	no	no	no	no	4.326586624	3.458968238	9.287748627	5.691101163	10
sRNA106	no	no	no	no	no	no	no	no	5.80357406	6.373829112	3.208969329	5.128790834	10
sRNA109	no	no	no	no	no	no	no	no	18.54167507	23.12719379	21.48089554	21.04992147	21.04992147
sRNA110	no	no	no	no	no	no	no	no	18.54167507	23.12719379	21.48089554	21.04992147	21.04992147
sRNA13	no	no	no	no	no	no	no	no	49.14411296	50.32240888	45.381804	48.28277528	48.28277528
sRNA14	no	no	no	no	no	no	no	no	6.260825349	4.916346855	3.807976937	4.995049714	10
sRNA15	no	no	no	no	no	no	no	no	838.0788363	872.0890831	625.4240602	778.5306599	778.5306599
sRNA17	no	no	no	no	no	no	no	no	39.0971372	45.23805042	41.50748419	41.94755727	41.94755727
sRNA18	no	no	no	no	no	no	no	no	17.35674354	18.25376308	20.2652238	18.62524347	18.62524347
sRNA19	no	no	no	no	no	no	no	no	34.71137864	42.25588545	59.14884811	45.3720374	45.3720374
sRNA2	no	no	no	no	no	no	no	no	55091.47468	53815.20948	42433.27336	50446.65251	50446.65251
sRNA20	no	no	no	no	no	no	no	no	14.68588662	18.90902637	14.88715263	16.16068854	16.16068854
sRNA21	no	no	no	no	no	no	no	no	1.215694243	1.101496681	7.702218724	3.339803216	10
sRNA22	no	no	no	no	no	no	no	no	0	0.207033135	0	0.069011045	10
sRNA24	no	no	no	no	no	no	no	no	215.1480156	211.8248156	146.009135	190.9939887	190.9939887
sRNA25	no	no	no	no	no	no	no	no	2.141861304	2.687072168	1.002099194	1.943677555	10
sRNA26	no	no	no	no	no	no	no	no	451.1381183	434.9076064	322.785545	402.9437566	402.9437566
sRNA27	no	no	no	no	no	no	no	no	18.54509878	16.13092297	12.63309884	15.76970686	15.76970686
sRNA28	no	no	no	no	no	no	no	no	5.354653259	5.598067016	3.966642643	4.973120973	10
sRNA29	no	no	no	no	no	no	no	no	4.173883566	6.239978701	5.711965405	5.375275891	10
sRNA3	no	no	no	no	no	no	no	no	974.5468932	834.1119854	956.1696476	921.6095087	921.6095087
sRNA30	no	no	no	no	no	no	no	no	1.707497823	1.547102157	2.596347912	1.950315964	10
sRNA31	no	no	no	no	no	no	no	no	5.568512546	6.409069033	5.797400785	5.924997455	10
sRNA32	no	no	no	no	no	no	no	no	2.921718496	12.4799574	6.769736777	7.390470892	10
sRNA37	no	no	no	no	no	no	no	no	3546.836478	3383.126726	2841.316125	3257.09311	3257.09311
sRNA38	no	no	no	no	no	no	no	no	19.85960729	19.51899496	23.88516	21.08792075	21.08792075
sRNA39	no	no	no	no	no	no	no	no	0.813094201	0.368357656	0	0.393817286	10
sRNA4	no	no	no	no	no	no	no	no	4.192516975	4.811671888	1.133326469	3.379171777	10
sRNA40	no	no	no	no	no	no	no	no	0.326084654	0	0.330553554	0.218879402	10
sRNA42	no	no	no	no	no	no	no	no	23.24378273	22.07940204	21.47212544	22.26510341	22.26510341
sRNA43_truncated	no	no	no	no	no	no	no	no	1.916579189	1.736543238	0.647615125	1.433579184	10
sRNA44	no	no	no	no	no	no	no	no	0.355728713	0	2.16362326	0.839783991	10
sRNA46	no	no	no	no	no	no	no	no	808.0167339	696.7366247	540.998874	681.9174109	681.9174109
sRNA48	no	no	no	no	no	no	no	no	53.58842036	64.4188643	62.92843243	60.31191308	60.31191308
sRNA49	no	no	no	no	no	no	no	no	15.82792925	11.79158386	19.96692027	15.86214446	15.86214446
sRNA5	no	no	no	no	no	no	no	no	0.460354805	0.417110876	0.933327681	0.603597787	10
sRNA50	no	no	no	no	no	no	no	no	28.5829704	24.92553475	23.55945327	25.64776169	25.64776169
sRNA53	no	no	no	no	no	no	no	no	263.4533145	252.2597986	214.8305573	243.5145568	243.5145568
sRNA54	no	no	no	no	no	no	no	no	224.742041	221.6268297	194.7758318	213.7149008	213.7149008
sRNA55	no	no	no	no	no	no	no	no	6.047388122	11.28095323	9.736304668	9.021548673	10
sRNA56	no	no	no	no	no	no	no	no	0	0.609968592	1.023649714	0.544539436	10
sRNA57	no	no	no	no	no	no	no	no	12.44621907	18.11165778	11.85213705	14.1366713	14.1366713
sRNA58	no	no	no	no	no	no	no	no	36.41047366	52.90504185	65.04168645	51.45240066	51.45240066
sRNA59	no	no	no	no	no	no	no	no	3.889861903	2.517473924	3.004321055	3.137218961	10
sRNA6	no	no	no	no	no	no	no	no	78.26031687	64.46258988	52.08722662	64.93671112	64.93671112
sRNA60	no	no	no	no	no	no	no	no	3.890908409	3.685657681	3.047815816	3.541460636	10
sRNA61	no	no	no	no	no	no	no	no	22.11908357	19.70162029	18.81186211	20.21085532	20.21085532
sRNA62	no	no	no	no	no	no	no	no	132.2851808	128.703373	97.929156	119.6392366	119.6392366
sRNA63	no	no	no	no	no	no	no	no	8.203840113	4.499044204	2.626190991	5.109691769	10
sRNA64	no	no	no	no	no	no	no	no	20.75957879	25.37790381	18.70585162	21.61444474	21.61444474
sRNA65	no	no	no	no	no	no	no	no	25.77986909	29.1977613	34.29979226	29.75914088	29.75914088
sRNA69	no	no	no	no	no	no	no	no	14.00447776	14.71491901	16.94024828	15.21988168	15.21988168
sRNA7	no	no	no	no	no	no	no	no	142.9555121	148.9085826	128.5192216	140.1277721	140.1277721
sRNA70	no	no	no	no	no	no	no	no	409.6757457	446.4174485	352.2838567	402.7923503	402.7923503
sRNA71	no	no	no	no	no	no	no	no	21.93163371	26.83496556	20.14199378	22.96953102	22.96953102
sRNA72	no	no	no	no	no	no	no	no	3.421908592	5.397110764	2.569485113	3.796168156	10
sRNA73	no	no	no	no	no	no	no	no	0.549195206	2.985635742	2.226887098	1.920572682	10
sRNA74	no	no	no	no	no	no	no	no	7.745350948	10.52667447	13.0858314	10.45261894	10.45261894
sRNA75	no	no	no	no	no	no	no	no	16.24270727	16.58999483	8.981077682	13.9379266	13.9379266
sRNA76	no	no	no	no	no	no	no	no	5014.878222	4669.881943	3446.958119	4377.239428	4377.239428
sRNA77	no	no	no	no	no	no	no	no	6.027502666	7.927697389	7.48980971	7.148336588	10
sRNA8	no	no	no	no	no	no	no	no	31.5467944	36.27894593	28.04324101	31.95632711	31.95632711
sRNA81	no	no	no	no	no	no	no	no	92.24529657	91.13255606	78.11234743	87.16340002	87.16340002
sRNA84	no	no	no	no	no	no	no	no	774.9510488	869.3424872	609.1000147	751.1311836	751.1311836
sRNA85	no	no	no	no	no	no	no	no	34.05010278	34.83241699	22.26887098	30.38379691	30.38379691
sRNA86	no	no	no	no	no	no	no	no	32.86933308	32.01028035	32.18647173	32.35536172	32.35536172
sRNA87	no	no	no	no	no	no	no	no	169.4105683	222.4591337	185.4210992	192.4302671	192.4302671
sRNA88	no	no	no	no	no	no	no	no	91.14596904	103.9556705	75.42155871	90.17439943	90.17439943
sRNA89	no	no	no	no	no	no	no	no	22560.17497	23513.82862	14943.55007	20339.18455	20339.18455
sRNA9	no	no	no	no	no	no	no	no	321.0750699	333.3343409	226.6251761	293.6781956	293.6781956
sRNA90	no	no	no	no	no	no	no	no	350.3927823	348.5814548	411.4490232	370.1410868	370.1410868
sRNA91	no	no	no	no	no	no	no	no	41.40232315	38.88549777	41.96963828	40.75245607	40.75245607
sRNA92	no	no	no	no	no	no	no	no	84.70528414	93.88786621	66.52080924	81.70465319	81.70465319
sRNA93	no	no	no	no	no	no	no	no	134.6697334	120.0535956	100.0693609	118.26423	118.26423
sRNA94	no	no	no	no	no	no	no	no	110.7425559	113.4541582	86.32779257	103.5081689	103.5081689
sRNA95	no	no	no	no	no	no	no	no	40.77774405	61.95194165	64.71890628	55.81619732	55.81619732
sRNA96	no	no	no	no	no	no	no	no	619.0138612	618.2467376	694.1807419	643.8137802	643.8137802
sRNA97	no	no	no	no	no	no	no	no	684.615695	686.599055	475.0582668	615.4243389	615.4243389
sRNA98	no	no	no	no	no	no	no	no	4.53086045	4.851658081	5.01049597	4.7976715	10
sRNA99	no	no	no	no	no	no	no	no	2755.183343	2648.4693	2147.204893	2516.952512	2516.952512

Table S 27. sRNAs expression TPM values (LowFe)

locus_tag	"old_locus_tag"	chrom	start	stop	strand	refseq_id	symbol	name	LowFe_1	LowFe_2	LowFe_3	LowFe_Mean	lowfe_Mean_10
newcandnsRNA1	no	no	no	no	no	no	no	no	0.756730837	0.575550079	1.107932345	0.81340442	10
sRNA1	no	no	no	no	no	no	no	no	552.1108188	461.878938	542.0251239	518.6716269	518.6716269
sRNA10	no	no	no	no	no	no	no	no	2.167931588	2.061091497	1.763375804	1.997466296	10
sRNA100	no	no	no	no	no	no	no	no	312.8915086	237.4725972	276.0914903	275.4851987	275.4851987
sRNA101	no	no	no	no	no	no	no	no	168.8704605	105.9617987	207.066724	160.6329944	160.6329944
sRNA102	no	no	no	no	no	no	no	no	92.52345652	129.1141179	108.5261782	110.0545842	110.0545842
sRNA103	no	no	no	no	no	no	no	no	3.881296875	4.510022793	3.858569636	4.083296434	10
sRNA104	no	no	no	no	no	no	no	no	5.347564583	2.859764453	4.893367857	4.366898964	10
sRNA105	no	no	no	no	no	no	no	no	5.543207189	4.340021933	5.834910181	5.239379768	10
sRNA106	no	no	no	no	no	no	no	no	1.351912395	1.285287394	3.115627474	1.917609088	10
sRNA109	no	no	no	no	no	no	no	no	28.3832274	16.71862295	17.31499395	20.80561477	20.80561477
sRNA110	no	no	no	no	no	no	no	no	28.3832274	16.71862295	17.31499395	20.80561477	20.80561477
sRNA13	no	no	no	no	no	no	no	no	36.2254375	37.72019063	38.2349173	37.39351514	37.39351514
sRNA14	no	no	no	no	no	no	no	no	5.347564583	4.067220555	5.219592381	4.878125839	10
sRNA15	no	no	no	no	no	no	no	no	866.1023903	531.8920551	794.5012453	730.8318969	730.8318969
sRNA17	no	no	no	no	no	no	no	no	44.50662928	36.36043692	45.56131535	42.14279385	42.14279385
sRNA18	no	no	no	no	no	no	no	no	18.66352986	18.31004303	17.28020992	18.08459427	18.08459427
sRNA19	no	no	no	no	no	no	no	no	34.78645328	26.3279902	38.1704885	33.09497733	33.09497733
sRNA2	no	no	no	no	no	no	no	no	51732.32274	48025.34201	49385.19824	49714.28766	49714.28766
sRNA20	no	no	no	no	no	no	no	no	22.2815191	9.885605515	11.27689712	14.48134058	14.48134058
sRNA21	no	no	no	no	no	no	no	no	2.336314624	5.552940685	3.167228386	3.685494565	10
sRNA22	no	no	no	no	no	no	no	no	0.585499772	0.278322574	0.23812009	0.367314146	10
sRNA24	no	no	no	no	no	no	no	no	212.3570444	134.4475003	208.7459814	185.1835087	185.1835087
sRNA25	no	no	no	no	no	no	no	no	1.899792681	1.404796573	0.34394236	1.21594496	10
sRNA26	no	no	no	no	no	no	no	no	460.8096668	326.8869645	475.9140058	421.2035457	421.2035457
sRNA27	no	no	no	no	no	no	no	no	19.76824822	18.61331682	18.08922715	18.82359739	18.82359739
sRNA28	no	no	no	no	no	no	no	no	3.166321135	5.267987149	6.009399122	4.814569135	10
sRNA29	no	no	no	no	no	no	no	no	8.021346874	10.93065524	6.30700746	8.419669858	10
sRNA3	no	no	no	no	no	no	no	no	937.758776	804.2460381	852.4761898	864.8270013	864.8270013
sRNA30	no	no	no	no	no	no	no	no	3.646066761	0.346638115	0.593135498	1.528613458	10
sRNA31	no	no	no	no	no	no	no	no	7.327191856	4.582955853	2.82309684	4.911081517	10
sRNA32	no	no	no	no	no	no	no	no	7.486590416	7.117635971	10.43918476	8.347803716	10
sRNA37	no	no	no	no	no	no	no	no	2798.371559	2472.374512	3759.532033	3010.092701	3010.092701
sRNA38	no	no	no	no	no	no	no	no	22.85652604	16.40008288	28.41310368	22.55657087	22.55657087
sRNA39	no	no	no	no	no	no	no	no	0	0	0	0	10
sRNA4	no	no	no	no	no	no	no	no	4.297150111	6.128066684	7.281797406	5.902338067	10
sRNA40	no	no	no	no	no	no	no	no	0.835556966	0	0	0.278518989	10
sRNA42	no	no	no	no	no	no	no	no	23.05536826	21.46250368	23.44128315	22.65305169	22.65305169
sRNA43_inuncat	no	no	no	no	no	no	no	no	0.818504783	1.556334396	5.991879008	2.788906062	10
sRNA44	no	no	no	no	no	no	no	no	0	0	0.370709686	0.123569895	10
sRNA46	no	no	no	no	no	no	no	no	666.5049244	496.1025072	727.5157659	630.0410658	630.0410658
sRNA48	no	no	no	no	no	no	no	no	72.05616684	63.9811708	72.98582566	69.67438777	69.67438777
sRNA49	no	no	no	no	no	no	no	no	41.0080093	31.70375573	27.49083066	33.40086523	33.40086523
sRNA5	no	no	no	no	no	no	no	no	1.769414752	1.121476256	0	0.963630336	10
sRNA50	no	no	no	no	no	no	no	no	38.89137878	32.73804424	29.49201503	33.70714602	33.70714602
sRNA53	no	no	no	no	no	no	no	no	242.4150405	213.5965662	213.3450647	223.1188905	223.1188905
sRNA54	no	no	no	no	no	no	no	no	211.3210004	192.4917314	192.8099427	198.8742248	198.8742248
sRNA55	no	no	no	no	no	no	no	no	6.380616832	6.066167021	6.67277435	6.373186067	10
sRNA56	no	no	no	no	no	no	no	no	0	0	0	0	10
sRNA57	no	no	no	no	no	no	no	no	10.14748701	11.4849978	16.11470539	12.58239673	12.58239673
sRNA58	no	no	no	no	no	no	no	no	52.90675598	81.66892337	54.83348378	63.13638771	63.13638771
sRNA59	no	no	no	no	no	no	no	no	3.322451368	5.189316166	3.860645252	4.124137595	10
sRNA6	no	no	no	no	no	no	no	no	96.4182099	73.56431117	67.88106252	79.2878612	79.2878612
sRNA60	no	no	no	no	no	no	no	no	4.305242673	2.369672993	4.607691014	3.760868893	10
sRNA61	no	no	no	no	no	no	no	no	18.73248671	19.1792586	24.6133473	20.84169754	20.84169754
sRNA62	no	no	no	no	no	no	no	no	108.2450573	88.35544653	114.0031938	103.5345659	103.5345659
sRNA63	no	no	no	no	no	no	no	no	5.80856153	3.418569001	4.499648604	4.575593045	10
sRNA64	no	no	no	no	no	no	no	no	19.84227911	13.64659528	25.0677792	19.51888453	19.51888453
sRNA65	no	no	no	no	no	no	no	no	32.14436799	30.84059704	37.41987185	33.46827896	33.46827896
sRNA69	no	no	no	no	no	no	no	no	13.26839333	8.887488524	11.89615745	11.35067977	11.35067977
sRNA7	no	no	no	no	no	no	no	no	290.7738242	180.8006637	153.0536724	208.2093868	208.2093868
sRNA70	no	no	no	no	no	no	no	no	396.9985446	297.3049808	394.7789527	363.0274927	363.0274927
sRNA71	no	no	no	no	no	no	no	no	24.73648886	31.28045749	24.80869133	26.94187923	26.94187923
sRNA72	no	no	no	no	no	no	no	no	4.871263284	4.939943994	3.169792944	4.327000074	10
sRNA73	no	no	no	no	no	no	no	no	2.110880756	0.668950749	5.150913533	2.64358168	10
sRNA74	no	no	no	no	no	no	no	no	11.99067316	6.289516322	7.062592783	8.447594089	10
sRNA75	no	no	no	no	no	no	no	no	17.97235738	12.77001737	15.38794924	15.37677466	15.37677466
sRNA76	no	no	no	no	no	no	no	no	4645.788299	4071.050985	5081.952444	4599.597243	4599.597243
sRNA77	no	no	no	no	no	no	no	no	10.96084666	2.84200194	9.523324607	7.775391069	10
sRNA8	no	no	no	no	no	no	no	no	46.63573764	24.82896269	40.20906921	37.22458985	37.22458985
sRNA81	no	no	no	no	no	no	no	no	72.38197623	67.00986528	80.68748576	73.35977576	73.35977576
sRNA84	no	no	no	no	no	no	no	no	758.6857252	656.6866521	741.0733765	718.8152513	718.8152513
sRNA85	no	no	no	no	no	no	no	no	47.14300356	20.73747322	32.62245238	33.50097639	33.50097639
sRNA86	no	no	no	no	no	no	no	no	26.64233069	24.23990822	36.35073265	29.07765719	29.07765719
sRNA87	no	no	no	no	no	no	no	no	193.4560128	139.4368812	188.0588431	173.650579	173.650579
sRNA88	no	no	no	no	no	no	no	no	63.98423204	60.29890939	77.99042103	67.42452082	67.42452082
sRNA89	no	no	no	no	no	no	no	no	27329.94026	23059.95388	19863.4156	23417.76992	23417.76992
sRNA9	no	no	no	no	no	no	no	no	344.8114375	224.2257792	311.0680747	293.3684305	293.3684305
sRNA90	no	no	no	no	no	no	no	no	422.9437443	327.7896679	323.0734915	357.9356346	357.9356346
sRNA91	no	no	no	no	no	no	no	no	45.92867968	39.36019892	38.14722254	41.14536705	41.14536705
sRNA92	no	no	no	no	no	no	no	no	74.85160586	57.90895576	76.25335663	69.66530608	69.66530608
sRNA93	no	no	no	no	no	no	no	no	123.6955223	70.0311955	112.886605	102.204441	102.204441
sRNA94	no	no	no	no	no	no	no	no	103.9325052	89.9954582	108.5661184	100.8313595	100.8313595
sRNA95	no	no	no	no	no	no	no	no	30.08005078	42.64561026	47.21670739	39.98078948	39.98078948
sRNA96	no	no	no	no	no	no	no	no	413.6353526	446.6679716	432.0595767	430.7876336	430.7876336
sRNA97	no	no	no	no	no	no	no	no	1018.568662	756.7376705	721.3615653	832.2226327	832.2226327
sRNA98	no	no	no	no	no	no	no	no	4.221761513	9.030835113	2.575456767	5.276017798	10
sRNA99	no	no	no	no	no	no	no	no	5900.265889	4191.250309	3362.302021	4484.606073	4484.606073

Table S 28. sRNAs expression TPM values (ChI)

locus_tag	"old_locus_tag"	chrom	start	stop	strand	refseq_id	symbol	name	ChI_1	ChI_2	ChI_3	ChI_Mean	ChI_Mean_10
newcandsRNA1	no	no	no	no	no	no	no	no	2.324104126	6.788802731	4.653992935	4.588966597	10
	sRNA1	no	no	no	no	no	no	no	297.0011398	325.173812	425.5954065	349.2567861	349.2567861
	sRNA10	no	no	no	no	no	no	no	9.36315598	15.85516501	13.59621336	12.93817812	12.93817812
	sRNA100	no	no	no	no	no	no	no	13.01968258	15.52873515	18.85281387	15.80041053	15.80041053
	sRNA101	no	no	no	no	no	no	no	947.332364	1284.709715	1283.187071	1171.74305	1171.74305
	sRNA102	no	no	no	no	no	no	no	69.61765701	121.8458094	134.6420285	108.7018316	108.7018316
	sRNA103	no	no	no	no	no	no	no	6.070576637	17.10160451	9.073574228	10.74858512	10.74858512
	sRNA104	no	no	no	no	no	no	no	55.60096329	77.7842651	28.93946703	54.10823181	54.10823181
	sRNA105	no	no	no	no	no	no	no	2.503608103	7.2071536	8.707567012	6.139442905	10
	sRNA106	no	no	no	no	no	no	no	8.505938204	13.76885491	12.21638743	11.49706018	11.49706018
sRNA109	no	no	no	no	no	no	no	10.46219309	21.05891148	16.22773852	15.91628103	15.91628103	
sRNA110	no	no	no	no	no	no	no	10.46219309	21.05891148	16.22773852	15.91628103	15.91628103	
sRNA13	no	no	no	no	no	no	no	76.71001387	76.53668904	76.77639731	76.67436674	76.67436674	
sRNA14	no	no	no	no	no	no	no	52.69260521	62.22741208	58.41985868	57.77995866	57.77995866	
sRNA15	no	no	no	no	no	no	no	598.346491	857.4366201	1317.528036	924.4370492	924.4370492	
sRNA17	no	no	no	no	no	no	no	95.39327879	91.09026449	99.96834702	95.48396343	95.48396343	
sRNA18	no	no	no	no	no	no	no	22.86711362	29.42886074	30.84877026	27.71491487	27.71491487	
sRNA19	no	no	no	no	no	no	no	52.63325096	80.87931795	82.2426204	71.91839644	71.91839644	
sRNA2	no	no	no	no	no	no	no	1546.257068	1349.48213	1884.484896	1593.408032	1593.408032	
sRNA20	no	no	no	no	no	no	no	36.75049425	45.06433732	50.48629763	44.1003764	44.1003764	
sRNA21	no	no	no	no	no	no	no	10.4641096	18.22574308	31.51017189	20.06667486	20.06667486	
sRNA22	no	no	no	no	no	no	no	1.685823704	9.135043979	7.580841354	6.133903012	10	
sRNA24	no	no	no	no	no	no	no	90.78111925	144.9836207	252.8900755	162.8849385	162.8849385	
sRNA25	no	no	no	no	no	no	no	7.023279574	8.508011355	12.98219082	9.504039316	10	
sRNA26	no	no	no	no	no	no	no	164.397079	204.3738111	394.3678539	254.3795813	254.3795813	
sRNA27	no	no	no	no	no	no	no	26.63494924	45.96745471	35.37800815	35.9934707	35.9934707	
sRNA28	no	no	no	no	no	no	no	11.64918968	15.7809888	24.98217641	17.47078496	17.47078496	
sRNA29	no	no	no	no	no	no	no	2.224038532	1.912015455	5.409246174	1.318176672	10	
sRNA3	no	no	no	no	no	no	no	198.8803687	212.3572189	201.5655943	204.2677273	204.2677273	
sRNA30	no	no	no	no	no	no	no	5.832268877	9.007014954	9.146543531	7.995275787	10	
sRNA31	no	no	no	no	no	no	no	15.91536449	15.04207963	16.53981042	15.83241818	15.83241818	
sRNA32	no	no	no	no	no	no	no	61.58875934	206.8453083	115.5414983	127.9918553	127.9918553	
sRNA37	no	no	no	no	no	no	no	835.8474482	1571.606592	2499.889938	1635.781326	1635.781326	
sRNA38	no	no	no	no	no	no	no	27.31759487	62.79933459	72.58859382	54.23517443	54.23517443	
sRNA39	no	no	no	no	no	no	no	0.999817522	1.015828754	2.528998211	1.514881496	10	
sRNA4	no	no	no	no	no	no	no	29.55710549	42.36852429	36.51241168	36.14601382	36.14601382	
sRNA40	no	no	no	no	no	no	no	0.801936971	0.814779313	2.704623087	1.440446457	10	
sRNA42	no	no	no	no	no	no	no	76.3712909	89.61596662	105.1401981	90.37581854	90.37581854	
sRNA43_1uncatex	no	no	no	no	no	no	no	no	1.57114182	2.66050388	4.636496721	2.956047473	10
	sRNA44	no	no	no	no	no	no	no	3.207747882	3.851684026	5.90095826	4.320142578	10
	sRNA46	no	no	no	no	no	no	no	771.6530712	906.2448619	1448.980007	1042.292647	1042.292647
	sRNA48	no	no	no	no	no	no	no	19.13775008	28.72442325	28.60482723	25.48900018	25.48900018
	sRNA49	no	no	no	no	no	no	no	21.62526662	45.99383449	41.93685236	36.51865116	36.51865116
	sRNA5	no	no	no	no	no	no	no	5.283349453	11.50276678	14.79587924	10.52733182	10.52733182
	sRNA50	no	no	no	no	no	no	no	11.9237497	20.2789518	15.57207232	15.92492461	15.92492461
	sRNA53	no	no	no	no	no	no	no	142.1628442	218.5050647	307.0345572	222.5674887	222.5674887
	sRNA54	no	no	no	no	no	no	no	157.6884614	245.6250575	327.240741	243.5180866	243.5180866
	sRNA55	no	no	no	no	no	no	no	15.74712597	13.3327524	13.64605285	14.24197707	14.24197707
sRNA56	no	no	no	no	no	no	no	35.31971862	46.81914677	43.97193664	42.03693401	42.03693401	
sRNA57	no	no	no	no	no	no	no	8.347874007	16.02072095	30.10929798	18.15929765	18.15929765	
sRNA58	no	no	no	no	no	no	no	111.7479262	237.9849024	157.2134101	168.9820796	168.9820796	
sRNA59	no	no	no	no	no	no	no	7.136764519	14.50210754	17.4760261	13.03829939	13.03829939	
sRNA6	no	no	no	no	no	no	no	42.25154786	45.9568453	46.22446731	44.81095349	44.81095349	
sRNA60	no	no	no	no	no	no	no	10.72873868	25.63102382	18.88652054	18.41542768	18.41542768	
sRNA61	no	no	no	no	no	no	no	20.59105227	39.65584586	46.44825757	35.5650519	35.5650519	
sRNA62	no	no	no	no	no	no	no	128.9997535	138.354784	174.6663039	147.3402805	147.3402805	
sRNA63	no	no	no	no	no	no	no	21.23750322	22.11704398	23.27841112	22.21098611	22.21098611	
sRNA64	no	no	no	no	no	no	no	10.53491936	18.93718656	27.67256464	19.04822352	19.04822352	
sRNA65	no	no	no	no	no	no	no	132.0837363	203.5989719	195.6874351	177.1233811	177.1233811	
sRNA69	no	no	no	no	no	no	no	46.40381147	98.50865682	69.42543774	71.44596868	71.44596868	
sRNA7	no	no	no	no	no	no	no	139.6439578	137.1001991	399.47283	225.4056623	225.4056623	
sRNA70	no	no	no	no	no	no	no	424.3525024	546.7759612	600.1911407	523.7732014	523.7732014	
sRNA71	no	no	no	no	no	no	no	114.6337686	116.3134062	131.9596941	120.9689563	120.9689563	
sRNA72	no	no	no	no	no	no	no	14.44135889	19.84498926	36.92303259	23.73646025	23.73646025	
sRNA73	no	no	no	no	no	no	no	98.14582994	135.8537297	170.2489059	134.7494885	134.7494885	
sRNA74	no	no	no	no	no	no	no	31.21767011	53.22104875	51.52725222	45.32199036	45.32199036	
sRNA75	no	no	no	no	no	no	no	130.9729513	258.1466835	195.6514135	194.9236828	194.9236828	
sRNA76	no	no	no	no	no	no	no	13637.23479	13801.87047	14351.54519	13930.21682	13930.21682	
sRNA77	no	no	no	no	no	no	no	70.45091001	63.48193606	96.15691025	76.69658544	76.69658544	
sRNA8	no	no	no	no	no	no	no	131.4927969	233.847979	183.1595914	182.8334558	182.8334558	
sRNA81	no	no	no	no	no	no	no	85.48932817	109.3829175	165.5421374	120.1381277	120.1381277	
sRNA84	no	no	no	no	no	no	no	373.8095532	373.7121117	381.8927799	376.4714816	376.4714816	
sRNA85	no	no	no	no	no	no	no	58.52732978	74.10203438	137.2240345	89.9511329	89.9511329	
sRNA86	no	no	no	no	no	no	no	31.16097943	39.10940704	46.82861688	39.03300111	39.03300111	
sRNA87	no	no	no	no	no	no	no	102.8995203	155.1595429	358.2830113	205.4473582	205.4473582	
sRNA88	no	no	no	no	no	no	no	90.47341003	106.9596806	104.7632608	100.7321172	100.7321172	
sRNA89	no	no	no	no	no	no	no	3615.814519	2773.635567	3126.86612	3172.105402	3172.105402	
sRNA9	no	no	no	no	no	no	no	121.610548	148.9387743	296.5511509	189.0334911	189.0334911	
sRNA90	no	no	no	no	no	no	no	2168.291762	2528.33428	3116.094609	2604.240217	2604.240217	
sRNA91	no	no	no	no	no	no	no	32.2844303	23.12921921	23.55639463	26.32334805	26.32334805	
sRNA92	no	no	no	no	no	no	no	90.43447505	112.3785457	171.6495551	124.8208586	124.8208586	
sRNA93	no	no	no	no	no	no	no	56.78666548	75.25011321	128.3758721	86.80421692	86.80421692	
sRNA94	no	no	no	no	no	no	no	159.4906044	201.4344728	307.1055892	222.6768888	222.6768888	
sRNA95	no	no	no	no	no	no	no	55.71351585	68.6129948	73.4518691	65.92612658	65.92612658	
sRNA96	no	no	no	no	no	no	no	978.9396117	970.5861445	1175.127572	1041.551109	1041.551109	
sRNA97	no	no	no	no	no								

Table S 29. sRNAs expression TPM values (Tet)

locus_tag	old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	TET_1	TET_2	TET_3	TET_Mean	TET_Mean_10
newcandansRNA1	no	no	no	no	no	no	no	no	4.981293612	2.192097212	7.857284741	5.010225189	10
sRNA1	no	no	no	no	no	no	no	no	428.3912507	262.2625104	405.6726875	365.4421495	365.4421495
sRNA10	no	no	no	no	no	no	no	no	10.0543801	5.652056055	15.03240241	10.24627952	10.24627952
sRNA100	no	no	no	no	no	no	no	no	14.64753382	7.175894697	15.10042233	12.30795028	12.30795028
sRNA101	no	no	no	no	no	no	no	no	792.0256844	437.0857243	695.3612022	641.4908703	641.4908703
sRNA102	no	no	no	no	no	no	no	no	100.7557426	46.70252258	95.45327469	80.9705133	80.9705133
sRNA103	no	no	no	no	no	no	no	no	20.38775792	9.24452179	19.01534663	16.21587545	16.21587545
sRNA104	no	no	no	no	no	no	no	no	65.80213388	30.40073483	32.80147294	43.00144722	43.00144722
sRNA105	no	no	no	no	no	no	no	no	5.268463532	4.156073738	7.652517548	5.692351606	10
sRNA106	no	no	no	no	no	no	no	no	10.65203082	6.135409163	9.294017737	8.693819242	10
sRNA109	no	no	no	no	no	no	no	no	19.93910814	11.43937499	19.30789043	16.89545785	16.89545785
sRNA110	no	no	no	no	no	no	no	no	19.93910814	11.43937499	19.30789043	16.89545785	16.89545785
sRNA13	no	no	no	no	no	no	no	no	58.58254492	47.22201671	56.12594248	53.97683471	53.97683471
sRNA14	no	no	no	no	no	no	no	no	64.96210664	22.30678123	48.29898045	45.18928944	45.18928944
sRNA15	no	no	no	no	no	no	no	no	968.8415449	601.4948261	915.2639946	828.5334552	828.5334552
sRNA17	no	no	no	no	no	no	no	no	55.79927785	61.66915169	68.96071912	62.14304956	62.14304956
sRNA18	no	no	no	no	no	no	no	no	18.0599916	13.45860872	19.0963274	17.14274435	17.14274435
sRNA19	no	no	no	no	no	no	no	no	56.08345137	37.54152878	62.09092779	51.90530264	51.90530264
sRNA2	no	no	no	no	no	no	no	no	1134.457171	1064.278555	1435.234762	1211.323496	1211.323496
sRNA20	no	no	no	no	no	no	no	no	30.81581413	33.27657694	51.41186312	38.50141806	38.50141806
sRNA21	no	no	no	no	no	no	no	no	25.39888191	16.46839634	34.06147043	25.30958289	25.30958289
sRNA22	no	no	no	no	no	no	no	no	5.080456723	2.374505301	3.539352841	3.664771622	10
sRNA24	no	no	no	no	no	no	no	no	242.2275083	100.1978492	198.8367749	180.4207108	180.4207108
sRNA25	no	no	no	no	no	no	no	no	14.77942665	9.294492179	14.26150998	12.77847627	12.77847627
sRNA26	no	no	no	no	no	no	no	no	367.761926	198.113069	354.0122737	306.6290896	306.6290896
sRNA27	no	no	no	no	no	no	no	no	38.90173547	24.55772223	32.17288506	31.87744759	31.87744759
sRNA28	no	no	no	no	no	no	no	no	18.15848359	7.949236732	23.64408233	16.58393422	16.58393422
sRNA29	no	no	no	no	no	no	no	no	1.28004151	0.774541015	2.09168813	1.382090218	10
sRNA3	no	no	no	no	no	no	no	no	256.1135686	336.3138617	279.6006561	290.6760288	290.6760288
sRNA30	no	no	no	no	no	no	no	no	8.291177963	4.013530713	9.075506348	7.126738342	10
sRNA31	no	no	no	no	no	no	no	no	15.34665152	8.043310539	13.43873055	12.27623087	12.27623087
sRNA32	no	no	no	no	no	no	no	no	140.8045661	48.02154292	117.5148422	102.1136504	102.1136504
sRNA37	no	no	no	no	no	no	no	no	3102.756081	1145.800002	2824.498043	2357.684709	2357.684709
sRNA38	no	no	no	no	no	no	no	no	69.16353321	25.73474985	74.52789084	56.4753913	56.4753913
sRNA39	no	no	no	no	no	no	no	no	2.493587357	1.207076906	2.963430644	2.221364969	10
sRNA4	no	no	no	no	no	no	no	no	25.07224163	12.24051425	16.04419872	17.78565154	17.78565154
sRNA40	no	no	no	no	no	no	no	no	2.00006486	1.210220336	2.376918329	1.862401175	10
sRNA42	no	no	no	no	no	no	no	no	90.1107066	71.6566388	94.10888619	85.2920772	85.2920772
sRNA43_truncate	no	no	no	no	no	no	no	no	5.387929826	1.422626354	6.403126928	4.404561036	10
sRNA44	no	no	no	no	no	no	no	no	4.363777875	1.056192293	4.861878401	3.427282856	10
sRNA46	no	no	no	no	no	no	no	no	948.8049621	457.8536806	796.037616	734.2320862	734.2320862
sRNA48	no	no	no	no	no	no	no	no	8.542649908	7.482853873	6.768174226	7.597892669	10
sRNA49	no	no	no	no	no	no	no	no	33.97862997	20.10325555	39.09897117	31.06028557	31.06028557
sRNA5	no	no	no	no	no	no	no	no	13.05924702	3.075383441	12.58368527	9.572771913	10
sRNA50	no	no	no	no	no	no	no	no	36.60724773	28.63454661	31.11602177	32.11927204	32.11927204
sRNA53	no	no	no	no	no	no	no	no	214.3078347	103.0208093	224.6503341	180.6596594	180.6596594
sRNA54	no	no	no	no	no	no	no	no	225.7728388	112.9761549	264.5755989	201.1081975	201.1081975
sRNA55	no	no	no	no	no	no	no	no	11.72765304	8.449538344	11.34438294	10.50719144	10.50719144
sRNA56	no	no	no	no	no	no	no	no	12.38749848	7.495558209	27.90962167	15.93089279	15.93089279
sRNA57	no	no	no	no	no	no	no	no	18.21745824	7.838728343	23.02460647	16.36026435	16.36026435
sRNA58	no	no	no	no	no	no	no	no	154.5582036	57.34899429	132.2982628	114.7351536	114.7351536
sRNA59	no	no	no	no	no	no	no	no	10.65123298	9.349489174	9.620190161	9.873637438	10
sRNA6	no	no	no	no	no	no	no	no	44.36507507	42.24769172	40.76775074	42.46017251	42.46017251
sRNA60	no	no	no	no	no	no	no	no	18.71247123	12.20886684	14.01978947	14.98037585	14.98037585
sRNA61	no	no	no	no	no	no	no	no	44.12119127	29.35835104	49.18939968	40.88964733	40.88964733
sRNA62	no	no	no	no	no	no	no	no	171.8765415	137.5434931	153.3495696	154.2565347	154.2565347
sRNA63	no	no	no	no	no	no	no	no	20.52480352	14.58273773	17.11381197	17.40711774	17.40711774
sRNA64	no	no	no	no	no	no	no	no	17.93742379	5.625613687	15.31235808	12.95846519	12.95846519
sRNA65	no	no	no	no	no	no	no	no	173.4762138	91.5780847	188.3358229	151.1300405	151.1300405
sRNA69	no	no	no	no	no	no	no	no	90.58940386	34.06815742	96.39922908	73.68559679	73.68559679
sRNA7	no	no	no	no	no	no	no	no	322.8104683	125.2820092	332.5308743	260.2077839	260.2077839
sRNA70	no	no	no	no	no	no	no	no	476.88503	357.2991377	485.7180934	439.9674204	439.9674204
sRNA71	no	no	no	no	no	no	no	no	77.46358989	66.64763104	110.5053527	84.7219122	84.7219122
sRNA72	no	no	no	no	no	no	no	no	19.04515202	19.00290911	36.14455565	24.73087226	24.73087226
sRNA73	no	no	no	no	no	no	no	no	163.3737191	99.8750256	191.1542741	151.4676729	151.4676729
sRNA74	no	no	no	no	no	no	no	no	68.53830508	34.25547375	67.92595473	56.90657785	56.90657785
sRNA75	no	no	no	no	no	no	no	no	90.90860843	23.01702073	70.36575205	61.4304604	61.4304604
sRNA76	no	no	no	no	no	no	no	no	7062.311213	4000.292139	6886.941776	5983.181709	5983.181709
sRNA77	no	no	no	no	no	no	no	no	54.26262923	35.35948111	60.05778735	49.89329923	49.89329923
sRNA8	no	no	no	no	no	no	no	no	146.9815106	54.21787104	146.8161647	116.0051821	116.0051821
sRNA81	no	no	no	no	no	no	no	no	161.3306755	90.74504198	125.2312474	125.7689883	125.7689883
sRNA84	no	no	no	no	no	no	no	no	378.945622	426.3848287	478.8698127	428.0667545	428.0667545
sRNA85	no	no	no	no	no	no	no	no	104.0033727	43.61888873	106.5860219	84.73609445	84.73609445
sRNA86	no	no	no	no	no	no	no	no	30.85814355	14.93757672	35.04256737	26.94609588	26.94609588
sRNA87	no	no	no	no	no	no	no	no	272.4794244	111.3972224	273.2057891	219.0274787	219.0274787
sRNA88	no	no	no	no	no	no	no	no	129.9390975	102.8878669	108.6528062	113.8265902	113.8265902
sRNA89	no	no	no	no	no	no	no	no	4375.391316	6366.035904	3923.38382	4888.270347	4888.270347
sRNA9	no	no	no	no	no	no	no	no	214.0954384	173.6548373	238.0283877	208.5928878	208.5928878
sRNA90	no	no	no	no	no	no	no	no	301.1006734	213.3508432	306.4604019	273.6373061	273.6373061
sRNA91	no	no	no	no	no	no	no	no	14.32304512	14.80372746	19.55207013	16.2262809	16.2262809
sRNA92	no	no	no	no	no	no	no	no	129.1164865	76.7913926	127.8197365	111.2425385	111.2425385
sRNA93	no	no	no	no	no	no	no	no	89.94351081	69.82372218	99.12455448	86.29726249	86.29726249
sRNA94	no	no	no	no	no	no	no	no	292.9127246	134.1704919	240.2987756	222.460664	222.460664
sRNA95	no	no	no	no	no	no	no	no	40.10656376	54.7274375	72.43345856	55.75581994	55.75581994
sRNA96	no	no	no	no	no	no	no	no	430.1337643	483.356425	518.1462887	477.2121594	477.2121594
sRNA97	no	no	no	no	no	no	no	no	119.438258	61.0466646	126.5814495	102.3546466	102.3546466
sRNA98	no	no	no	no	no	no	no	no	8.210792581	4.891837989	6.004846306	6.369158958	

Table S 30. sRNAs expression TPM values (AT)

locus_tag	'old_locus_tag'	chrom	start	stop	strand	refseq_id	symbol	name	AT_1	ATC_2	ATC_3	AT_Mean	AT_Mean_10
newcandsRNA1	no	no	no	no	no	no	no	no	1.388231147	3.727545545	2.082312917	2.399363203	10
sRNA1	no	no	no	no	no	no	no	no	207.4413971	228.6656388	234.6072553	223.5714304	223.5714304
sRNA10	no	no	no	no	no	no	no	no	0.710195471	0	1.491386279	0.733860583	10
sRNA100	no	no	no	no	no	no	no	no	210.9907191	345.3792105	286.7263228	281.0320841	281.0320841
sRNA101	no	no	no	no	no	no	no	no	139.1310306	149.5144902	127.4010187	138.6821798	138.6821798
sRNA102	no	no	no	no	no	no	no	no	202.4127408	204.0350767	192.3149989	199.5876055	199.5876055
sRNA103	no	no	no	no	no	no	no	no	37.57926787	43.58477893	49.05003761	43.4046948	43.4046948
sRNA104	no	no	no	no	no	no	no	no	2.408746305	2.554654059	2.145939145	2.369779836	10
sRNA105	no	no	no	no	no	no	no	no	3.418176575	5.815472655	3.289941547	4.174530259	10
sRNA106	no	no	no	no	no	no	no	no	2.214373518	2.104958401	4.753444656	3.024258858	10
sRNA109	no	no	no	no	no	no	no	no	9.500230182	18.07909026	17.26184016	14.94705353	14.94705353
sRNA110	no	no	no	no	no	no	no	no	9.500230182	18.07909026	17.26184016	14.94705353	14.94705353
sRNA13	no	no	no	no	no	no	no	no	34.75375901	36.259606	51.81899134	40.94411878	40.94411878
sRNA14	no	no	no	no	no	no	no	no	2.802904791	3.179125051	3.433502632	3.138510825	10
sRNA15	no	no	no	no	no	no	no	no	565.4594318	674.7736038	457.7486104	565.993882	565.993882
sRNA17	no	no	no	no	no	no	no	no	39.80390902	48.77267235	38.02930131	42.18496089	42.18496089
sRNA18	no	no	no	no	no	no	no	no	20.81364944	30.52094948	22.58244306	24.63901399	24.63901399
sRNA19	no	no	no	no	no	no	no	no	6.435240592	10.07958744	6.256382348	7.590403461	10
sRNA2	no	no	no	no	no	no	no	no	29330.41251	27711.54211	30442.49969	29161.48477	29161.48477
sRNA20	no	no	no	no	no	no	no	no	14.92287273	22.28751689	11.80834239	16.33957734	16.33957734
sRNA21	no	no	no	no	no	no	no	no	6.377969034	7.606089755	3.57160468	5.851887823	10
sRNA22	no	no	no	no	no	no	no	no	0.575413849	0.248628132	0.268522104	0.364188028	10
sRNA24	no	no	no	no	no	no	no	no	109.5137837	142.1549311	105.6844018	119.1177055	119.1177055
sRNA25	no	no	no	no	no	no	no	no	3.734133028	1.075643814	3.67875282	2.829509888	10
sRNA26	no	no	no	no	no	no	no	no	230.7469472	234.3540286	187.0032684	217.3680814	217.3680814
sRNA27	no	no	no	no	no	no	no	no	19.92586345	33.41632798	36.09013431	29.81077524	29.81077524
sRNA28	no	no	no	no	no	no	no	no	5.359172401	7.395051223	2.178208907	4.977477511	10
sRNA29	no	no	no	no	no	no	no	no	190.7727074	475.9604362	224.1586719	296.9639385	296.9639385
sRNA3	no	no	no	no	no	no	no	no	624.08427	668.6919046	634.5848615	642.4536787	642.4536787
sRNA30	no	no	no	no	no	no	no	no	0.238883931	0.619310075	0	0.286064669	10
sRNA31	no	no	no	no	no	no	no	no	4.295316838	5.731595645	2.652946746	4.226619743	10
sRNA32	no	no	no	no	no	no	no	no	5.605809583	6.812410824	1.962001504	4.793407304	10
sRNA37	no	no	no	no	no	no	no	no	1994.640676	2268.41831	2122.856775	2128.638587	2128.638587
sRNA38	no	no	no	no	no	no	no	no	6.498670383	12.81905263	13.44920386	10.92230896	10.92230896
sRNA39	no	no	no	no	no	no	no	no	0	0	0.477760107	0.159253369	10
sRNA4	no	no	no	no	no	no	no	no	1.876945173	1.520627416	1.313840293	1.570470961	10
sRNA40	no	no	no	no	no	no	no	no	0.273721171	0.354813064	0.383203419	0.337245885	10
sRNA42	no	no	no	no	no	no	no	no	21.39942281	33.04223214	17.4024834	23.94804612	23.94804612
sRNA43_truncated	no	no	no	no	no	no	no	no	1.608810148	5.561151693	4.50459529	3.891519044	10
sRNA44	no	no	no	no	no	no	no	no	0	1.548275187	0	0.516091729	10
sRNA46	no	no	no	no	no	no	no	no	226.3232599	199.0615743	144.1833767	189.8560703	189.8560703
sRNA48	no	no	no	no	no	no	no	no	49.88220391	62.35087873	31.17587136	47.80298467	47.80298467
sRNA49	no	no	no	no	no	no	no	no	7.085995259	13.01247011	6.200145203	8.766203525	10
sRNA5	no	no	no	no	no	no	no	no	0	0.500912561	0	0.166970854	10
sRNA50	no	no	no	no	no	no	no	no	17.12001506	15.9988436	13.56307858	15.56064575	15.56064575
sRNA53	no	no	no	no	no	no	no	no	258.3540285	346.6492233	285.1847319	296.7293279	296.7293279
sRNA54	no	no	no	no	no	no	no	no	223.0846421	298.3366119	242.7976862	254.7396467	254.7396467
sRNA55	no	no	no	no	no	no	no	no	5.972098277	6.967238343	1.25412028	4.7311523	10
sRNA56	no	no	no	no	no	no	no	no	0	0	0	0	10
sRNA57	no	no	no	no	no	no	no	no	0.316593162	1.231158583	0	0.515917248	10
sRNA58	no	no	no	no	no	no	no	no	41.55902716	42.27559909	26.35134999	36.72865875	36.72865875
sRNA59	no	no	no	no	no	no	no	no	1.865838988	2.217056777	1.088388408	1.723761391	10
sRNA6	no	no	no	no	no	no	no	no	26.01180583	39.39500199	55.5528835	40.31989711	40.31989711
sRNA60	no	no	no	no	no	no	no	no	4.899145027	3.656378691	4.572461133	4.37599495	10
sRNA61	no	no	no	no	no	no	no	no	24.54639675	19.9885108	18.724191	21.08636618	21.08636618
sRNA62	no	no	no	no	no	no	no	no	72.89812865	69.4060135	70.21275544	70.83896586	70.83896586
sRNA63	no	no	no	no	no	no	no	no	4.349335021	4.463303643	3.551899275	4.121512646	10
sRNA64	no	no	no	no	no	no	no	no	40.38395719	41.59156082	30.59173398	37.52241733	37.52241733
sRNA65	no	no	no	no	no	no	no	no	76.51311793	90.66517347	84.93591071	84.03806737	84.03806737
sRNA69	no	no	no	no	no	no	no	no	12.74346986	16.77492139	8.574536649	12.69764263	12.69764263
sRNA7	no	no	no	no	no	no	no	no	34.59835602	99.34765785	33.72190085	55.88930491	55.88930491
sRNA70	no	no	no	no	no	no	no	no	214.7878128	212.764425	174.3408945	200.6310441	200.6310441
sRNA71	no	no	no	no	no	no	no	no	7.867434856	11.01407738	6.167968801	8.349827012	10
sRNA72	no	no	no	no	no	no	no	no	7.234217832	8.274183187	8.191554863	7.89985294	10
sRNA73	no	no	no	no	no	no	no	no	7.376065241	8.963698453	7.099347548	7.813037081	10
sRNA74	no	no	no	no	no	no	no	no	6.230683976	14.74851828	10.99833317	10.65917848	10.65917848
sRNA75	no	no	no	no	no	no	no	no	13.75836226	16.22767673	14.05561219	14.68055039	14.68055039
sRNA76	no	no	no	no	no	no	no	no	3542.746869	3966.596193	3386.46835	3631.937137	3631.937137
sRNA77	no	no	no	no	no	no	no	no	7.834205939	12.05923655	6.397830992	8.763757828	10
sRNA8	no	no	no	no	no	no	no	no	26.68463137	41.98346206	41.3503224	36.67280528	36.67280528
sRNA81	no	no	no	no	no	no	no	no	38.09421268	43.53493308	31.56326384	37.7308032	37.7308032
sRNA84	no	no	no	no	no	no	no	no	530.9460795	533.071147	542.0029156	535.3400473	535.3400473
sRNA85	no	no	no	no	no	no	no	no	36.8803262	65.13620876	43.24148052	48.41933849	48.41933849
sRNA86	no	no	no	no	no	no	no	no	14.82786687	19.9506317	13.40117099	16.05988985	16.05988985
sRNA87	no	no	no	no	no	no	no	no	89.39411421	174.6515128	122.264432	128.7700197	128.7700197
sRNA88	no	no	no	no	no	no	no	no	65.99863026	50.06329815	41.40735733	52.48976191	52.48976191
sRNA89	no	no	no	no	no	no	no	no	39723.47865	30091.05776	37957.742	35924.09281	35924.09281
sRNA9	no	no	no	no	no	no	no	no	148.5942612	179.6547279	123.8730485	150.7073459	150.7073459
sRNA90	no	no	no	no	no	no	no	no	458.6571477	450.9351483	488.897889	466.163395	466.163395
sRNA91	no	no	no	no	no	no	no	no	18.43644533	27.46939848	26.70062531	24.20215637	24.20215637
sRNA92	no	no	no	no	no	no	no	no	111.4323279	81.96750992	56.65672793	83.35218857	83.35218857
sRNA93	no	no	no	no	no	no	no	no	29.52936514	28.83470918	24.94995725	27.77134386	27.77134386
sRNA94	no	no	no	no	no	no	no	no	35.74268711	35.16083006	29.46957905	33.45769874	33.45769874
sRNA95	no	no	no	no	no	no	no	no	33.53804664	60.05677963	36.7875282	43.46078483	43.46078483
sRNA96	no	no	no	no	no	no	no	no	517.189215	420.8311848	302.2680313	413.429477	413.429477
sRNA97	no	no	no	no	no	no	no	no	1172.368831	1335.071281	1089.694475	1199.044862	1199.044862
sRNA98	no	no	no	no	no	no	no	no	2.074518349	1.792739691	1.936185695	1.934481245	10
sRNA99	no	no	no	no	no	no	no	no	616.8977114	1332.992198	961.4136566	970.4345222	970.4345222

Table S 31. sRNAs expression TPM values (Col)

locus_tag	*old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	Col_1	Col_2	Col_3	Col_Mean	Col_Mean_10
newcandnsRNA1	no	no	no	no	no	no	no	no	0.766497109	0.320552082	0	0.36234973	10
sRNA1	no	no	no	no	no	no	no	no	247.2500674	282.406384	144.9214305	224.8592939	224.8592939
sRNA10	no	no	no	no	no	no	no	no	1.960634496	7.461499471	3.300320463	4.240818143	10
sRNA100	no	no	no	no	no	no	no	no	81.29136616	109.930508	100.3382356	97.18670325	97.18670325
sRNA101	no	no	no	no	no	no	no	no	109.6551916	104.6180768	118.5770402	110.9501029	110.9501029
sRNA102	no	no	no	no	no	no	no	no	60.04588736	106.3931402	104.580947	90.33999151	90.33999151
sRNA103	no	no	no	no	no	no	no	no	4.368209329	5.023706013	5.580380568	4.990765303	10
sRNA104	no	no	no	no	no	no	no	no	5.803478109	10.61828771	9.921588393	8.78111807	10
sRNA105	no	no	no	no	no	no	no	no	4.482361141	3.107791524	5.212091463	4.26741471	10
sRNA106	no	no	no	no	no	no	no	no	1.304152384	2.147518862	2.058065008	1.836578751	10
sRNA109	no	no	no	no	no	no	no	no	4.687424626	11.43507907	3.757287912	6.626597203	10
sRNA110	no	no	no	no	no	no	no	no	4.687424626	11.43507907	3.757287912	6.626597203	10
sRNA13	no	no	no	no	no	no	no	no	34.63365968	30.14223608	30.52796429	31.76795335	31.76795335
sRNA14	no	no	no	no	no	no	no	no	3.095188325	14.15771694	7.326711428	8.193205566	10
sRNA15	no	no	no	no	no	no	no	no	539.9438494	746.7747659	362.0848422	549.6011525	549.6011525
sRNA17	no	no	no	no	no	no	no	no	27.42571933	30.82439639	31.68725407	29.97912326	29.97912326
sRNA18	no	no	no	no	no	no	no	no	8.906327791	14.92868173	11.48576874	11.77359275	11.77359275
sRNA19	no	no	no	no	no	no	no	no	21.22020057	24.9927044	22.013362	22.74208899	22.74208899
sRNA2	no	no	no	no	no	no	no	no	16592.77232	22486.42228	21760.79961	20279.99807	20279.99807
sRNA20	no	no	no	no	no	no	no	no	10.74718168	24.64491468	13.19109568	16.19430735	16.19430735
sRNA21	no	no	no	no	no	no	no	no	3.38066686	2.886524814	2.371104022	2.879431899	10
sRNA22	no	no	no	no	no	no	no	no	0.21180577	1.860137993	0.222831856	0.764925206	10
sRNA24	no	no	no	no	no	no	no	no	97.45146767	126.1919048	68.64380409	97.42905885	97.42905885
sRNA25	no	no	no	no	no	no	no	no	1.679954189	3.129600588	3.213469925	2.674341567	10
sRNA26	no	no	no	no	no	no	no	no	209.1670235	699.8814793	119.4088603	199.4857877	199.4857877
sRNA27	no	no	no	no	no	no	no	no	9.214052922	12.27896778	10.70648984	10.73317018	10.73317018
sRNA28	no	no	no	no	no	no	no	no	2.290846622	3.912000735	4.016837406	3.406561588	10
sRNA29	no	no	no	no	no	no	no	no	5.416579568	23.50181013	6.716152143	11.87818061	11.87818061
sRNA3	no	no	no	no	no	no	no	no	352.408572	323.0194892	328.9789835	334.8023483	334.8023483
sRNA30	no	no	no	no	no	no	no	no	0.791383378	3.86119553	0	1.550859636	10
sRNA31	no	no	no	no	no	no	no	no	4.603720615	5.717539535	4.256302713	4.859187621	10
sRNA32	no	no	no	no	no	no	no	no	11.60695622	23.21865579	12.2118571	15.67893257	15.67893257
sRNA37	no	no	no	no	no	no	no	no	2302.615285	1799.933611	1481.760687	1861.436527	1861.436527
sRNA38	no	no	no	no	no	no	no	no	19.03291208	34.252541	18.71068779	23.99871362	23.99871362
sRNA39	no	no	no	no	no	no	no	no	0.376849228	0	0	0.125616409	10
sRNA4	no	no	no	no	no	no	no	no	10.36335377	12.51441051	8.177133291	10.35163252	10.35163252
sRNA40	no	no	no	no	no	no	no	no	0.302264485	0	0.317999628	0.206754704	10
sRNA42	no	no	no	no	no	no	no	no	24.6734698	27.72199665	25.22670103	25.87405583	25.87405583
sRNA43_truncated	no	no	no	no	no	no	no	no	1.184383288	0	0.623019679	0.602467656	10
sRNA44	no	no	no	no	no	no	no	no	2.637944595	1.930597765	0.346908685	1.638483682	10
sRNA46	no	no	no	no	no	no	no	no	324.6515576	400.7547296	220.7532901	315.3865258	315.3865258
sRNA48	no	no	no	no	no	no	no	no	8.852763217	13.67779434	4.656808111	9.062455222	10
sRNA49	no	no	no	no	no	no	no	no	14.99775242	13.839566	10.97634671	13.27122171	13.27122171
sRNA5	no	no	no	no	no	no	no	no	0	1.249210319	0.897881303	0.715697207	10
sRNA50	no	no	no	no	no	no	no	no	25.20702613	25.9558144	28.06105808	26.4079662	26.4079662
sRNA53	no	no	no	no	no	no	no	no	152.0203115	230.031578	127.2448777	169.7655891	169.7655891
sRNA54	no	no	no	no	no	no	no	no	138.082755	222.617894	128.0069123	162.9025204	162.9025204
sRNA55	no	no	no	no	no	no	no	no	5.27588919	8.205040502	2.77526948	5.418733057	10
sRNA56	no	no	no	no	no	no	no	no	0.312014952	2.283502733	0.656515361	1.084011015	10
sRNA57	no	no	no	no	no	no	no	no	0.349607115	11.25794359	0.735613597	4.114388102	10
sRNA58	no	no	no	no	no	no	no	no	15.22898511	27.11052181	17.10432042	19.81460911	19.81460911
sRNA59	no	no	no	no	no	no	no	no	5.66611768	5.78036964	6.683637151	6.043374824	10
sRNA6	no	no	no	no	no	no	no	no	23.74150135	30.24603165	20.8145211	24.93401804	24.93401804
sRNA60	no	no	no	no	no	no	no	no	11.14792405	10.79825869	7.933821227	9.960001321	10
sRNA61	no	no	no	no	no	no	no	no	12.51049173	15.76847516	9.322911249	12.53395938	12.53395938
sRNA62	no	no	no	no	no	no	no	no	73.94754365	68.50508199	52.35710004	64.93657522	64.93657522
sRNA63	no	no	no	no	no	no	no	no	4.402638565	3.222101098	3.368602956	3.66444754	10
sRNA64	no	no	no	no	no	no	no	no	2.138123514	3.57668686	3.213469925	2.976093275	10
sRNA65	no	no	no	no	no	no	no	no	24.53676406	44.65926889	42.64936187	37.28179827	37.28179827
sRNA69	no	no	no	no	no	no	no	no	11.67240898	18.04310543	12.96864648	14.22805363	14.22805363
sRNA7	no	no	no	no	no	no	no	no	364.6518745	702.5767034	330.2108137	465.8131305	465.8131305
sRNA70	no	no	no	no	no	no	no	no	281.3425257	344.090771	320.3224079	315.2530035	315.2530035
sRNA71	no	no	no	no	no	no	no	no	24.49971297	31.02828983	30.52796429	28.68532236	28.68532236
sRNA72	no	no	no	no	no	no	no	no	72.01481945	136.8770367	65.13456347	91.34213987	91.34213987
sRNA73	no	no	no	no	no	no	no	no	6.108924325	14.15771694	4.284626566	8.183755945	10
sRNA74	no	no	no	no	no	no	no	no	8.974450684	9.195218222	6.609146907	8.259605271	10
sRNA75	no	no	no	no	no	no	no	no	6.022477283	6.811731738	4.175995114	5.670068045	10
sRNA76	no	no	no	no	no	no	no	no	2452.963247	1776.890447	2790.381393	2340.078363	2340.078363
sRNA77	no	no	no	no	no	no	no	no	6.488360619	6.859018147	5.498825865	6.28206821	10
sRNA8	no	no	no	no	no	no	no	no	13.04657869	27.98618466	14.19905316	18.4106055	18.4106055
sRNA81	no	no	no	no	no	no	no	no	48.24785055	56.54709431	37.9341568	47.57636722	47.57636722
sRNA84	no	no	no	no	no	no	no	no	394.1528882	336.7177013	365.6571722	365.5092539	365.5092539
sRNA85	no	no	no	no	no	no	no	no	19.85400406	31.29600588	19.28081955	23.47694316	23.47694316
sRNA86	no	no	no	no	no	no	no	no	6.010745184	7.887870869	5.887535969	6.595384008	10
sRNA87	no	no	no	no	no	no	no	no	83.35387676	128.6686628	79.01355462	97.0120314	97.0120314
sRNA88	no	no	no	no	no	no	no	no	29.82717819	32.20057482	24.2803809	28.76937797	28.76937797
sRNA89	no	no	no	no	no	no	no	no	7913.248246	6388.661672	6805.221146	7035.710355	7035.710355
sRNA9	no	no	no	no	no	no	no	no	161.0079889	183.6118069	102.6604109	149.0934056	149.0934056
sRNA90	no	no	no	no	no	no	no	no	604.9136699	601.6225286	525.3932035	577.3098007	577.3098007
sRNA91	no	no	no	no	no	no	no	no	14.9767177	13.7010164	15.26398214	14.64723875	14.64723875
sRNA92	no	no	no	no	no	no	no	no	39.87951535	51.55831679	29.05870397	40.16551204	40.16551204
sRNA93	no	no	no	no	no	no	no	no	50.27765688	58.6634113	40.20019059	49.71375293	49.71375293
sRNA94	no	no	no	no	no	no	no	no	49.45436991	69.90663008	46.77671947	54.37923982	54.37923982
sRNA95	no	no	no	no	no	no	no	no	22.14485068	42.47315083	34.94648543	33.18816231	33.18816231
sRNA96	no	no	no	no	no	no	no	no	319.3250167	351.528935	343.4044277	338.0861265	338.0861265
sRNA97	no	no	no	no	no	no	no	no	337.9066544	445.5911031	506.3306739	429.9428105	429.9428105
sRNA98	no	no	no	no	no	no	no	no	1.145423311	2.235428991	1.606734962	1.662529088	10
sRNA99	no	no	no	no	no	no	no	no	1309.677526	1897.039052	2024.88504	1743.867206	1743.867206

Table S 32. sRNAs expression TPM values (TS)

locus_tag	*old_locus_tag	chrom	start	stop	strand	refseq_id	symbol	name	TS_1	TS_2	TS_3	TS_4	TS_Mean	TS_Mean_10
newcandRNA1	no	no	no	no	no	no	no	no	104.829139	35.15240923	17.27900311	74.60884522	57.96734915	57.96734915
sRNA1	no	no	no	no	no	no	no	no	463.5890566	289.8754227	293.605918	546.0336407	398.2760095	398.2760095
sRNA10	no	no	no	no	no	no	no	no	0.728935236	0.756057824	2.94654815	2.051288477	1.620707422	10
sRNA100	no	no	no	no	no	no	no	no	1551.008028	1435.937263	993.2250503	615.5524561	1148.930699	1148.930699
sRNA101	no	no	no	no	no	no	no	no	270.2738395	214.9591771	157.9866747	316.7729221	239.9961533	239.9961533
sRNA102	no	no	no	no	no	no	no	no	188.7942261	148.7337911	136.3678043	176.217866	162.5284219	162.5284219
sRNA103	no	no	no	no	no	no	no	no	139.203116	93.5479288	61.34945592	69.77680351	90.96934857	90.96934857
sRNA104	no	no	no	no	no	no	no	no	48.09757665	41.26185573	28.76976874	12.33337197	32.61564327	32.61564327
sRNA105	no	no	no	no	no	no	no	no	4.385464021	10.4618733	11.227272683	5.553488315	7.907013116	10
sRNA106	no	no	no	no	no	no	no	no	3.333445405	4.086110261	0	3.837522825	2.814269623	10
sRNA109	no	no	no	no	no	no	no	no	84.4387363	80.69463311	75.19741984	73.27044648	78.40030893	78.40030893
sRNA110	no	no	no	no	no	no	no	no	84.4387363	80.69463311	75.19741984	73.27044648	78.40030893	78.40030893
sRNA13	no	no	no	no	no	no	no	no	64.96145415	77.00408287	56.66032554	44.06961695	60.67386988	60.67386988
sRNA14	no	no	no	no	no	no	no	no	4.315296597	5.967816422	8.721782524	1.517953473	5.130712254	10
sRNA15	no	no	no	no	no	no	no	no	3927.466143	1626.395223	1247.086098	997.7181529	1949.666404	1949.666404
sRNA17	no	no	no	no	no	no	no	no	41.87840579	46.50553146	44.31426071	38.90956687	42.90194121	42.90194121
sRNA18	no	no	no	no	no	no	no	no	109.484629	111.4811004	111.1811386	89.61185725	105.4396813	105.4396813
sRNA19	no	no	no	no	no	no	no	no	15.22830007	16.74642363	20.14810872	10.06805875	15.54772279	15.54772279
sRNA2	no	no	no	no	no	no	no	no	32715.85769	28524.00059	25446.17087	53339.62813	35006.41432	35006.41432
sRNA20	no	no	no	no	no	no	no	no	14.31772791	25.55662125	23.77852231	14.05512475	19.42699906	19.42699906
sRNA21	no	no	no	no	no	no	no	no	24.35209851	17.92517675	15.52420838	12.89523581	17.67417986	17.67417986
sRNA22	no	no	no	no	no	no	no	no	0.590597162	1.633526393	0.795783077	0.553997618	0.893476062	10
sRNA24	no	no	no	no	no	no	no	no	477.9876939	187.2488643	161.9579558	179.6537419	251.712064	251.712064
sRNA25	no	no	no	no	no	no	no	no	3.548763649	5.30036327	4.972946176	1.797576481	3.904912394	10
sRNA26	no	no	no	no	no	no	no	no	783.8331709	332.7757009	301.5147474	343.3183831	440.3605006	440.3605006
sRNA27	no	no	no	no	no	no	no	no	69.91905327	53.03154404	49.25809245	44.06381527	54.06812626	54.06812626
sRNA28	no	no	no	no	no	no	no	no	7.98471821	12.698787	15.0622889	5.492594803	10.30959723	10.30959723
sRNA29	no	no	no	no	no	no	no	no	518.7346118	486.7500269	666.4895479	670.934535	585.7274054	585.7274054
sRNA3	no	no	no	no	no	no	no	no	859.1556794	636.4116732	732.0750572	1144.457026	843.024859	843.024859
sRNA30	no	no	no	no	no	no	no	no	4.168184213	7.375000408	5.616299352	1.724947128	4.721107775	10
sRNA31	no	no	no	no	no	no	no	no	16.20829551	13.44910552	13.97721558	10.94677985	13.64534912	13.64534912
sRNA32	no	no	no	no	no	no	no	no	11.14784954	7.832759054	10.65995642	6.071813891	8.928094726	10
sRNA37	no	no	no	no	no	no	no	no	3248.711209	2445.268898	2006.071057	3472.478018	2793.132296	2793.132296
sRNA38	no	no	no	no	no	no	no	no	33.64075304	20.45420951	41.02989091	18.3623404	28.37179846	28.37179846
sRNA39	no	no	no	no	no	no	no	no	0.700535162	1.453202051	0	0	0.538434303	10
sRNA4	no	no	no	no	no	no	no	no	3.130516504	4.246074742	7.138363673	2.032973401	4.13698208	10
sRNA40	no	no	no	no	no	no	no	no	1.9666006522	0.582794572	3.02839671	0.790600767	1.592099643	10
sRNA42	no	no	no	no	no	no	no	no	43.12066585	42.21247395	55.92560151	28.40481798	42.41588982	42.41588982
sRNA43_truncatex	no	no	no	no	no	no	no	no	8.256307265	7.99261128	8.899778086	2.323396173	6.868023701	10
sRNA44	no	no	no	no	no	no	no	no	2.145388933	4.132543332	2.890742314	1.724947128	2.723405427	10
sRNA46	no	no	no	no	no	no	no	no	669.6249894	306.9635413	238.5595085	454.5699378	417.4294943	417.4294943
sRNA48	no	no	no	no	no	no	no	no	32.91327913	72.06896951	90.54392874	170.4481654	91.49358569	91.49358569
sRNA49	no	no	no	no	no	no	no	no	78.79052775	60.97733774	60.84014963	78.45602219	69.76600933	69.76600933
sRNA5	no	no	no	no	no	no	no	no	0.396626525	0.411384404	0.534422949	0	0.33560847	10
sRNA50	no	no	no	no	no	no	no	no	28.4689706	26.13745355	31.20166307	27.21583247	28.25597992	28.25597992
sRNA53	no	no	no	no	no	no	no	no	233.1883172	169.5777482	285.9020894	202.1699094	222.709516	222.709516
sRNA54	no	no	no	no	no	no	no	no	217.9968798	173.0538146	275.4379021	188.4356035	213.73105	213.73105
sRNA55	no	no	no	no	no	no	no	no	11.33991293	17.16594923	11.56296926	20.26812876	15.08424004	15.08424004
sRNA56	no	no	no	no	no	no	no	no	1.450032459	2.40637759	2.73532606	0.408052009	1.749947029	10
sRNA57	no	no	no	no	no	no	no	no	0.324947033	4.381491726	3.502723905	12.80201724	5.252794976	10
sRNA58	no	no	no	no	no	no	no	no	15.3024702	30.15651916	31.95925038	39.29454025	29.178195	29.178195
sRNA59	no	no	no	no	no	no	no	no	7.660289817	4.303713766	5.590886233	5.389183927	5.736018436	10
sRNA6	no	no	no	no	no	no	no	no	81.45667187	98.19205524	105.718576	89.12226829	93.62239286	93.62239286
sRNA60	no	no	no	no	no	no	no	no	8.07594349	7.428161331	8.623231309	7.075206885	7.800635749	10
sRNA61	no	no	no	no	no	no	no	no	15.98856149	21.94378606	12.83895132	15.67945962	16.6126896	16.6126896
sRNA62	no	no	no	no	no	no	no	no	238.0953297	172.9583893	120.940488	120.5793686	163.1433939	163.1433939
sRNA63	no	no	no	no	no	no	no	no	20.0884968	11.96135619	10.27566332	10.20692852	13.13309943	13.13309943
sRNA64	no	no	no	no	no	no	no	no	47.69538344	47.1134018	16.44897581	21.17145633	33.10753894	33.10753894
sRNA65	no	no	no	no	no	no	no	no	3945.045735	1056.229458	479.1101736	2000.964036	1870.337351	1870.337351
sRNA69	no	no	no	no	no	no	no	no	27.9845362	32.07561106	37.57033512	21.97037921	29.9002154	29.9002154
sRNA7	no	no	no	no	no	no	no	no	83.60887157	140.3369331	170.8015744	42.05996081	109.201835	109.201835
sRNA70	no	no	no	no	no	no	no	no	584.7539592	569.2129251	395.5349442	511.4843224	515.2465377	515.2465377
sRNA71	no	no	no	no	no	no	no	no	23.74059131	25.62900204	26.98355871	30.67720342	26.75758887	26.75758887
sRNA72	no	no	no	no	no	no	no	no	26.97060373	23.67042571	19.86235899	12.59839927	20.77544692	20.77544692
sRNA73	no	no	no	no	no	no	no	no	8.990201244	11.28781067	18.48915886	6.65769067	11.35621536	11.35621536
sRNA74	no	no	no	no	no	no	no	no	17.79503751	21.91788248	17.60840973	13.69287927	17.75355225	17.75355225
sRNA75	no	no	no	no	no	no	no	no	46.56245738	51.98967432	21.77017257	26.67158814	36.7484731	36.7484731
sRNA76	no	no	no	no	no	no	no	no	5325.770586	3369.350978	3815.282036	7504.512443	5003.729011	5003.729011
sRNA77	no	no	no	no	no	no	no	no	72.87088586	42.74309511	26.63484311	24.98494847	41.80844313	41.80844313
sRNA8	no	no	no	no	no	no	no	no	193.8102129	139.0032822	142.2642175	118.5533429	148.4082139	148.4082139
sRNA81	no	no	no	no	no	no	no	no	71.81521704	58.43119075	54.8338919	67.36479909	63.11122469	63.11122469
sRNA84	no	no	no	no	no	no	no	no	1269.716089	943.8163837	560.8590706	1339.383113	1028.443664	1028.443664
sRNA85	no	no	no	no	no	no	no	no	131.0676708	96.68255224	86.70777948	113.1807414	106.909686	106.909686
sRNA86	no	no	no	no	no	no	no	no	37.56619805	30.77155343	32.4471076	47.70710915	37.12299206	37.12299206
sRNA87	no	no	no	no	no	no	no	no	112.1130979	101.7490759	124.3424061	100.8248508	109.7573577	109.7573577
sRNA88	no	no	no	no	no	no	no	no	104.2445195	96.54330927	66.42752969	95.84287625	90.76455869	90.76455869
sRNA89	no	no	no	no	no	no	no	no	27901.67588	25250.21366	15055.13717	34746.45866	25738.37134	25738.37134
sRNA9	no	no	no	no	no	no	no	no	775.1065099	382.4782787	284.2940911	220.9764126	415.7138231	415.7138231
sRNA90	no	no	no	no	no	no	no	no	2173.891958	1480.086289	1367.114633	1		

Appendix III

Table S 33. Kegg Pathways Sets AB5075-UW

gene	KEGG function	KEGG Pathway ID	KEGG Pathway
ABUW_RS00005	DNA replication initiator protein [KO:K02313]	AB02020	Two-component system
ABUW_RS00100	putative glutathione S-transferase [KO:K00799] [EC:2.5.1.18]	AB00480	Glutathione metabolism
ABUW_RS00130	dihydroxy-acid dehydratase [KO:K01687] [EC:4.2.1.9]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS00155	phosphoenolpyruvate carboxylase [KO:K01595] [EC:4.1.1.31]	AB00680	Methane metabolism
ABUW_RS00155	phosphoenolpyruvate carboxylase [KO:K01595] [EC:4.1.1.31]	AB00620	Pyruvate metabolism
ABUW_RS00225	putative alcohol dehydrogenase [KO:K12957] [EC:1.1.1.2 1.1.1.183]	AB00620	Pyruvate metabolism
ABUW_RS00225	putative alcohol dehydrogenase [KO:K12957] [EC:1.1.1.2 1.1.1.183]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS00290	phosphoribosylaminimidazole-succinocarboxamide synthase [KO:K01923] [EC:6.3.2.6]	AB00230	Purine metabolism
ABUW_RS00300	dihydrodipicolinate synthase [KO:K01714] [EC:4.3.3.7]	AB00300	Lysine biosynthesis
ABUW_RS00305	hypothetical protein [KO:K08281] [EC:3.5.1.19 3.5.1.-]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS00325	4-hydroxyphenylpyruvate dioxygenase [KO:K00457] [EC:1.13.11.27]	AB00360	Phenylalanine metabolism
ABUW_RS00325	4-hydroxyphenylpyruvate dioxygenase [KO:K00457] [EC:1.13.11.27]	AB00350	Tyrosine metabolism
ABUW_RS00340	Maleylacetoacetate isomerase [KO:K01800] [EC:5.2.1.2]	AB00350	Tyrosine metabolism
ABUW_RS00345	Fumarylacetoacetase [KO:K01555] [EC:3.7.1.2]	AB00350	Tyrosine metabolism
ABUW_RS00380	Urocanase [KO:K01712] [EC:4.2.1.49]	AB00340	Histidine metabolism
ABUW_RS00385	histidine ammonia-lyase [KO:K01745] [EC:4.3.1.3]	AB00340	Histidine metabolism
ABUW_RS00395	imidazolepropionase [KO:K01468] [EC:3.5.2.7]	AB00340	Histidine metabolism
ABUW_RS00400	Arginase/argininase/formiminoglutamate hydrolase [KO:K01479] [EC:3.5.3.8]	AB00340	Histidine metabolism
ABUW_RS00440	glucosamine-fructose-6-phosphate aminotransferase [KO:K00820] [EC:2.6.1.16]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS00440	glucosamine-fructose-6-phosphate aminotransferase [KO:K00820] [EC:2.6.1.16]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS00450	phosphatidylglycerophosphatase A [KO:K01095] [EC:3.1.3.27]	AB00564	Glycerophospholipid metabolism
ABUW_RS00470	hypothetical protein [KO:K14652] [EC:4.1.99.12 3.5.4.25]	AB00797	Folate biosynthesis
ABUW_RS00480	phosphoserine phosphatase [KO:K01079] [EC:3.1.3.3]	AB00680	Methane metabolism
ABUW_RS00480	phosphoserine phosphatase [KO:K01079] [EC:3.1.3.3]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS00500	nicotinate phosphoribosyltransferase [KO:K00763] [EC:6.3.4.21]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS00505	thiosulfate sulfatransferase [KO:K01011] [EC:2.8.1.1 2.8.1.2]	AB00920	Sulfur metabolism
ABUW_RS00505	thiosulfate sulfatransferase [KO:K01011] [EC:2.8.1.1 2.8.1.2]	AB00270	Cysteine and methionine metabolism
ABUW_RS00510	phosphatidylserine decarboxylase [KO:K01613] [EC:4.1.1.65]	AB00564	Glycerophospholipid metabolism
ABUW_RS00520	two-component sensor [KO:K07636] [EC:2.7.13.3]	AB02020	Two-component system
ABUW_RS00565	gamma-glutamate-cysteine ligase [KO:K01919] [EC:6.3.3.2]	AB00480	Glutathione metabolism
ABUW_RS00565	gamma-glutamate-cysteine ligase [KO:K01919] [EC:6.3.3.2]	AB00270	Cysteine and methionine metabolism
ABUW_RS00620	ureidoglycolate amidohydrolase(decarboxylating) [KO:K01483] [EC:4.3.2.3]	AB00230	Purine metabolism
ABUW_RS00625	allantoinase [KO:K01477] [EC:3.5.3.4]	AB00230	Purine metabolism
ABUW_RS00630	putative flavoprotein monooxygenase [KO:K16839] [EC:1.14.13.113]	AB00230	Purine metabolism
ABUW_RS00645	putative transthyretin-like protein precursor [KO:K07127] [EC:3.5.2.17]	AB00230	Purine metabolism
ABUW_RS00650	hypothetical protein [KO:K16840] [EC:4.1.1.97]	AB00230	Purine metabolism
ABUW_RS00655	putative deacetylase [KO:K16842] [EC:3.5.2.5]	AB00230	Purine metabolism
ABUW_RS00705	orotate phosphoribosyltransferase [KO:K00762] [EC:2.4.2.10]	AB00240	Pyrimidine metabolism
ABUW_RS00720	glutathione synthetase [KO:K01920] [EC:6.3.2.3]	AB00480	Glutathione metabolism
ABUW_RS00720	glutathione synthetase [KO:K01920] [EC:6.3.2.3]	AB00270	Cysteine and methionine metabolism
ABUW_RS00725	γ-glucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [KO:K02563] [EC:2.4.1.12]	AB00550	Peptidoglycan biosynthesis
ABUW_RS00730	UDP-N-acetylmutarinate-alanine ligase [KO:K01924] [EC:6.3.3.26]	AB00550	Peptidoglycan biosynthesis
ABUW_RS00735	D-alanine-D-alanine ligase B [KO:K01921] [EC:6.3.2.4]	AB00550	Peptidoglycan biosynthesis
ABUW_RS00755	UDP-3-O-acetyl-N-acetylglucosamine deacetylase [KO:K02535] [EC:3.5.1.108]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS00770	pyruvate decarboxylase E1 component of the pyruvate dehydrogenase complex [KO:K00163] [EC:1.2.4.1]	AB00620	Pyruvate metabolism
ABUW_RS00770	pyruvate decarboxylase E1 component of the pyruvate dehydrogenase complex [KO:K00163] [EC:1.2.4.1]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS00770	pyruvate decarboxylase E1 component of the pyruvate dehydrogenase complex [KO:K00163] [EC:1.2.4.1]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS00775	dihydropyrimidine S-acetyltransferase E2 component of the pyruvate dehydrogenase complex [KO:K00627] [EC:2.3.1.12]	AB00620	Pyruvate metabolism
ABUW_RS00775	dihydropyrimidine S-acetyltransferase E2 component of the pyruvate dehydrogenase complex [KO:K00627] [EC:2.3.1.12]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS00775	dihydropyrimidine S-acetyltransferase E2 component of the pyruvate dehydrogenase complex [KO:K00627] [EC:2.3.1.12]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS00805	IMP dehydrogenase [KO:K00088] [EC:1.1.1.205]	AB00230	Purine metabolism
ABUW_RS00810	phosphoglucoamine mutase [KO:K03431] [EC:5.4.2.10]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS00845	3-deoxy-D-manno-2-oxulosonate transferase [KO:K02527] [EC:2.4.99.12 2.4.99.13 2.4.99.14 2.4.99.15]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS00865	acetyl-CoA synthetase [KO:K01895] [EC:6.2.1.1]	AB00680	Methane metabolism
ABUW_RS00865	acetyl-CoA synthetase [KO:K01895] [EC:6.2.1.1]	AB00640	Propanoate metabolism
ABUW_RS00865	acetyl-CoA synthetase [KO:K01895] [EC:6.2.1.1]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS00865	acetyl-CoA synthetase [KO:K01895] [EC:6.2.1.1]	AB00620	Pyruvate metabolism
ABUW_RS00865	acetyl-CoA synthetase [KO:K01895] [EC:6.2.1.1]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS00880	putative sulfonate monooxygenase (MsdU) [KO:K17228] [EC:1.14.14.35]	AB00920	Sulfur metabolism
ABUW_RS00885	NADH-dependent FMN reductase [KO:K00299] [EC:1.5.1.38]	AB00920	Sulfur metabolism
ABUW_RS01005	4-aminobutyrate aminotransferase PLP-dependent [KO:K00823] [EC:2.6.1.19]	AB00650	Butanoate metabolism
ABUW_RS01005	4-aminobutyrate aminotransferase PLP-dependent [KO:K00823] [EC:2.6.1.19]	AB00640	Propanoate metabolism
ABUW_RS01005	4-aminobutyrate aminotransferase PLP-dependent [KO:K00823] [EC:2.6.1.19]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS01010	NADP+ dependent succinate semialdehyde dehydrogenase [KO:K00135] [EC:1.2.1.16 1.2.1.79 1.2.1.20]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS01010	NADP+ dependent succinate semialdehyde dehydrogenase [KO:K00135] [EC:1.2.1.16 1.2.1.79 1.2.1.20]	AB00650	Butanoate metabolism
ABUW_RS01010	NADP+ dependent succinate semialdehyde dehydrogenase [KO:K00135] [EC:1.2.1.16 1.2.1.79 1.2.1.20]	AB00350	Tyrosine metabolism
ABUW_RS01010	NADP+ dependent succinate semialdehyde dehydrogenase [KO:K00135] [EC:1.2.1.16 1.2.1.79 1.2.1.20]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS01175	imidazole glycerol phosphate synthase cyclase subunit [KO:K02500] [EC:4.3.2.10]	AB00340	Histidine metabolism
ABUW_RS01180	putative homoserine kinase (ThrB) [KO:K02204] [EC:2.7.1.39]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS01205	phosphoribosylformimino-5-aminoimidazole carboxamide isomerase [KO:K01814] [EC:5.3.1.16]	AB00340	Histidine metabolism
ABUW_RS01220	imidazole glycerol phosphate synthetase glutamine amidotransferase subunit [KO:K02501] [EC:4.3.2.10]	AB00340	Histidine metabolism
ABUW_RS01225	hypothetical protein [KO:K01693] [EC:4.2.1.19]	AB00340	Histidine metabolism
ABUW_RS01250	putative acetyl-CoA hydrolase/transferase [KO:K18118] [EC:2.8.3.18]	AB00650	Butanoate metabolism
ABUW_RS01250	putative acetyl-CoA hydrolase/transferase [KO:K18118] [EC:2.8.3.18]	AB00620	Pyruvate metabolism
ABUW_RS01250	putative acetyl-CoA hydrolase/transferase [KO:K18118] [EC:2.8.3.18]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS01255	sensory histidine kinase (OmpR) [KO:K07638] [EC:2.7.13.3]	AB00200	Two-component system
ABUW_RS01260	two-component response regulator [KO:K07659]	AB00200	Two-component system
ABUW_RS01270	putative sulfate permease [KO:K01673] [EC:4.2.1.1]	AB00910	Nitrogen metabolism
ABUW_RS01280	homocysteine synthase [KO:K01740] [EC:2.5.1.49]	AB00270	Cysteine and methionine metabolism
ABUW_RS01375	sulfate transport protein [KO:K23163]	AB02010	ABC transporters
ABUW_RS01375	sulfate transport protein [KO:K23163]	AB00920	Sulfur metabolism
ABUW_RS01390	septum formation penicillin binding protein 3, peptidoglycan synthetase [KO:K03587] [EC:3.4.16.4]	AB00550	Peptidoglycan biosynthesis
ABUW_RS01395	UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate ligase [KO:K01928] [EC:6.3.2.13]	AB00550	Peptidoglycan biosynthesis
ABUW_RS01395	UDP-N-acetylmuramoylalanine-D-glutamate-2,6-diaminopimelate ligase [KO:K01928] [EC:6.3.2.13]	AB00300	Lysine biosynthesis
ABUW_RS01400	UDP-N-acetylmuramoyl-tripeptide-D-alanine-D-alanine ligase [KO:K01929] [EC:6.3.2.10]	AB00550	Peptidoglycan biosynthesis
ABUW_RS01400	UDP-N-acetylmuramoyl-tripeptide-D-alanine-D-alanine ligase [KO:K01929] [EC:6.3.2.10]	AB00300	Lysine biosynthesis
ABUW_RS01405	phospho-N-acetylmuramoyl-pentapeptide transferase [KO:K01000] [EC:2.7.8.13]	AB00550	Peptidoglycan biosynthesis
ABUW_RS01420	putative penicillin binding protein (PonA) [KO:K05366] [EC:2.4.1.129 3.4.16.4]	AB00550	Peptidoglycan biosynthesis
ABUW_RS01450	shikimate-kinase [KO:K00891] [EC:2.7.1.71]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS01455	3-dehydroquinate synthase [KO:K01713] [EC:4.2.3.4]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS01465	glutamate synthase large chain precursor [KO:K00265] [EC:1.4.1.13]	AB00910	Nitrogen metabolism
ABUW_RS01465	glutamate synthase large chain precursor [KO:K00265] [EC:1.4.1.13]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS01470	glutamate synthase small chain [KO:K00266] [EC:1.4.1.13]	AB00910	Nitrogen metabolism
ABUW_RS01470	glutamate synthase small chain [KO:K00266] [EC:1.4.1.13]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS01505	bacterioferritin [KO:K03594] [EC:1.16.3.1]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS01520	hypothetical protein (Spot) [KO:K01139] [EC:2.7.6.5 3.1.7.2]	AB00230	Purine metabolism
ABUW_RS01530	guanylate kinase [KO:K00942] [EC:2.7.4.8]	AB00230	Purine metabolism
ABUW_RS01535	4-hydroxy-3-methylbut-2-enyl diphosphate reductase [KO:K03527] [EC:1.17.7.4]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS01630	D-3-phosphoglycerate dehydrogenase [KO:K00058] [EC:1.1.1.95 1.1.1.399]	AB00680	Methane metabolism

ABUW_RS01630	D-3-phosphoglycerate dehydrogenase [KO:K00058] [EC:1.1.1.95 1.1.1.399]	AB00270	Cysteine and methionine metabolism
ABUW_RS01630	D-3-phosphoglycerate dehydrogenase [KO:K00058] [EC:1.1.1.95 1.1.1.399]	AB00280	Glycine, serine and threonine metabolism
ABUW_RS01715	glutamate dehydrogenase (NAD(P ⁺)) oxidoreductase protein [KO:K00261] [EC:1.4.1.3]	AB00910	Nitrogen metabolism
ABUW_RS01715	glutamate dehydrogenase (NAD(P ⁺)) oxidoreductase protein [KO:K00261] [EC:1.4.1.3]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS01715	glutamate dehydrogenase (NAD(P ⁺)) oxidoreductase protein [KO:K00261] [EC:1.4.1.3]	AB00220	Arginine biosynthesis
ABUW_RS01725	arginine succinyltransferase [KO:K00673] [EC:2.3.1.109]	AB00330	Arginine and proline metabolism
ABUW_RS01730	succinylglutamic semialdehyde dehydrogenase [KO:K06447] [EC:1.2.1.71]	AB00330	Arginine and proline metabolism
ABUW_RS01735	succinylarginine dihydrolase [KO:K01484] [EC:3.5.3.23]	AB00330	Arginine and proline metabolism
ABUW_RS01740	succinylglutamate desuccinylase [KO:K05526] [EC:3.5.1.96]	AB00330	Arginine and proline metabolism
ABUW_RS01845	dehydroximate reductase NAD(P)-binding [KO:K00014] [EC:1.1.1.25]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS01850	coproporphyrinogen III oxidase [KO:K00228] [EC:1.3.3.3]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS01855	GTP cyclohydrolase II [KO:K01497] [EC:3.5.4.25]	AB02024	Quorum sensing
ABUW_RS01855	GTP cyclohydrolase II [KO:K01497] [EC:3.5.4.25]	AB00796	Folate biosynthesis
ABUW_RS01860	1-deoxyxylulose-5-phosphate synthase [KO:K01662] [EC:2.2.2.17]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS01880	toluene tolerance efflux transporter [KO:K02065]	AB02010	ABC transporters
ABUW_RS01890	toluene tolerance efflux transporter [KO:K02067]	AB02010	ABC transporters
ABUW_RS01895	putative toluene tolerance protein (Tg2D) [KO:K07323]	AB02010	ABC transporters
ABUW_RS01900	putative toluene-tolerance protein (Tg2E) [KO:K07122]	AB02010	ABC transporters
ABUW_RS01940	glycerol-3-phosphate acyltransferase [KO:K00631] [EC:2.3.1.15]	AB00564	Glycerophospholipid metabolism
ABUW_RS01980	putative cystathionine beta-lyase PLP-dependent [KO:K01760] [EC:4.4.1.13]	AB00270	Cysteine and methionine metabolism
ABUW_RS02095	secretion protein [KO:K03076]	AB03070	Bacterial secretion system
ABUW_RS02095	secretion protein [KO:K03076]	AB03060	Protein export
ABUW_RS02095	secretion protein [KO:K03076]	AB02024	Quorum sensing
ABUW_RS02250	xanthine phosphoribosyltransferase [KO:K03816] [EC:2.4.2.22]	AB00230	Purine metabolism
ABUW_RS02295	malate dehydrogenase [KO:K00024] [EC:1.1.1.37]	AB00680	Methane metabolism
ABUW_RS02295	malate dehydrogenase [KO:K00024] [EC:1.1.1.37]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS02295	malate dehydrogenase [KO:K00024] [EC:1.1.1.37]	AB00620	Pyruvate metabolism
ABUW_RS02295	malate dehydrogenase [KO:K00024] [EC:1.1.1.37]	AB00270	Cysteine and methionine metabolism
ABUW_RS02295	malate dehydrogenase [KO:K00024] [EC:1.1.1.37]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS02320	phosphatidylserine synthase [KO:K17103] [EC:2.7.8.8]	AB00564	Glycerophospholipid metabolism
ABUW_RS02320	phosphatidylserine synthase [KO:K17103] [EC:2.7.8.8]	AB00280	Glycine, serine and threonine metabolism
ABUW_RS02365	acyl-CoA dehydrogenase [KO:K00249] [EC:1.3.8.7]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS02365	acyl-CoA dehydrogenase [KO:K00249] [EC:1.3.8.7]	AB00071	Fatty acid degradation
ABUW_RS02440	bis(5'-nucleosyl)-tetraphosphatase symmetrical [KO:K01525] [EC:3.6.1.41]	AB00230	Purine metabolism
ABUW_RS02470	putative phospholipase D protein [KO:K06132] [EC:2.7.8.-]	AB00564	Glycerophospholipid metabolism
ABUW_RS02520	putative pyridine nucleotide-disulfide oxidoreductase class I [KO:K00382] [EC:1.8.1.4]	AB00640	Propanoate metabolism
ABUW_RS02520	putative pyridine nucleotide-disulfide oxidoreductase class I [KO:K00382] [EC:1.8.1.4]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS02520	putative pyridine nucleotide-disulfide oxidoreductase class I [KO:K00382] [EC:1.8.1.4]	AB00620	Pyruvate metabolism
ABUW_RS02520	putative pyridine nucleotide-disulfide oxidoreductase class I [KO:K00382] [EC:1.8.1.4]	AB00380	Tryptophan metabolism
ABUW_RS02520	putative pyridine nucleotide-disulfide oxidoreductase class I [KO:K00382] [EC:1.8.1.4]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS02520	putative pyridine nucleotide-disulfide oxidoreductase class I [KO:K00382] [EC:1.8.1.4]	AB00280	Glycine, serine and threonine metabolism
ABUW_RS02520	putative pyridine nucleotide-disulfide oxidoreductase class I [KO:K00382] [EC:1.8.1.4]	AB00010	Glycolysis / Gluconogenesis
ABUW_RS02520	putative pyridine nucleotide-disulfide oxidoreductase class I [KO:K00382] [EC:1.8.1.4]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS02600	hypothetical protein [KO:K13038] [EC:4.1.1.36 6.3.2.9]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS02610	preprotein translocase ISP family, part of the channel [KO:K03072]	AB03070	Bacterial secretion system
ABUW_RS02610	preprotein translocase ISP family, part of the channel [KO:K03072]	AB03060	Protein export
ABUW_RS02615	putative preprotein translocase ISP family membrane subunit [KO:K03210]	AB03070	Bacterial secretion system
ABUW_RS02615	putative preprotein translocase ISP family membrane subunit [KO:K03210]	AB03060	Protein export
ABUW_RS02615	putative preprotein translocase ISP family membrane subunit [KO:K03210]	AB02024	Quorum sensing
ABUW_RS02885	branched-chain amino acid transferase [KO:K00826] [EC:2.6.1.42]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS02885	branched-chain amino acid transferase [KO:K00826] [EC:2.6.1.42]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS02885	branched-chain amino acid transferase [KO:K00826] [EC:2.6.1.42]	AB00270	Cysteine and methionine metabolism
ABUW_RS02925	UDP-N-acetylglucosamine 2-epimerase [KO:K01791] [EC:5.1.3.14]	AB02020	Two-component system
ABUW_RS02925	UDP-N-acetylglucosamine 2-epimerase [KO:K01791] [EC:5.1.3.14]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS02990	two component signal transduction system kinase sensor component [KO:K07642] [EC:2.7.13.3]	AB02020	Two-component system
ABUW_RS02995	transcriptional regulator protein (OmpR family) [KO:K07664]	AB02020	Two-component system
ABUW_RS03015	putative glycerophosphodiester phosphodiesterase [KO:K01126] [EC:3.1.4.46]	AB00564	Glycerophospholipid metabolism
ABUW_RS03020	hypothetical protein [KO:K00798] [EC:2.5.1.17]	AB00860	Porphyryrin and chlorophyll metabolism
ABUW_RS03030	N-(5-phosphoribosyl)anthranilate isomerase [KO:K01817] [EC:5.3.1.24]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS03035	tryptophan synthase beta chain [KO:K01696] [EC:4.2.1.20]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS03035	tryptophan synthase beta chain [KO:K01696] [EC:4.2.1.20]	AB00280	Glycine, serine and threonine metabolism
ABUW_RS03060	tryptophan synthase alpha chain [KO:K01695] [EC:4.2.1.20]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS03060	tryptophan synthase alpha chain [KO:K01695] [EC:4.2.1.20]	AB00280	Glycine, serine and threonine metabolism
ABUW_RS03065	acetylCoA carboxylase beta subunit [KO:K01963] [EC:6.4.1.2.2.1.3.15]	AB00640	Propanoate metabolism
ABUW_RS03065	acetylCoA carboxylase beta subunit [KO:K01963] [EC:6.4.1.2.2.1.3.15]	AB00620	Pyruvate metabolism
ABUW_RS03065	acetylCoA carboxylase beta subunit [KO:K01963] [EC:6.4.1.2.2.1.3.15]	AB00061	Fatty acid biosynthesis
ABUW_RS03095	preprotein translocase secretion protein of ISP family [KO:K03070] [EC:7.4.2.8]	AB03070	Bacterial secretion system
ABUW_RS03095	preprotein translocase secretion protein of ISP family [KO:K03070] [EC:7.4.2.8]	AB03060	Protein export
ABUW_RS03095	preprotein translocase secretion protein of ISP family [KO:K03070] [EC:7.4.2.8]	AB02024	Quorum sensing
ABUW_RS03140	putative thiolase; putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB02020	Two-component system
ABUW_RS03140	putative thiolase; putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS03140	putative thiolase; putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00650	Butanoate metabolism
ABUW_RS03140	putative thiolase; putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00640	Propanoate metabolism
ABUW_RS03140	putative thiolase; putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS03140	putative thiolase; putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00620	Pyruvate metabolism
ABUW_RS03140	putative thiolase; putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00380	Tryptophan metabolism
ABUW_RS03140	putative thiolase; putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS03140	putative thiolase; putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00071	Fatty acid degradation
ABUW_RS03160	glucose dehydrogenase [KO:K00117] [EC:1.1.5.2]	AB00030	Pentose phosphate pathway
ABUW_RS03165	CysI-like sulfite reductase protein [KO:K00381] [EC:1.8.1.2]	AB00920	Sulfur metabolism
ABUW_RS03185	putative acetyl-CoA acetyltransferase [KO:K00626] [EC:2.3.1.9]	AB02020	Two-component system
ABUW_RS03185	putative acetyl-CoA acetyltransferase [KO:K00626] [EC:2.3.1.9]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS03185	putative acetyl-CoA acetyltransferase [KO:K00626] [EC:2.3.1.9]	AB00550	Butanoate metabolism
ABUW_RS03185	putative acetyl-CoA acetyltransferase [KO:K00626] [EC:2.3.1.9]	AB00640	Propanoate metabolism
ABUW_RS03185	putative acetyl-CoA acetyltransferase [KO:K00626] [EC:2.3.1.9]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS03185	putative acetyl-CoA acetyltransferase [KO:K00626] [EC:2.3.1.9]	AB00620	Pyruvate metabolism
ABUW_RS03185	putative acetyl-CoA acetyltransferase [KO:K00626] [EC:2.3.1.9]	AB00380	Tryptophan metabolism
ABUW_RS03185	putative acetyl-CoA acetyltransferase [KO:K00626] [EC:2.3.1.9]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS03185	putative acetyl-CoA acetyltransferase [KO:K00626] [EC:2.3.1.9]	AB00071	Fatty acid degradation
ABUW_RS03335	twitching motility protein [KO:K02657]	AB02020	Two-component system
ABUW_RS03340	twitching motility protein [KO:K02658]	AB02020	Two-component system
ABUW_RS03345	twitching motility protein [KO:K02659]	AB02020	Two-component system
ABUW_RS03350	Methyl-accepting chemotaxis protein [KO:K02660]	AB02020	Two-component system
ABUW_RS03375	succinyl-diaminopimelate desuccinylase [KO:K01439] [EC:3.5.1.18]	AB00300	Lysine biosynthesis
ABUW_RS03435	hypothetical protein [KO:K00380] [EC:1.8.1.2]	AB00920	Sulfur metabolism
ABUW_RS03475	threonine dehydratase [KO:K01754] [EC:4.3.1.19]	AB00280	Glycine, serine and threonine metabolism
ABUW_RS03555	3'-phosphoadenylylsulfate reductase [KO:K00390] [EC:1.8.4.8 1.8.4.10]	AB00920	Sulfur metabolism
ABUW_RS03560	putative homoserine kinase (ThH) [KO:K02203] [EC:3.1.3.3 2.7.1.39]	AB00680	Methane metabolism
ABUW_RS03560	putative homoserine kinase (ThH) [KO:K02203] [EC:3.1.3.3 2.7.1.39]	AB00280	Glycine, serine and threonine metabolism
ABUW_RS03590	bacitracin resistance protein [KO:K06153] [EC:3.6.1.27]	AB00550	Peptidoglycan biosynthesis

ABUW_RS03605	putative intracellular protease/amidase [KO:K05523] [EC:4.2.1.130 3.5.1.124]	AB00620	Pyruvate metabolism
ABUW_RS04005	hypothetical protein [KO:K09788] [EC:5.3.3.-]	AB00640	Propanoate metabolism
ABUW_RS04010	geranyltransferase [KO:K00795] [EC:2.5.1.1 2.5.1.10]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS04050	lipid A phosphoethanolamine transferase [KO:K03760] [EC:2.7.8.43]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS04055	transcriptional regulator [KO:K07666]	AB02024	Quorum sensing
ABUW_RS04055	transcriptional regulator [KO:K07666]	AB02020	Two-component system
ABUW_RS04060	two-component sensor kinase transcription regulator protein [KO:K07645] [EC:2.7.13.3]	AB02024	Quorum sensing
ABUW_RS04060	two-component sensor kinase transcription regulator protein [KO:K07645] [EC:2.7.13.3]	AB02020	Two-component system
ABUW_RS04125	AdeK [KO:K18139]	AB02024	Quorum sensing
ABUW_RS04150	solanesyl diphosphate synthase [KO:K02523] [EC:2.5.1.90]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS04185	multifunctional protein [KO:K02302] [EC:2.1.1.107 1.3.1.76 4.99.1.4]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS04210	putative alcohol dehydrogenase [KO:K00001] [EC:1.1.1.1]	AB00620	Pyruvate metabolism
ABUW_RS04210	putative alcohol dehydrogenase [KO:K00001] [EC:1.1.1.1]	AB00350	Tyrosine metabolism
ABUW_RS04210	putative alcohol dehydrogenase [KO:K00001] [EC:1.1.1.1]	AB00071	Fatty acid degradation
ABUW_RS04210	putative alcohol dehydrogenase [KO:K00001] [EC:1.1.1.1]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS04255	hypothetical protein [KO:K01647] [EC:2.3.3.1]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS04255	hypothetical protein [KO:K01647] [EC:2.3.3.1]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04260	succinate dehydrogenase cytochrome b556 subunit [KO:K00241]	AB00650	Butanoate metabolism
ABUW_RS04260	succinate dehydrogenase cytochrome b556 subunit [KO:K00241]	AB00190	Oxidative phosphorylation
ABUW_RS04260	succinate dehydrogenase cytochrome b556 subunit [KO:K00241]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04265	succinate dehydrogenase hydrophobic subunit [KO:K00242]	AB00650	Butanoate metabolism
ABUW_RS04265	succinate dehydrogenase hydrophobic subunit [KO:K00242]	AB00190	Oxidative phosphorylation
ABUW_RS04265	succinate dehydrogenase hydrophobic subunit [KO:K00242]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04270	succinate dehydrogenase flavoprotein subunit [KO:K00239] [EC:1.3.5.1 1.3.5.4]	AB00650	Butanoate metabolism
ABUW_RS04270	succinate dehydrogenase flavoprotein subunit [KO:K00239] [EC:1.3.5.1 1.3.5.4]	AB00190	Oxidative phosphorylation
ABUW_RS04270	succinate dehydrogenase flavoprotein subunit [KO:K00239] [EC:1.3.5.1 1.3.5.4]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04275	succinate dehydrogenase iron-sulfur subunit [KO:K00240] [EC:1.3.5.1 1.3.5.4]	AB00650	Butanoate metabolism
ABUW_RS04275	succinate dehydrogenase iron-sulfur subunit [KO:K00240] [EC:1.3.5.1 1.3.5.4]	AB00190	Oxidative phosphorylation
ABUW_RS04275	succinate dehydrogenase iron-sulfur subunit [KO:K00240] [EC:1.3.5.1 1.3.5.4]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04280	2-oxoglutarate decarboxylase component of the 2-oxoglutarate dehydrogenase complex (E1) [KO:K00164] [EC:1.2.4.2]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04285	dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex (E2) [KO:K00658] [EC:2.3.1.61]	AB00380	Tryptophan metabolism
ABUW_RS04285	dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex (E2) [KO:K00658] [EC:2.3.1.61]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04290	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]	AB00640	Propanoate metabolism
ABUW_RS04290	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS04290	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]	AB00620	Pyruvate metabolism
ABUW_RS04290	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]	AB00380	Tryptophan metabolism
ABUW_RS04290	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS04290	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS04290	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS04290	dihydrolipoamide dehydrogenase [KO:K00382] [EC:1.8.1.4]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04295	succinyl-CoA synthetase beta chain [KO:K01903] [EC:6.2.1.5]	AB00640	Propanoate metabolism
ABUW_RS04295	succinyl-CoA synthetase beta chain [KO:K01903] [EC:6.2.1.5]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04300	succinyl-CoA synthetase alpha chain [KO:K01902] [EC:6.2.1.5]	AB00640	Propanoate metabolism
ABUW_RS04300	succinyl-CoA synthetase alpha chain [KO:K01902] [EC:6.2.1.5]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04380	carbamoyl-phosphate synthase large subunit [KO:K01955] [EC:6.3.5.5]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS04380	carbamoyl-phosphate synthase large subunit [KO:K01955] [EC:6.3.5.5]	AB00240	Pyrimidine metabolism
ABUW_RS04385	carbamoyl-phosphate synthase small chain [KO:K01956] [EC:6.3.5.5]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS04385	carbamoyl-phosphate synthase small chain [KO:K01956] [EC:6.3.5.5]	AB00240	Pyrimidine metabolism
ABUW_RS04415	78-dihydropterate synthase [KO:K00796] [EC:2.5.1.15]	AB00794	Folate biosynthesis
ABUW_RS04435	Twin-arginine translocation pathway signal [KO:K01113] [EC:3.1.3.1]	AB00200	Two-component system
ABUW_RS04435	Twin-arginine translocation pathway signal [KO:K01113] [EC:3.1.3.1]	AB00791	Folate biosynthesis
ABUW_RS04475	FAD dependent oxidoreductase [KO:K00111] [EC:1.1.5.3]	AB00564	Glycerophospholipid metabolism
ABUW_RS04480	phosphoenolpyruvate carboxykinase [KO:K01596] [EC:4.1.1.32]	AB00620	Pyruvate metabolism
ABUW_RS04480	phosphoenolpyruvate carboxykinase [KO:K01596] [EC:4.1.1.32]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS04480	phosphoenolpyruvate carboxykinase [KO:K01596] [EC:4.1.1.32]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS04510	diacylglycerol kinase [KO:K00901] [EC:2.7.1.107]	AB00564	Glycerophospholipid metabolism
ABUW_RS04520	Glycerophosphoryl diester phosphodiesterase [KO:K01126] [EC:3.1.4.46]	AB00564	Glycerophospholipid metabolism
ABUW_RS04625	Glycerate kinase [KO:K00865] [EC:2.7.1.165]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS04625	Glycerate kinase [KO:K00865] [EC:2.7.1.165]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS04675	diaminopimelate decarboxylase [KO:K01586] [EC:4.1.1.20]	AB00300	Lysine biosynthesis
ABUW_RS04680	diaminopimelate epimerase [KO:K01778] [EC:5.1.1.7]	AB00300	Lysine biosynthesis
ABUW_RS04755	3-phosphoserine aminotransferase [KO:K00831] [EC:2.6.1.52]	AB00680	Methane metabolism
ABUW_RS04755	3-phosphoserine aminotransferase [KO:K00831] [EC:2.6.1.52]	AB00270	Cysteine and methionine metabolism
ABUW_RS04755	3-phosphoserine aminotransferase [KO:K00831] [EC:2.6.1.52]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS04775	transport protein of outer membrane lipoproteins [KO:K09808]	AB02010	ABC transporters
ABUW_RS04780	transport protein of outer membrane lipoproteins [KO:K09810] [EC:7.6.2.-]	AB02010	ABC transporters
ABUW_RS04790	putative lipid A biosynthesis lauroyl acyltransferase [KO:K02517] [EC:2.3.1.241 2.3.1.-]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS04805	phosphoribosylglycinamide formyltransferase 1 [KO:K11175] [EC:2.1.2.2]	AB00230	Purine metabolism
ABUW_RS04810	phosphoribosylaminimidazole synthetase [KO:K01933] [EC:6.3.3.1]	AB00230	Purine metabolism
ABUW_RS04855	fructose-16-bisphosphatase [KO:K03841] [EC:3.1.3.11]	AB00680	Methane metabolism
ABUW_RS04855	fructose-16-bisphosphatase [KO:K03841] [EC:3.1.3.11]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS04855	fructose-16-bisphosphatase [KO:K03841] [EC:3.1.3.11]	AB00030	Pentose phosphate pathway
ABUW_RS04910	deoxyguanosinetriphosphate triphosphohydrolase [KO:K01129] [EC:3.1.5.1]	AB00230	Purine metabolism
ABUW_RS04915	phosphoribosylformylglycinamide synthase [KO:K01952] [EC:6.3.5.3]	AB00230	Purine metabolism
ABUW_RS04965	hypothetical protein [KO:K06920] [EC:6.3.4.20]	AB00802	Folate biosynthesis
ABUW_RS04970	putative organic radical activating enzyme [KO:K10026] [EC:4.3.99.3]	AB00801	Folate biosynthesis
ABUW_RS04975	putative tetrahydropyridine-2-carboxylate N-succinyltransferase [KO:K00674] [EC:2.3.1.117]	AB00300	Lysine biosynthesis
ABUW_RS04990	putative ATPase [KO:K02045] [EC:7.3.2.3]	AB02010	ABC transporters
ABUW_RS04990	putative ATPase [KO:K02045] [EC:7.3.2.3]	AB00920	Sulfur metabolism
ABUW_RS04995	putative sulfate permease [KO:K02047]	AB02010	ABC transporters
ABUW_RS04995	putative sulfate permease [KO:K02047]	AB00920	Sulfur metabolism
ABUW_RS05000	sulfate transport protein [KO:K02046]	AB02010	ABC transporters
ABUW_RS05000	sulfate transport protein [KO:K02046]	AB00920	Sulfur metabolism
ABUW_RS05010	sulfate transport protein [KO:K02048]	AB02010	ABC transporters
ABUW_RS05010	sulfate transport protein [KO:K02048]	AB00920	Sulfur metabolism
ABUW_RS05015	4-amino-4-deoxychorismate lyase [KO:K02619] [EC:4.1.3.38]	AB00799	Folate biosynthesis
ABUW_RS05025	thymidylate kinase [KO:K00943] [EC:2.7.4.9]	AB00240	Pyrimidine metabolism
ABUW_RS05035	L-aspartate oxidase [KO:K00278] [EC:1.4.3.16]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS05035	L-aspartate oxidase [KO:K00278] [EC:1.4.3.16]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS05040	putative serine protease [KO:K04771] [EC:3.4.21.107]	AB02020	Two-component system
ABUW_RS05055	leader peptidase [KO:K03100] [EC:3.4.21.89]	AB03060	Protein export
ABUW_RS05095	Short-chain alcohol dehydrogenase of unknown specificity [KO:K16066] [EC:1.1.1.381 1.1.1.-]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS05095	Short-chain alcohol dehydrogenase of unknown specificity [KO:K16066] [EC:1.1.1.381 1.1.1.-]	AB00240	Pyrimidine metabolism
ABUW_RS05120	aspartate aminotransferase A [KO:K00812] [EC:2.6.1.1]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS05120	aspartate aminotransferase A [KO:K00812] [EC:2.6.1.1]	AB00360	Phenylalanine metabolism
ABUW_RS05120	aspartate aminotransferase A [KO:K00812] [EC:2.6.1.1]	AB00350	Tyrosine metabolism
ABUW_RS05120	aspartate aminotransferase A [KO:K00812] [EC:2.6.1.1]	AB00330	Arginine and proline metabolism
ABUW_RS05120	aspartate aminotransferase A [KO:K00812] [EC:2.6.1.1]	AB00270	Cysteine and methionine metabolism
ABUW_RS05120	aspartate aminotransferase A [KO:K00812] [EC:2.6.1.1]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS05120	aspartate aminotransferase A [KO:K00812] [EC:2.6.1.1]	AB00220	Arginine biosynthesis

ABUW_RS05155	glyceraldehyde-3-phosphate dehydrogenase [KO:K00134] [EC:1.2.1.12]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS05175	gamma-glutamyl kinase [KO:K00931] [EC:2.7.2.11]	AB00330	Arginine and proline metabolism
ABUW_RS05196	putative 2-nitropropane dioxygenase [KO:K00459] [EC:1.13.12.16]	AB00910	Nitrogen metabolism
ABUW_RS05210	UDP-N-acetyl glucosamine-2-epimerase [KO:K01791] [EC:5.3.1.3.14]	AB02020	Two-component system
ABUW_RS05210	UDP-N-acetyl glucosamine-2-epimerase [KO:K01791] [EC:5.3.1.3.14]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS05250	NADH dehydrogenase II [KO:K03885] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS05255	putative D-alta-D-ala-carboxypeptidase penicillin-binding protein [KO:K07258] [EC:3.4.16.4]	AB00550	Peptidoglycan biosynthesis
ABUW_RS05265	isocitrate dehydrogenase [KO:K00031] [EC:1.1.1.42]	AB00480	Glutathione metabolism
ABUW_RS05265	isocitrate dehydrogenase [KO:K00031] [EC:1.1.1.42]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS05275	isocitrate dehydrogenase [KO:K00031] [EC:1.1.1.42]	AB00480	Glutathione metabolism
ABUW_RS05275	isocitrate dehydrogenase [KO:K00031] [EC:1.1.1.42]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS05370	glutamate-1-semialdehyde aminotransferase [KO:K01845] [EC:5.4.3.8]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS05425	L-24-diaminobutyrate 2-ketoglutarate 4-aminotransferase [KO:K00836] [EC:2.6.1.76]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS05430	L-24-diaminobutyrate decarboxylase [KO:K13745] [EC:4.1.1.86]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS05455	putative phosphate transporter [KO:K02040]	AB02020	Two-component system
ABUW_RS05455	putative phosphate transporter [KO:K02040]	AB02010	ABC transporters
ABUW_RS05460	EvfO [KO:K02037]	AB02010	ABC transporters
ABUW_RS05465	high-affinity phosphate transport protein [KO:K02038]	AB02010	ABC transporters
ABUW_RS05470	high-affinity phosphate transport protein [KO:K02036] [EC:7.3.2.1]	AB02010	ABC transporters
ABUW_RS05490	adenylosuccinate lyase [KO:K01756] [EC:4.3.2.2]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS05490	adenylosuccinate lyase [KO:K01756] [EC:4.3.2.2]	AB00230	Purine metabolism
ABUW_RS05515	D-alta-D-ala-carboxypeptidase, penicillin-binding protein 5 (precursor) [KO:K07258] [EC:3.4.16.4]	AB00550	Peptidoglycan biosynthesis
ABUW_RS05530	survival protein (acid phosphatase) [KO:K03787] [EC:3.1.3.5]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS05530	survival protein (acid phosphatase) [KO:K03787] [EC:3.1.3.5]	AB00240	Pyrimidine metabolism
ABUW_RS05530	survival protein (acid phosphatase) [KO:K03787] [EC:3.1.3.5]	AB00230	Purine metabolism
ABUW_RS05555	lactoylglutathione lyase [KO:K01759] [EC:4.4.1.5]	AB00620	Pyruvate metabolism
ABUW_RS05770	putative acinetobactin biosynthesis protein [KO:K01590] [EC:4.1.1.22]	AB00340	Histidine metabolism
ABUW_RS05810	uroporphyrinogen decarboxylase [KO:K01599] [EC:4.1.1.37]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS05835	GTP cyclohydrolase I [KO:K01495] [EC:3.5.4.16]	AB00790	Folate biosynthesis
ABUW_RS05840	xanthine dehydrogenase small subunit [KO:K13481] [EC:1.17.1.4]	AB00230	Purine metabolism
ABUW_RS05860	indole-3-glycerol phosphate synthase (GPS) [KO:K01609] [EC:4.1.1.48]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS05865	anthranilate phosphoribosyltransferase [KO:K00766] [EC:2.4.2.16]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS05880	anthranilate synthase component II [KO:K01658] [EC:4.1.3.27]	AB00224	Quorum sensing
ABUW_RS05880	anthranilate synthase component II [KO:K01658] [EC:4.1.3.27]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS05960	hypothetical protein (MaeB) [KO:K00029] [EC:1.1.1.40]	AB00620	Pyruvate metabolism
ABUW_RS05980	S-adenosyl-L-homocysteine hydrolase [KO:K01251] [EC:3.3.1.1]	AB00270	Cysteine and methionine metabolism
ABUW_RS06005	soluble pyridine nucleotide transhydrogenase [KO:K00322] [EC:1.6.1.1]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS06020	putative nitrate transporter transmembrane protein (MFS superfamily) [KO:K02575]	AB00910	Nitrogen metabolism
ABUW_RS06090	EvfE1 [KO:K06879] [EC:1.7.1.13]	AB00803	Folate biosynthesis
ABUW_RS06505	serine hydroxymethyltransferase [KO:K00600] [EC:2.1.2.1]	AB00680	Methane metabolism
ABUW_RS06505	serine hydroxymethyltransferase [KO:K00600] [EC:2.1.2.1]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS06505	serine hydroxymethyltransferase [KO:K00600] [EC:2.1.2.1]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS06530	ABC Lysine-arginine-ornithine transporter periplasmic ligand binding protein [KO:K10014]	AB02010	ABC transporters
ABUW_RS06535	Amino acid ABC transporter permease protein [KO:K10016]	AB02010	ABC transporters
ABUW_RS06540	Amino acid ABC transporter permease protein [KO:K10015]	AB02010	ABC transporters
ABUW_RS06590	putative secretion pathway ATPase [KO:K02454] [EC:7.4.2.8]	AB03070	Bacterial secretion system
ABUW_RS06605	putative two-component system sensor protein [KO:K07645] [EC:2.7.13.3]	AB02024	Quorum sensing
ABUW_RS06605	putative two-component system sensor protein [KO:K07645] [EC:2.7.13.3]	AB02020	Two-component system
ABUW_RS06625	hypothetical protein [KO:K05365] [EC:2.4.1.129.3.4.16.4]	AB00550	Peptidoglycan biosynthesis
ABUW_RS06630	putative inorganic polyphosphate/ATP-NAD kinase [KO:K00858] [EC:2.7.1.23]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS06645	aerobic C4-dicarboxylate transport protein [KO:K11103]	AB00200	Two-component system
ABUW_RS06650	putative acyl coenzyme A dehydrogenase (HsdA-like) [KO:K00255] [EC:1.3.8.8]	AB00071	Fatty acid degradation
ABUW_RS06660	hypothetical protein [KO:K14170] [EC:5.4.99.5.4.2.1.51]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS06665	hypothetical protein [KO:K24018] [EC:1.3.1.43.1.3.1.2.5.1.19]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS06675	aminoacyl-L-histidine dipeptidase [KO:K01270] [EC:3.4.13.-]	AB00480	Glutathione metabolism
ABUW_RS06740	glycerol-3-phosphate dehydrogenase [KO:K00057] [EC:1.1.1.94]	AB00564	Glycerophospholipid metabolism
ABUW_RS07025	putative general secretion pathway protein L (GspL family) [KO:K02461]	AB03070	Bacterial secretion system
ABUW_RS07030	hypothetical protein [KO:K02462]	AB03070	Bacterial secretion system
ABUW_RS07035	dihydroxycarboxylate oxidase [KO:K00254] [EC:1.3.5.2]	AB00240	Pyrimidine metabolism
ABUW_RS07045	amidophosphoribosyltransferase [KO:K00764] [EC:2.4.2.14]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS07045	amidophosphoribosyltransferase [KO:K00764] [EC:2.4.2.14]	AB00230	Purine metabolism
ABUW_RS07060	2-keto-D-gluconate reductase [KO:K00090] [EC:1.1.1.79.1.1.81.1.1.1.215]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS07060	2-keto-D-gluconate reductase [KO:K00090] [EC:1.1.1.79.1.1.81.1.1.1.215]	AB00620	Pyruvate metabolism
ABUW_RS07060	2-keto-D-gluconate reductase [KO:K00090] [EC:1.1.1.79.1.1.81.1.1.1.215]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS07060	2-keto-D-gluconate reductase [KO:K00090] [EC:1.1.1.79.1.1.81.1.1.1.215]	AB00030	Pentose phosphate pathway
ABUW_RS07130	hypothetical protein [KO:K00822] [EC:2.6.1.18]	AB00640	Propanoate metabolism
ABUW_RS07130	hypothetical protein [KO:K00822] [EC:2.6.1.18]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS07135	methylmalonate-semialdehyde dehydrogenase [KO:K00140] [EC:1.2.1.18.1.2.1.27]	AB00640	Propanoate metabolism
ABUW_RS07135	methylmalonate-semialdehyde dehydrogenase [KO:K00140] [EC:1.2.1.18.1.2.1.27]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS07195	putative poly(R)-hydroxyalkanoic acid synthase [KO:K03821] [EC:2.3.1.-]	AB00650	Butanoate metabolism
ABUW_RS07415	Aspartate racemase [KO:K01779] [EC:5.1.1.13]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS07445	membrane-associated dicarboxylate transport protein [KO:K11103]	AB02020	Two-component system
ABUW_RS07455	putative hydroxyacylglutathione hydrolase [KO:K01069] [EC:3.1.2.6]	AB00620	Pyruvate metabolism
ABUW_RS07460	putative permease protein [KO:K02072]	AB02010	ABC transporters
ABUW_RS07465	D-and L-methionine transport protein [KO:K02071]	AB02010	ABC transporters
ABUW_RS07470	putative lipoprotein [KO:K02073]	AB02010	ABC transporters
ABUW_RS07475	phosphoribosylamine-glycine ligase [KO:K01945] [EC:6.3.4.13]	AB00230	Purine metabolism
ABUW_RS07480	hypothetical protein [KO:K00602] [EC:2.1.2.3.3.5.4.10]	AB00230	Purine metabolism
ABUW_RS07560	prothomase IX farnesyltransferase [KO:K02257] [EC:2.5.1.141]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS07560	prothomase IX farnesyltransferase [KO:K02257] [EC:2.5.1.141]	AB00190	Oxidative phosphorylation
ABUW_RS07565	cytochrome o ubiquinol oxidase subunit IV [KO:K02300]	AB00190	Oxidative phosphorylation
ABUW_RS07570	cytochrome o ubiquinol oxidase subunit III [KO:K02299]	AB00190	Oxidative phosphorylation
ABUW_RS07575	cytochrome o ubiquinol oxidase subunit I [KO:K02298] [EC:7.1.1.3]	AB00190	Oxidative phosphorylation
ABUW_RS07580	cytochrome o ubiquinol oxidase subunit II [KO:K02297] [EC:7.1.1.3]	AB00190	Oxidative phosphorylation
ABUW_RS07590	phosphoenolpyruvate synthase [KO:K01007] [EC:2.7.9.2]	AB00680	Methane metabolism
ABUW_RS07590	phosphoenolpyruvate synthase [KO:K01007] [EC:2.7.9.2]	AB00620	Pyruvate metabolism
ABUW_RS07590	phosphoenolpyruvate synthase [KO:K01007] [EC:2.7.9.2]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS07690	putative acetyl-CoA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00680	Methane metabolism
ABUW_RS07690	putative acetyl-CoA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00640	Propanoate metabolism
ABUW_RS07690	putative acetyl-CoA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS07690	putative acetyl-CoA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00620	Pyruvate metabolism
ABUW_RS07690	putative acetyl-CoA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS07710	dihydroxypteridin aldolase [KO:K01633] [EC:4.1.2.25.5.1.99.8.1.13.11.81]	AB00792	Folate biosynthesis
ABUW_RS07720	potassium-transporting ATPase A chain [KO:K01546]	AB02020	Two-component system
ABUW_RS07725	potassium-transporting ATPase B chain [KO:K01547] [EC:7.2.2.6]	AB02020	Two-component system
ABUW_RS07735	hypothetical protein [KO:K07646] [EC:2.7.13.3]	AB02020	Two-component system
ABUW_RS07740	hypothetical protein [KO:K07667]	AB02024	Quorum sensing
ABUW_RS07740	hypothetical protein [KO:K07667]	AB02020	Two-component system
ABUW_RS07745	Glutamine synthetase [KO:K09470] [EC:6.3.1.11]	AB00330	Arginine and proline metabolism
ABUW_RS07780	aconitate hydratase 2 [KO:K01682] [EC:4.2.1.3.4.2.1.99]	AB00640	Propanoate metabolism

ABUW_RS07780	aconitate hydratase 2 [KO:K01682] [EC:4.2.1.3.4.2.1.99]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS07780	aconitate hydratase 2 [KO:K01682] [EC:4.2.1.3.4.2.1.99]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS07860	hypothetical protein [KO:K03666]	AB02024	Quorum sensing
ABUW_RS07875	UDP-23-diacylglycerolamine hydrolase [KO:K03269] [EC:3.6.1.54]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS07890	putative glutamine amidotransferase [KO:K01951] [EC:6.3.3.5.2]	AB00230	Purine metabolism
ABUW_RS07900	ethanolamine ammonia-lyase heavy chain [KO:K03735] [EC:4.3.1.7]	AB00564	Glycerophospholipid metabolism
ABUW_RS07910	aldehyde dehydrogenase 1 [KO:K00138] [EC:1.2.1.-]	AB00620	Pyruvate metabolism
ABUW_RS07910	aldehyde dehydrogenase 1 [KO:K00138] [EC:1.2.1.-]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS07925	putative alcohol dehydrogenase [KO:K13954] [EC:1.1.1.1.1]	AB00620	Pyruvate metabolism
ABUW_RS07925	putative alcohol dehydrogenase [KO:K13954] [EC:1.1.1.1.1]	AB00350	Tyrosine metabolism
ABUW_RS07925	putative alcohol dehydrogenase [KO:K13954] [EC:1.1.1.1.1]	AB00071	Fatty acid degradation
ABUW_RS07925	putative alcohol dehydrogenase [KO:K13954] [EC:1.1.1.1.1]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS07935	putative 5-carboxymethyl-2-hydroxymuconate delta isomerase [KO:K01826] [EC:5.3.3.10]	AB00350	Tyrosine metabolism
ABUW_RS07955	aminopeptidase N [KO:K01256] [EC:3.4.11.2]	AB00480	Glutathione metabolism
ABUW_RS07980	putative glutathione S-transferase [KO:K00799] [EC:2.5.1.18]	AB00480	Glutathione metabolism
ABUW_RS07995	Chorismate mutase [KO:K04093] [EC:5.4.99.5]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS08140	transaldolase [KO:K00616] [EC:2.2.1.2]	AB00030	Pentose phosphate pathway
ABUW_RS08155	putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB02020	Two-component system
ABUW_RS08155	putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS08155	putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00650	Butanoate metabolism
ABUW_RS08155	putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00640	Propanoate metabolism
ABUW_RS08155	putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS08155	putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00620	Pyruvate metabolism
ABUW_RS08155	putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00380	Tryptophan metabolism
ABUW_RS08155	putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS08155	putative acyl-CoA thiolase [KO:K00626] [EC:2.3.1.9]	AB00071	Fatty acid degradation
ABUW_RS08160	putative short-chain dehydrogenase [KO:K00059] [EC:1.1.1.100]	AB00780	Biotin metabolism
ABUW_RS08160	putative short-chain dehydrogenase [KO:K00059] [EC:1.1.1.100]	AB00061	Fatty acid biosynthesis
ABUW_RS08190	Phospholipase C [KO:K01114] [EC:3.1.4.3]	AB02024	Quorum sensing
ABUW_RS08190	Phospholipase C [KO:K01114] [EC:3.1.4.3]	AB00564	Glycerophospholipid metabolism
ABUW_RS08200	putative iron-containing alcohol dehydrogenase [KO:K00001] [EC:1.1.1.1]	AB00620	Pyruvate metabolism
ABUW_RS08200	putative iron-containing alcohol dehydrogenase [KO:K00001] [EC:1.1.1.1]	AB00350	Tyrosine metabolism
ABUW_RS08200	putative iron-containing alcohol dehydrogenase [KO:K00001] [EC:1.1.1.1]	AB00071	Fatty acid degradation
ABUW_RS08200	putative iron-containing alcohol dehydrogenase [KO:K00001] [EC:1.1.1.1]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS08210	putative phosphotyrosine protein phosphatase [KO:K01104] [EC:3.1.3.48]	AB02020	Two-component system
ABUW_RS08215	UDP-N-acetylenolpyruvoylglucosamine reductase FAD-binding [KO:K00075] [EC:1.3.1.98]	AB00550	Peptidoglycan biosynthesis
ABUW_RS08215	UDP-N-acetylenolpyruvoylglucosamine reductase FAD-binding [KO:K00075] [EC:1.3.1.98]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS08260	biotin carboxylase (A subunit of acetyl-CoA carboxylase) [KO:K01961] [EC:6.4.1.2.6.3.4.14]	AB00640	Propanoate metabolism
ABUW_RS08260	biotin carboxylase (A subunit of acetyl-CoA carboxylase) [KO:K01961] [EC:6.4.1.2.6.3.4.14]	AB00620	Pyruvate metabolism
ABUW_RS08260	biotin carboxylase (A subunit of acetyl-CoA carboxylase) [KO:K01961] [EC:6.4.1.2.6.3.4.14]	AB00061	Fatty acid biosynthesis
ABUW_RS08265	biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP) [KO:K02160]	AB00640	Propanoate metabolism
ABUW_RS08265	biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP) [KO:K02160]	AB00620	Pyruvate metabolism
ABUW_RS08265	biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP) [KO:K02160]	AB00061	Fatty acid biosynthesis
ABUW_RS08270	3-dehydroquinate dehydratase type II [KO:K03786] [EC:4.2.1.10]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS08295	nitrile reductase [KO:K00362] [EC:1.7.1.15]	AB00910	Nitrogen metabolism
ABUW_RS08305	nitrate reductase large subunit [KO:K00372] [EC:1.7.99.-]	AB00910	Nitrogen metabolism
ABUW_RS08310	molybdopterin-guanine dinucleotide synthase [KO:K03752] [EC:2.7.7.77]	AB00806	Folate biosynthesis
ABUW_RS08330	molybdopterin converting factor large subunit [KO:K03635] [EC:2.8.1.12]	AB00804	Folate biosynthesis
ABUW_RS08340	molybdopterin biosynthesis protein [KO:K03750] [EC:2.10.1.1]	AB00805	Folate biosynthesis
ABUW_RS08380	putative UDP-galactose 4-epimerase (GalE-like) [KO:K01784] [EC:5.1.3.2]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS08385	fumarase C [KO:K01679] [EC:4.2.1.2]	AB00620	Pyruvate metabolism
ABUW_RS08385	fumarase C [KO:K01679] [EC:4.2.1.2]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS08405	D-amino acid dehydrogenase small subunit [KO:K00285] [EC:1.4.5.1]	AB00360	Phenylalanine metabolism
ABUW_RS08415	2C-methyl-D-erythritol 24-cyclophosphate synthase [KO:K01770] [EC:4.6.1.12]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS08425	ornithine carbamoyltransferase [KO:K00611] [EC:2.1.3.3]	AB00220	Arginine biosynthesis
ABUW_RS08435	response regulator protein [KO:K07712]	AB02020	Two-component system
ABUW_RS08440	two-component regulatory system sensory kinase [KO:K07708] [EC:2.7.13.3]	AB02020	Two-component system
ABUW_RS08450	uridylyl kinase [KO:K09903] [EC:2.7.4.22]	AB02440	Pyrimidine metabolism
ABUW_RS08460	undecaprenyl pyrophosphate synthetase [KO:K00806] [EC:2.5.1.31]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS08460	undecaprenyl pyrophosphate synthetase [KO:K00806] [EC:2.5.1.31]	AB00550	Peptidoglycan biosynthesis
ABUW_RS08465	phosphatidate cytidyltransferase [KO:K00981] [EC:2.7.7.41]	AB00564	Glycerophospholipid metabolism
ABUW_RS08470	1-deoxy-D-xylulose 5-phosphate reductoisomerase [KO:K00099] [EC:1.1.1.267]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS08490	hypothetical protein [KO:K02536] [EC:2.3.1.191]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS08495	hypothetical protein [KO:K02372] [EC:4.2.1.59]	AB00780	Biotin metabolism
ABUW_RS08495	hypothetical protein [KO:K02372] [EC:4.2.1.59]	AB00061	Fatty acid biosynthesis
ABUW_RS08500	UDP-acetylglucosamine acyltransferase [KO:K00677] [EC:2.3.1.129]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS08525	predicted hydrolase (HAD superfamily) [KO:K20881] [EC:3.1.3.5]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS08525	predicted hydrolase (HAD superfamily) [KO:K20881] [EC:3.1.3.5]	AB00240	Pyrimidine metabolism
ABUW_RS08525	predicted hydrolase (HAD superfamily) [KO:K20881] [EC:3.1.3.5]	AB00230	Purine metabolism
ABUW_RS08555	putative L-kynurenine hydrolase [KO:K01656] [EC:3.7.1.3]	AB00380	Tryptophan metabolism
ABUW_RS08585	hypothetical protein [KO:K00117] [EC:1.1.5.2]	AB00030	Pentose phosphate pathway
ABUW_RS08680	acetylornithine aminotransferase [KO:K00821] [EC:2.6.1.11.2.6.1.17]	AB00300	Lysine biosynthesis
ABUW_RS08680	acetylornithine aminotransferase [KO:K00821] [EC:2.6.1.11.2.6.1.17]	AB00220	Arginine biosynthesis
ABUW_RS08710	cell division protein [KO:K03110]	AB03070	Bacterial secretion system
ABUW_RS08710	cell division protein [KO:K03110]	AB03060	Protein export
ABUW_RS08710	cell division protein [KO:K03110]	AB02024	Quorum sensing
ABUW_RS08735	cytochrome d terminal oxidase polypeptide subunit II [KO:K00426] [EC:7.1.1.7]	AB02020	Two-component system
ABUW_RS08735	cytochrome d terminal oxidase polypeptide subunit II [KO:K00426] [EC:7.1.1.7]	AB00190	Oxidative phosphorylation
ABUW_RS08740	cytochrome d terminal oxidase polypeptide subunit I [KO:K00425] [EC:7.1.1.7]	AB02020	Two-component system
ABUW_RS08740	cytochrome d terminal oxidase polypeptide subunit I [KO:K00425] [EC:7.1.1.7]	AB00190	Oxidative phosphorylation
ABUW_RS08775	putative phospholipase A1 precursor (PldA) [KO:K01058] [EC:3.1.1.32.3.1.1.4]	AB00564	Glycerophospholipid metabolism
ABUW_RS08790	threonine dehydratase [KO:K01754] [EC:4.3.1.19]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS08795	ribose 5-phosphate isomerase [KO:K01807] [EC:5.3.1.6]	AB00030	Pentose phosphate pathway
ABUW_RS08810	N-acetyl-gamma-glutamyl-phosphate reductase [KO:K00145] [EC:1.2.1.38]	AB00220	Arginine biosynthesis
ABUW_RS08835	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase [KO:K01626] [EC:2.5.1.54]	AB02024	Quorum sensing
ABUW_RS08835	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase [KO:K01626] [EC:2.5.1.54]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS08880	CTP synthase [KO:K01937] [EC:6.3.4.2]	AB00240	Pyrimidine metabolism
ABUW_RS08885	2-dehydro-3-deoxyphosphocarbonate aldolase [KO:K01627] [EC:2.5.1.55]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS08890	enolase [KO:K01689] [EC:4.2.1.11]	AB00680	Methane metabolism
ABUW_RS08890	enolase [KO:K01689] [EC:4.2.1.11]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS08905	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase [KO:K00991] [EC:2.7.7.60]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS08955	catabolic dihydroquinate dehydratase [KO:K03785] [EC:4.2.1.10]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS08970	pyrroloquinoline-quinone QuA [KO:K05358] [EC:1.1.5.8]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS09070	Short-chain dehydrogenase/reductase SDR [KO:K00059] [EC:1.1.1.100]	AB00780	Biotin metabolism
ABUW_RS09070	Short-chain dehydrogenase/reductase SDR [KO:K00059] [EC:1.1.1.100]	AB00061	Fatty acid biosynthesis
ABUW_RS09080	p-hydroxyphenylacetate hydroxylase C1:reductase component [KO:K23470] [EC:1.5.1.36]	AB00350	Tyrosine metabolism
ABUW_RS09090	Cu2+-containing amine oxidase [KO:K00276] [EC:1.4.3.21]	AB00360	Phenylalanine metabolism
ABUW_RS09090	Cu2+-containing amine oxidase [KO:K00276] [EC:1.4.3.21]	AB00350	Tyrosine metabolism
ABUW_RS09090	Cu2+-containing amine oxidase [KO:K00276] [EC:1.4.3.21]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS09100	phenylacetaldehyde dehydrogenase [KO:K00146] [EC:1.2.1.38]	AB00360	Phenylalanine metabolism

ABUW_RS09390	hypothetical protein [KO-K09936]	AB02024	Quorum sensing
ABUW_RS09395	hypothetical protein [KO-K09936]	AB02024	Quorum sensing
ABUW_RS09445	6-phosphogluconate dehydrogenase NAD-binding [KO-K00042] [EC:1.1.1.60]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS09450	putative ribose-phosphate pyrophosphokinase [KO-K00948] [EC:2.7.6.1]	AB00230	Purine metabolism
ABUW_RS09450	putative ribose-phosphate pyrophosphokinase [KO-K00948] [EC:2.7.6.1]	AB00030	Pentose phosphate pathway
ABUW_RS09455	putative nicotinamide phosphoribosyl transferase [KO-K03462] [EC:2.4.2.12]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS10160	3-hydroxybutyrate dehydrogenase [KO-K00019] [EC:1.1.1.30]	AB00650	Butanoate metabolism
ABUW_RS10180	acetoacetyl-CoA transferase alpha subunit [KO-K01028] [EC:2.8.3.5]	AB00650	Butanoate metabolism
ABUW_RS10180	acetoacetyl-CoA transferase alpha subunit [KO-K01028] [EC:2.8.3.5]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS10185	acetoacetyl-CoA transferase beta subunit [KO-K01028] [EC:2.8.3.5]	AB00650	Butanoate metabolism
ABUW_RS10185	acetoacetyl-CoA transferase beta subunit [KO-K01028] [EC:2.8.3.5]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS10190	short-chain fatty acid transporter (scFAT family) [KO-K02106]	AB02020	Two-component system
ABUW_RS10195	putative acetyl-CoA acetyltransferase [KO-K00626] [EC:2.3.1.9]	AB02020	Two-component system
ABUW_RS10195	putative acetyl-CoA acetyltransferase [KO-K00626] [EC:2.3.1.9]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS10195	putative acetyl-CoA acetyltransferase [KO-K00626] [EC:2.3.1.9]	AB00650	Butanoate metabolism
ABUW_RS10195	putative acetyl-CoA acetyltransferase [KO-K00626] [EC:2.3.1.9]	AB00640	Propanoate metabolism
ABUW_RS10195	putative acetyl-CoA acetyltransferase [KO-K00626] [EC:2.3.1.9]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS10195	putative acetyl-CoA acetyltransferase [KO-K00626] [EC:2.3.1.9]	AB00620	Pyruvate metabolism
ABUW_RS10195	putative acetyl-CoA acetyltransferase [KO-K00626] [EC:2.3.1.9]	AB00380	Tryptophan metabolism
ABUW_RS10195	putative acetyl-CoA acetyltransferase [KO-K00626] [EC:2.3.1.9]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS10195	putative acetyl-CoA acetyltransferase [KO-K00626] [EC:2.3.1.9]	AB00071	Fatty acid degradation
ABUW_RS10220	aspartate ammonia-lyase (aspartase) [KO-K01744] [EC:4.3.1.1]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS10300	homoserine dehydrogenase putative [KO-K00003] [EC:1.1.1.3]	AB00300	Lysine biosynthesis
ABUW_RS10300	homoserine dehydrogenase putative [KO-K00003] [EC:1.1.1.3]	AB00270	Cysteine and methionine metabolism
ABUW_RS10300	homoserine dehydrogenase putative [KO-K00003] [EC:1.1.1.3]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS10310	hypothetical protein [KO-K17218] [EC:1.8.5.4]	AB00920	Sulfur metabolism
ABUW_RS10330	putative (RR)-butanediol dehydrogenase [KO-K00004] [EC:1.1.1.4 1.1.1.1. 1.1.1.303]	AB00650	Butanoate metabolism
ABUW_RS10335	acetoin dehydrogenase [KO-K03366] [EC:1.1.1.- 1.1.1.76 1.1.1.304]	AB00650	Butanoate metabolism
ABUW_RS10340	dihydroliponamide dehydrogenase [KO-K00382] [EC:1.8.1.4]	AB00640	Propanoate metabolism
ABUW_RS10340	dihydroliponamide dehydrogenase [KO-K00382] [EC:1.8.1.4]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS10340	dihydroliponamide dehydrogenase [KO-K00382] [EC:1.8.1.4]	AB00620	Pyruvate metabolism
ABUW_RS10340	dihydroliponamide dehydrogenase [KO-K00382] [EC:1.8.1.4]	AB00380	Tryptophan metabolism
ABUW_RS10340	dihydroliponamide dehydrogenase [KO-K00382] [EC:1.8.1.4]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS10340	dihydroliponamide dehydrogenase [KO-K00382] [EC:1.8.1.4]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS10340	dihydroliponamide dehydrogenase [KO-K00382] [EC:1.8.1.4]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS10340	dihydroliponamide dehydrogenase [KO-K00382] [EC:1.8.1.4]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS10345	dihydroliponamide acetyltransferase [KO-K00627] [EC:2.3.1.12]	AB00620	Pyruvate metabolism
ABUW_RS10345	dihydroliponamide acetyltransferase [KO-K00627] [EC:2.3.1.12]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS10345	dihydroliponamide acetyltransferase [KO-K00627] [EC:2.3.1.12]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS10380	chorismate synthase [KO-K01736] [EC:4.2.3.5]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS10390	tryptophan synthase subunit beta [KO-K08001] [EC:4.2.1.20]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS10390	tryptophan synthase subunit beta [KO-K08001] [EC:4.2.1.20]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS10450	o-succinylhomoserine sulphydrylase [KO-K10764] [EC:2.5.1.-]	AB00920	Sulfur metabolism
ABUW_RS10450	o-succinylhomoserine sulphydrylase [KO-K10764] [EC:2.5.1.-]	AB00270	Cysteine and methionine metabolism
ABUW_RS10515	lipid A-disaccharide synthase [KO-K00748] [EC:2.4.1.182]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS10545	phospho-2-dehydro-3-deoxyheptonate aldolase [KO-K01626] [EC:2.5.1.54]	AB02024	Quorum sensing
ABUW_RS10545	phospho-2-dehydro-3-deoxyheptonate aldolase [KO-K01626] [EC:2.5.1.54]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS10550	Cobalamin-5-phosphate synthase CobS [KO-K02233] [EC:2.7.8.26]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS10560	Fructose-26-bisphosphatase [KO-K02226] [EC:3.1.3.73]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS10565	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase [KO-K00768] [EC:2.4.2.21]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS10570	Cobalamin biosynthesis enzyme [KO-K02231] [EC:2.7.1.156 2.7.7.62]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS10665	putative acyl-CoA dehydrogenase [KO-K00249] [EC:1.3.8.7]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS10665	putative acyl-CoA dehydrogenase [KO-K00249] [EC:1.3.8.7]	AB00071	Fatty acid degradation
ABUW_RS10670	alkane 1-monoxygenase [KO-K00496] [EC:1.14.15.3]	AB00071	Fatty acid degradation
ABUW_RS10785	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) x [KO-K01082] [EC:3.1.3.7]	AB00920	Sulfur metabolism
ABUW_RS10800	putative ABC transporter ATP-binding protein [KO-K02031 K02032]	AB02024	Quorum sensing
ABUW_RS10805	ABC-type dipeptide/oligopeptide/nickel transport systems permease component [KO-K02034]	AB02024	Quorum sensing
ABUW_RS10810	ABC-type dipeptide/oligopeptide/nickel transport systems permease component [KO-K02033]	AB02024	Quorum sensing
ABUW_RS10855	hypothetical protein [KO-K00657] [EC:2.3.1.57]	AB00330	Arginine and proline metabolism
ABUW_RS10860	malate synthase G [KO-K01638] [EC:2.3.3.9]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS10860	malate synthase G [KO-K01638] [EC:2.3.3.9]	AB00620	Pyruvate metabolism
ABUW_RS10885	crotonine-5-phosphate decarboxylase [KO-K01591] [EC:4.1.1.23]	AB00240	Pyrimidine metabolism
ABUW_RS10905	cytidylate kinase [KO-K00945] [EC:2.7.4.25]	AB00240	Pyrimidine metabolism
ABUW_RS10930	putative 6-pyruvoyl-tetrahydropterin synthase [KO-K01737] [EC:4.2.3.12 4.1.2.50]	AB00800	Folate biosynthesis
ABUW_RS10935	general secretion pathway protein K [KO-K02460]	AB03070	Bacterial secretion system
ABUW_RS10940	general secretion pathway protein J precursor [KO-K02459]	AB03070	Bacterial secretion system
ABUW_RS10945	general secretion pathway protein I precursor [KO-K02458]	AB03070	Bacterial secretion system
ABUW_RS10950	putative general secretion pathway protein G precursor [KO-K02456]	AB03070	Bacterial secretion system
ABUW_RS10975	3-deoxy-manno-octulosonate cytidyltransferase [KO-K00979] [EC:2.7.7.38]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS10990	tetracycline-saccharide 4'-kinase [KO-K00912] [EC:2.7.1.130]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS10985	lipid transport protein flippase [KO-K11085] [EC:7.5.2.6]	AB02010	ABC transporters
ABUW_RS11015	putative nucleotidyl transferase [KO-K00962] [EC:2.7.7.96]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS11020	putative phosphotransferase [KO-K07102] [EC:2.7.1.221]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS11035	fructose-16-bisphosphate aldolase, class II [KO-K01624] [EC:4.1.2.13]	AB00680	Methane metabolism
ABUW_RS11035	fructose-16-bisphosphate aldolase, class II [KO-K01624] [EC:4.1.2.13]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS11035	fructose-16-bisphosphate aldolase, class II [KO-K01624] [EC:4.1.2.13]	AB00030	Pentose phosphate pathway
ABUW_RS11045	phosphoglycerate kinase [KO-K00927] [EC:2.7.2.3]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS11090	putative transport protein [KO-K18893]	AB02010	ABC transporters
ABUW_RS11105	glycine cleavage complex protein H [KO-K02437]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS11105	glycine cleavage complex protein H [KO-K02437]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS11110	putative cobalamin biosynthetic protein (CobE) [KO-K12410] [EC:2.3.1.286]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS11125	hypothetical protein [KO-K13821] [EC:1.5.5.2 1.2.1.88]	AB00330	Arginine and proline metabolism
ABUW_RS11125	hypothetical protein [KO-K13821] [EC:1.5.5.2 1.2.1.88]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS11165	transketolase [KO-K00615] [EC:2.2.2.1.1]	AB00030	Pentose phosphate pathway
ABUW_RS11170	methionine adenosyltransferase [KO-K00789] [EC:2.5.1.6]	AB00270	Cysteine and methionine metabolism
ABUW_RS11220	biotin synthase [KO-K01012] [EC:2.8.1.6]	AB00780	Biotin metabolism
ABUW_RS11330	glutamate/aspartate transport protein [KO-K10004] [EC:7.4.2.1]	AB02020	Two-component system
ABUW_RS11330	glutamate/aspartate transport protein [KO-K10004] [EC:7.4.2.1]	AB02010	ABC transporters
ABUW_RS11335	glutamate/aspartate transport protein [KO-K10002]	AB02020	Two-component system
ABUW_RS11335	glutamate/aspartate transport protein [KO-K10002]	AB02010	ABC transporters
ABUW_RS11340	glutamate/aspartate transport protein [KO-K10003]	AB02020	Two-component system
ABUW_RS11340	glutamate/aspartate transport protein [KO-K10003]	AB02010	ABC transporters
ABUW_RS11345	glutamate/aspartate transport protein [KO-K10001]	AB02020	Two-component system
ABUW_RS11345	glutamate/aspartate transport protein [KO-K10001]	AB02010	ABC transporters
ABUW_RS11350	putative glutathione S-transferase [KO-K00799] [EC:2.5.1.18]	AB00480	Glutathione metabolism
ABUW_RS11370	D-methionine transport protein [KO-K02073]	AB02010	ABC transporters
ABUW_RS11375	D-methionine transport protein [KO-K02073]	AB02010	ABC transporters
ABUW_RS11380	D- and L-methionine transport protein [KO-K02071]	AB02010	ABC transporters
ABUW_RS11385	D- and L-methionine transport protein x [KO-K02072]	AB02010	ABC transporters
ABUW_RS11400	hypothetical protein [KO-K10914]	AB02024	Quorum sensing

ABUW_RS11400	hypothetical protein [KO-K10914]	AB02020	Two-component system
ABUW_RS11430	phosphoribosylglycinamide formyltransferase 2 [KO-K08289] [EC:2.1.2.2]	AB00230	Purine metabolism
ABUW_RS11435	uridylyltransferase [KO-K00900] [EC:2.7.7.59]	AB02020	Two-component system
ABUW_RS11440	putative aminotransferase [KO-K14267] [EC:2.6.1.17]	AB00300	Lysine biosynthesis
ABUW_RS11455	glutathione peroxidase [KO-K00432] [EC:1.11.1.9]	AB00480	Glutathione metabolism
ABUW_RS11465	putative PLP-dependent aminotransferase [KO-K14260] [EC:2.6.1.66 2.6.1.2]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS11465	putative PLP-dependent aminotransferase [KO-K14260] [EC:2.6.1.66 2.6.1.2]	AB00220	Arginine biosynthesis
ABUW_RS11475	glutaminase-asparaginase [KO-K05597] [EC:3.5.1.38]	AB02020	Two-component system
ABUW_RS11475	glutaminase-asparaginase [KO-K05597] [EC:3.5.1.38]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS11475	glutaminase-asparaginase [KO-K05597] [EC:3.5.1.38]	AB00220	Arginine biosynthesis
ABUW_RS11490	serine acetyltransferase [KO-K00640] [EC:2.3.1.30]	AB00920	Sulfur metabolism
ABUW_RS11490	serine acetyltransferase [KO-K00640] [EC:2.3.1.30]	AB00270	Cysteine and methionine metabolism
ABUW_RS11570	hydantoin racemase [KO-K16841] [EC:5.1.90.3]	AB00230	Purine metabolism
ABUW_RS11575	taurine dioxygenase [KO-K03119] [EC:1.14.11.17]	AB00920	Sulfur metabolism
ABUW_RS11580	ABC taurine transporter permease subunit [KO-K15552]	AB02010	ABC transporters
ABUW_RS11580	ABC taurine transporter permease subunit [KO-K15552]	AB00920	Sulfur metabolism
ABUW_RS11585	taurine ATP-binding transport system component [KO-K10831] [EC:7.6.2.7]	AB02010	ABC transporters
ABUW_RS11585	taurine ATP-binding transport system component [KO-K10831] [EC:7.6.2.7]	AB00920	Sulfur metabolism
ABUW_RS11590	taurine ABC transporter periplasmic taurine-binding protein [KO-K15551]	AB02010	ABC transporters
ABUW_RS11590	taurine ABC transporter periplasmic taurine-binding protein [KO-K15551]	AB00920	Sulfur metabolism
ABUW_RS11620	ubiquinol oxidase subunit I [KO-K00425] [EC:7.1.1.7]	AB02020	Two-component system
ABUW_RS11620	ubiquinol oxidase subunit I [KO-K00425] [EC:7.1.1.7]	AB00190	Oxidative phosphorylation
ABUW_RS11625	ubiquinol oxidase subunit II [KO-K00426] [EC:7.1.1.7]	AB02020	Two-component system
ABUW_RS11625	ubiquinol oxidase subunit II [KO-K00426] [EC:7.1.1.7]	AB00190	Oxidative phosphorylation
ABUW_RS11725	Glutathione S-transferase-like protein [KO-K00799] [EC:2.5.1.18]	AB00480	Glutathione metabolism
ABUW_RS11740	putative short-chain dehydrogenase [KO-K00059] [EC:1.1.1.100]	AB00780	Biotin metabolism
ABUW_RS11740	putative short-chain dehydrogenase [KO-K00059] [EC:1.1.1.100]	AB00061	Fatty acid biosynthesis
ABUW_RS11750	serine acetyltransferase [KO-K00640] [EC:2.3.1.30]	AB00920	Sulfur metabolism
ABUW_RS11750	serine acetyltransferase [KO-K00640] [EC:2.3.1.30]	AB00270	Cysteine and methionine metabolism
ABUW_RS11855	Catalase [KO-K03781] [EC:1.11.1.6]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS11855	Catalase [KO-K03781] [EC:1.11.1.6]	AB00380	Tryptophan metabolism
ABUW_RS11865	CinA-like protein [KO-K03743] [EC:3.5.1.42]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS11930	Acyl-CoA dehydrogenase [KO-K00253] [EC:1.3.8.4]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS11935	putative propionyl-CoA carboxylase (Beta subunit) [KO-K01969] [EC:6.4.1.4]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS11940	3-methylglutaconyl-CoA hydratase [KO-K13766] [EC:4.2.1.18]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS11945	putative acyl-CoA carboxylase alpha chain protein [KO-K01968] [EC:6.4.1.4]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS11950	hypothetical protein [KO-K01640] [EC:4.1.3.4]	AB00650	Butanoate metabolism
ABUW_RS11950	hypothetical protein [KO-K01640] [EC:4.1.3.4]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS12085	ABC-type Fe3+ transport system permease component [KO-K02011]	AB02010	ABC transporters
ABUW_RS12095	ABC-type Fe3+ transport system [KO-K02012]	AB02010	ABC transporters
ABUW_RS12185	Catalase-like protein [KO-K03781] [EC:1.11.1.6]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS12185	Catalase-like protein [KO-K03781] [EC:1.11.1.6]	AB00380	Tryptophan metabolism
ABUW_RS12265	thioesterase domain protein [KO-K02614] [EC:3.1.2.-]	AB00360	Phenylalanine metabolism
ABUW_RS12280	Paac [KO-K01912] [EC:6.2.1.30]	AB00360	Phenylalanine metabolism
ABUW_RS12290	Paac [KO-K00074] [EC:1.1.1.157]	AB00650	Butanoate metabolism
ABUW_RS12290	Paac [KO-K00074] [EC:1.1.1.157]	AB00360	Phenylalanine metabolism
ABUW_RS12290	putative enoyl-CoA hydratase I [KO-K15866] [EC:5.3.3.18]	AB00360	Phenylalanine metabolism
ABUW_RS12300	Enoyl-CoA hydratase/camithine racemase [KO-K01692] [EC:4.2.1.17]	AB00650	Butanoate metabolism
ABUW_RS12300	Enoyl-CoA hydratase/camithine racemase [KO-K01692] [EC:4.2.1.17]	AB00640	Propanoate metabolism
ABUW_RS12300	Enoyl-CoA hydratase/camithine racemase [KO-K01692] [EC:4.2.1.17]	AB00380	Tryptophan metabolism
ABUW_RS12300	Enoyl-CoA hydratase/camithine racemase [KO-K01692] [EC:4.2.1.17]	AB00360	Phenylalanine metabolism
ABUW_RS12300	Enoyl-CoA hydratase/camithine racemase [KO-K01692] [EC:4.2.1.17]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS12300	Enoyl-CoA hydratase/camithine racemase [KO-K01692] [EC:4.2.1.17]	AB00071	Fatty acid degradation
ABUW_RS12305	Phenylacetate-CoA oxygenase/reductase Paac subunit [KO-K02613]	AB00360	Phenylalanine metabolism
ABUW_RS12310	Phenylacetate-CoA oxygenase Paaj subunit [KO-K02612]	AB00360	Phenylalanine metabolism
ABUW_RS12315	hypothetical protein [KO-K02611] [EC:1.14.13.149]	AB00360	Phenylalanine metabolism
ABUW_RS12320	Phenylacetic acid degradation B [KO-K02610]	AB00360	Phenylalanine metabolism
ABUW_RS12325	hypothetical protein [KO-K02609] [EC:1.14.13.149]	AB00360	Phenylalanine metabolism
ABUW_RS12330	Phenylacetic acid degradation protein paan [KO-K02618] [EC:3.3.2.12 1.2.1.91]	AB00360	Phenylalanine metabolism
ABUW_RS12335	Iron-sulfur-dependent L-serine dehydratase single chain form [KO-K01752] [EC:4.3.1.17]	AB00270	Cysteine and methionine metabolism
ABUW_RS12335	Iron-sulfur-dependent L-serine dehydratase single chain form [KO-K01752] [EC:4.3.1.17]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS12370	putative oxidoreductase [KO-K22549] [EC:1.5.99.-]	AB00330	Arginine and proline metabolism
ABUW_RS12375	hypothetical protein [KO-K22550]	AB00330	Arginine and proline metabolism
ABUW_RS12380	hypothetical protein [KO-K21061] [EC:1.5.99.-]	AB00330	Arginine and proline metabolism
ABUW_RS12385	hypothetical protein [KO-K12658] [EC:5.1.1.8]	AB00330	Arginine and proline metabolism
ABUW_RS12400	Dihydropicolinate synthetase [KO-K21062] [EC:3.5.4.22]	AB00330	Arginine and proline metabolism
ABUW_RS12465	hypothetical protein [KO-K11892]	AB03070	Bacterial secretion system
ABUW_RS12480	putative ClpA/B-type chaperone [KO-K11907]	AB03070	Bacterial secretion system
ABUW_RS12500	putative membrane protein [KO-K11891]	AB03070	Bacterial secretion system
ABUW_RS12525	hypothetical protein [KO-K11903]	AB03070	Bacterial secretion system
ABUW_RS12565	putative amidase [KO-K01457] [EC:3.5.1.54]	AB00220	Arginine biosynthesis
ABUW_RS12590	Allophanate hydrolase subunit 2 [KO-K01941] [EC:6.3.4.6]	AB00220	Arginine biosynthesis
ABUW_RS12645	hypothetical protein [KO-K11263] [EC:6.4.1.2 6.4.1.3 6.3.4.14]	AB00640	Propanoate metabolism
ABUW_RS12645	hypothetical protein [KO-K11263] [EC:6.4.1.2 6.4.1.3 6.3.4.14]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS12645	hypothetical protein [KO-K11263] [EC:6.4.1.2 6.4.1.3 6.3.4.14]	AB00620	Pyruvate metabolism
ABUW_RS12645	hypothetical protein [KO-K11263] [EC:6.4.1.2 6.4.1.3 6.3.4.14]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS12645	hypothetical protein [KO-K11263] [EC:6.4.1.2 6.4.1.3 6.3.4.14]	AB00061	Fatty acid biosynthesis
ABUW_RS12650	putative allophanate hydrolase subunit 1 and 2 [KO-K01457] [EC:3.5.1.54]	AB00220	Arginine biosynthesis
ABUW_RS12660	putative lactam utilization protein [KO-K07160] [EC:3.5.2.9]	AB00480	Glutathione metabolism
ABUW_RS12760	lipid A biosynthesis lauroyl acyltransferase [KO-K02517] [EC:2.3.1.241 2.3.1.-]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS12825	putative ABC family drug transporter [KO-K12541]	AB02010	ABC transporters
ABUW_RS12835	putative transport protein [KO-K08861] [EC:7.5.2.5]	AB02010	ABC transporters
ABUW_RS12850	3-Deoxy-D-manno-octulosonate 8-phosphate (KDO 8-P) phosphatase [KO-K03270] [EC:3.1.3.45]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS12855	D-arabinose 5-phosphate isomerase [KO-K06041] [EC:5.3.1.13]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS13045	pyrimidine-S-carboxylate reductase [KO-K00286] [EC:1.5.1.2]	AB00330	Arginine and proline metabolism
ABUW_RS13225	putative glutathione S-transferase [KO-K00799] [EC:2.5.1.18]	AB00480	Glutathione metabolism
ABUW_RS13240	putative glutathione S-transferase [KO-K00799] [EC:2.5.1.18]	AB00480	Glutathione metabolism
ABUW_RS13255	aspartate carbamoyltransferase non-catalytic chain [KO-K01465] [EC:3.5.2.3]	AB00240	Pyrimidine metabolism
ABUW_RS13260	aspartate carbamoyltransferase catalytic subunit [KO-K00609] [EC:2.1.3.2]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS13260	aspartate carbamoyltransferase catalytic subunit [KO-K00609] [EC:2.1.3.2]	AB00240	Pyrimidine metabolism
ABUW_RS13280	CinA-like protein [KO-K03743] [EC:3.5.1.42]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS13305	cyclic AMP receptor protein [KO-K10914]	AB02024	Quorum sensing
ABUW_RS13305	cyclic AMP receptor protein [KO-K10914]	AB02020	Two-component system
ABUW_RS13325	adenylosuccinate synthetase [KO-K01939] [EC:6.3.4.4]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS13325	adenylosuccinate synthetase [KO-K01939] [EC:6.3.4.4]	AB00230	Purine metabolism
ABUW_RS13330	ATP phosphoribosyltransferase [KO-K02502]	AB00340	Histidine metabolism
ABUW_RS13335	glycylidihydrate 3-phosphate dehydrogenase [KO-K00134] [EC:1.2.1.12]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS13345	aspartate kinase [KO-K00028] [EC:2.7.2.4]	AB00300	Lysine biosynthesis
ABUW_RS13345	aspartate kinase [KO-K00028] [EC:2.7.2.4]	AB00270	Cysteine and methionine metabolism
ABUW_RS13345	aspartate kinase [KO-K00028] [EC:2.7.2.4]	AB00260	Glycine, serine and threonine metabolism

ABUW_RS13350	Carbon storage regulator [KO:K03563]	AB02020	Two-component system
ABUW_RS13370	adenosine deaminase [KO:K21053] [EC:3.5.4.2]	AB00230	Purine metabolism
ABUW_RS13505	acyl coenzyme A dehydrogenase [KO:K00255] [EC:1.3.8.8]	AB00071	Fatty acid degradation
ABUW_RS13595	Arginine/ornithine N-succinyltransferase beta subunit [KO:K00673] [EC:2.3.1.109]	AB00330	Arginine and proline metabolism
ABUW_RS13610	hypothetical protein [KO:K00130] [EC:1.2.1.8]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS13635	Glycine/D-amino acid oxidases (deaminating) [KO:K09471] [EC:1.4.3.-]	AB00330	Arginine and proline metabolism
ABUW_RS13705	putative lipoprotein [KO:K02073]	AB02010	ABC transporters
ABUW_RS13720	argininosuccinate synthetase [KO:K01940] [EC:6.3.4.5]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS13720	argininosuccinate synthetase [KO:K01940] [EC:6.3.4.5]	AB00220	Arginine biosynthesis
ABUW_RS13730	dihydroorotase [KO:K01465] [EC:3.5.2.3]	AB00240	Pyrimidine metabolism
ABUW_RS13790	putative oligopeptide transport protein [KO:K13895]	AB02010	ABC transporters
ABUW_RS13795	putative oligopeptide transport protein [KO:K13894]	AB02010	ABC transporters
ABUW_RS13800	putative oligopeptide transport protein [KO:K13893]	AB02010	ABC transporters
ABUW_RS13820	putative NADH pyrophosphatase [KO:K03426] [EC:3.6.1.22]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS13940	glutamate dehydrogenase [KO:K00262] [EC:1.4.1.4]	AB00910	Nitrogen metabolism
ABUW_RS13940	glutamate dehydrogenase [KO:K00262] [EC:1.4.1.4]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS13940	glutamate dehydrogenase [KO:K00262] [EC:1.4.1.4]	AB00220	Arginine biosynthesis
ABUW_RS13955	adenylate kinase [KO:K00939] [EC:2.7.4.3]	AB00230	Purine metabolism
ABUW_RS13970	penicillin-binding protein 2 [KO:K05515] [EC:3.4.16.4]	AB00550	Peptidoglycan biosynthesis
ABUW_RS14000	urease alpha subunit [KO:K01428] [EC:3.5.1.5]	AB00230	Purine metabolism
ABUW_RS14000	urease alpha subunit [KO:K01428] [EC:3.5.1.5]	AB00220	Arginine biosynthesis
ABUW_RS14005	urease beta subunit [KO:K01429] [EC:3.5.1.5]	AB00230	Purine metabolism
ABUW_RS14005	urease beta subunit [KO:K01429] [EC:3.5.1.5]	AB00220	Arginine biosynthesis
ABUW_RS14010	EaVc [KO:K01430] [EC:3.5.1.5]	AB00230	Purine metabolism
ABUW_RS14010	EaVc [KO:K01430] [EC:3.5.1.5]	AB00220	Arginine biosynthesis
ABUW_RS14030	isocitrate lyase [KO:K01637] [EC:4.1.3.1]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS14060	ATP-sulfurylase subunit 1 [KO:K00956] [EC:2.7.7.4]	AB00920	Sulfur metabolism
ABUW_RS14060	ATP-sulfurylase subunit 1 [KO:K00956] [EC:2.7.7.4]	AB00230	Purine metabolism
ABUW_RS14065	sulfate adenylyltransferase subunit 2 [KO:K00957] [EC:2.7.7.4]	AB00920	Sulfur metabolism
ABUW_RS14065	sulfate adenylyltransferase subunit 2 [KO:K00957] [EC:2.7.7.4]	AB00230	Purine metabolism
ABUW_RS14095	rubredoxin reductase [KO:K05297] [EC:1.18.1.1]	AB00071	Fatty acid degradation
ABUW_RS14115	polyporphosphatase [KO:K00937] [EC:2.7.4.1]	AB00190	Oxidative phosphorylation
ABUW_RS14120	monofunctional biosynthetic peptidoglycan transglycosylase [KO:K03814] [EC:2.4.1.129]	AB00550	Peptidoglycan biosynthesis
ABUW_RS14145	putative carbonic anhydrase [KO:K01673] [EC:4.2.1.1]	AB00910	Nitrogen metabolism
ABUW_RS14160	ferric enterobactin receptor precursor [KO:K19611]	AB02020	Two-component system
ABUW_RS14195	D-serine deaminase (dehydratase) [KO:K01753] [EC:4.3.1.18]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS14205	methionine synthase [KO:K00548] [EC:2.1.1.13]	AB00270	Cysteine and methionine metabolism
ABUW_RS14210	putative transketolase beta subunit protein [KO:K00615] [EC:2.2.1.1]	AB00030	Pentose phosphate pathway
ABUW_RS14215	transketolase [KO:K00615] [EC:2.2.1.1]	AB00030	Pentose phosphate pathway
ABUW_RS14240	mutarotase precursor [KO:K01785] [EC:5.1.3.3]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS14255	putative glutaminase [KO:K01425] [EC:3.5.1.2]	AB00200	Two-component system
ABUW_RS14255	putative glutaminase [KO:K01425] [EC:3.5.1.2]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS14255	putative glutaminase [KO:K01425] [EC:3.5.1.2]	AB00220	Arginine biosynthesis
ABUW_RS14275	putative acetolactate synthase (M8-like) [KO:K01652] [EC:2.2.2.16]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS14275	putative acetolactate synthase (M8-like) [KO:K01652] [EC:2.2.2.16]	AB00650	Butanoate metabolism
ABUW_RS14280	putative aldehyde dehydrogenase [KO:K00130] [EC:1.2.1.8]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS14285	putative dinucleotide-utilizing enzyme [KO:K00699] [EC:1.4.1.12]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS14385	aerobic C4-dicarboxylate transport protein [KO:K11103]	AB02020	Two-component system
ABUW_RS14425	NAD ⁺ -dependent betaine aldehyde dehydrogenase [KO:K00130] [EC:1.2.1.8]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS14430	choline dehydrogenase [KO:K00108] [EC:1.1.99.1]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS14435	malate dehydrogenase FAD/NAD(P)-binding domain [KO:K00116] [EC:1.1.5.4]	AB00620	Pyruvate metabolism
ABUW_RS14435	malate dehydrogenase FAD/NAD(P)-binding domain [KO:K00116] [EC:1.1.5.4]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS14515	dihydropicolinate synthetase [KO:K01714] [EC:4.3.3.7]	AB00300	Lysine biosynthesis
ABUW_RS14645	gamma-glutamyltranspeptidase precursor [KO:K00681] [EC:2.3.2.2 3.4.19.13]	AB00480	Glutathione metabolism
ABUW_RS14665	delta-aminolevulinic acid dehydratase [KO:K01698] [EC:4.2.1.24]	AB00960	Porphyrin and chlorophyll metabolism
ABUW_RS14755	acetylglutamate kinase [KO:K00930] [EC:2.7.2.8]	AB00220	Arginine biosynthesis
ABUW_RS14760	phosphomannomutase [KO:K15778] [EC:5.4.2.8 5.4.2.2]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS14760	phosphomannomutase [KO:K15778] [EC:5.4.2.8 5.4.2.2]	AB00230	Purine metabolism
ABUW_RS14760	phosphomannomutase [KO:K15778] [EC:5.4.2.8 5.4.2.2]	AB00010	Glycolysis / Gluconeogenesis
ABUW_RS14760	phosphomannomutase [KO:K15778] [EC:5.4.2.8 5.4.2.2]	AB00030	Pentose phosphate pathway
ABUW_RS14765	deoxyuridine 5'-triphosphate nucleotidylhydrolase [KO:K01520] [EC:3.6.1.23]	AB00240	Pyrimidine metabolism
ABUW_RS14880	putative membrane protein [KO:K08973] [EC:1.3.99.-]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS14935	Tartrate dehydrogenase [KO:K07246] [EC:1.1.1.93 4.1.1.73 1.1.1.83]	AB00650	Butanoate metabolism
ABUW_RS14935	Tartrate dehydrogenase [KO:K07246] [EC:1.1.1.93 4.1.1.73 1.1.1.83]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS14960	phosphopantetheine adenylyltransferase [KO:K00954] [EC:2.7.7.3]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS14995	glutamyl tRNA reductase [KO:K02492] [EC:1.2.1.70]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS15010	4-diphosphocytidylyl-2-C-methyl-D-erythritol kinase [KO:K00919] [EC:2.7.1.148]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS15035	ribose-phosphate pyrophosphokinase [KO:K00948] [EC:2.7.6.1]	AB00230	Purine metabolism
ABUW_RS15035	ribose-phosphate pyrophosphokinase [KO:K00948] [EC:2.7.6.1]	AB00030	Pentose phosphate pathway
ABUW_RS15050	aspartate 1-decarboxylase precursor [KO:K01579] [EC:4.1.1.11]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS15070	putative hydrolase [KO:K01091] [EC:3.1.3.16]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS15090	hypothetical protein [KO:K00059] [EC:1.1.1.100]	AB00780	Biotin metabolism
ABUW_RS15090	hypothetical protein [KO:K00059] [EC:1.1.1.100]	AB00061	Fatty acid biosynthesis
ABUW_RS15095	hypothetical protein [KO:K00645] [EC:2.3.1.39]	AB00061	Fatty acid biosynthesis
ABUW_RS15135	dethiobiotin synthetase x [KO:K01935] [EC:6.3.3.3]	AB00780	Biotin metabolism
ABUW_RS15140	putative biotin biosynthesis protein (BioC) [KO:K02169] [EC:2.1.1.197]	AB00780	Biotin metabolism
ABUW_RS15145	8-amino-7-oxononanoate synthase [KO:K00652] [EC:2.3.1.47]	AB00780	Biotin metabolism
ABUW_RS15150	adenosylmethionine-8-amino-7-oxononanoate aminotransferase [KO:K00833] [EC:2.6.1.62]	AB00780	Biotin metabolism
ABUW_RS15155	putative hydrolase biotin biosynthesis (BioH) [KO:K02170] [EC:3.1.1.85]	AB00780	Biotin metabolism
ABUW_RS15175	bacterioferritin [KO:K03594] [EC:1.16.3.1]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS15205	hypothetical protein [KO:K03624] [EC:6.3.4.15]	AB00780	Biotin metabolism
ABUW_RS15210	putative transcriptional regulator [KO:K03525] [EC:2.7.1.33]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS15255	deoxycytidine triphosphate deaminase [KO:K01494] [EC:3.5.4.13]	AB00240	Pyrimidine metabolism
ABUW_RS15270	putative MTA/SAH nucleosidase [KO:K01243] [EC:3.2.2.9]	AB00270	Cysteine and methionine metabolism
ABUW_RS15315	putative D-cysteine desulfhydrase (DcyD) [KO:K05396] [EC:4.4.1.15]	AB00270	Cysteine and methionine metabolism
ABUW_RS15365	uracil phosphoribosyltransferase [KO:K00761] [EC:2.4.2.9]	AB00240	Pyrimidine metabolism
ABUW_RS15370	NADH dehydrogenase I chain N [KO:K00343] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15375	NADH dehydrogenase I chain M membrane subunit [KO:K00342] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15380	NADH dehydrogenase I chain L [KO:K00341] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15385	NADH dehydrogenase I chain K [KO:K00340] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15390	NADH dehydrogenase I chain J [KO:K00339] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15395	NADH dehydrogenase I chain I 2Fe-2S ferredoxin-related [KO:K00338] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15400	NADH dehydrogenase I chain H [KO:K00337] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15405	NADH dehydrogenase I chain G [KO:K00336] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15410	NADH dehydrogenase I chain F [KO:K00335] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15415	NADH dehydrogenase I chain E [KO:K00334] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15420	NADH dehydrogenase I chain CD [KO:K13378] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15425	NADH dehydrogenase I chain B [KO:K00331] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15430	NADH dehydrogenase I chain A [KO:K00330] [EC:7.1.1.2]	AB00190	Oxidative phosphorylation
ABUW_RS15445	BimS [KO:K07639] [EC:2.7.13.3]	AB02020	Two-component system

ABUW_RS15450	two-component regulatory activator (OmpR family) [KO:K07661]	AB02020	Two-component system
ABUW_RS15460	ribonucleoside diphosphate reductase alpha subunit [KO:K00525] [EC:1.17.4.1]	AB00240	Pyrimidine metabolism
ABUW_RS15460	ribonucleoside diphosphate reductase alpha subunit [KO:K00525] [EC:1.17.4.1]	AB00230	Purine metabolism
ABUW_RS15470	ribonucleoside-diphosphate reductase beta subunit [KO:K00526] [EC:1.17.4.1]	AB00240	Pyrimidine metabolism
ABUW_RS15470	ribonucleoside-diphosphate reductase beta subunit [KO:K00526] [EC:1.17.4.1]	AB00230	Purine metabolism
ABUW_RS15515	putative flavoprotein oxidoreductase [KO:K09024] [EC:1.5.1.1-]	AB00240	Pyrimidine metabolism
ABUW_RS15520	5-methyltetrahydropteroylglutamate-homocysteine methyltransferase [KO:K00549] [EC:2.1.1.14]	AB00270	Cysteine and methionine metabolism
ABUW_RS15570	putative substrate-binding protein [KO:K02020]	AB02010	ABC transporters
ABUW_RS15600	glutaryl-CoA dehydrogenase [KO:K00252] [EC:1.3.8.6]	AB00380	Tryptophan metabolism
ABUW_RS15600	glutaryl-CoA dehydrogenase [KO:K00252] [EC:1.3.8.6]	AB00071	Fatty acid degradation
ABUW_RS15615	adenosine deaminase [KO:K01488] [EC:3.5.4.4]	AB00230	Purine metabolism
ABUW_RS15640	quinolinate synthetase A [KO:K03517] [EC:2.5.1.72]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS15645	hypothetical protein [KO:K00620] [EC:2.3.1.35 2.3.1.1]	AB00220	Arginine biosynthesis
ABUW_RS15685	D-ribulose-5-phosphate 3-epimerase [KO:K01783] [EC:5.1.3.1]	AB00030	Pentose phosphate pathway
ABUW_RS15695	putative esterase [KO:K01070] [EC:3.1.2.12]	AB00680	Methane metabolism
ABUW_RS15760	p-aminobenzoate synthetase [KO:K01665] [EC:2.6.1.85]	AB00798	Folate biosynthesis
ABUW_RS15765	histidinol-phosphate aminotransferase [KO:K00817] [EC:2.6.1.9]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS15765	histidinol-phosphate aminotransferase [KO:K00817] [EC:2.6.1.9]	AB00360	Phenylalanine metabolism
ABUW_RS15765	histidinol-phosphate aminotransferase [KO:K00817] [EC:2.6.1.9]	AB00350	Tyrosine metabolism
ABUW_RS15765	histidinol-phosphate aminotransferase [KO:K00817] [EC:2.6.1.9]	AB00340	Histidine metabolism
ABUW_RS15770	histidinol dehydrogenase [KO:K00013] [EC:1.1.1.25]	AB00340	Histidine metabolism
ABUW_RS15775	ATP-phosphoribosyltransferase [KO:K00765] [EC:2.4.2.17]	AB00340	Histidine metabolism
ABUW_RS15780	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [KO:K00790] [EC:2.5.1.7]	AB00550	Peptidoglycan biosynthesis
ABUW_RS15780	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [KO:K00790] [EC:2.5.1.7]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS15795	RNA polymerase sigma-54 factor [KO:K03092]	AB02020	Two-component system
ABUW_RS15860	secretion protein XcpR [KO:K02454] [EC:7.4.2.8]	AB03070	Bacterial secretion system
ABUW_RS15890	pyrroline-5-carboxylate reductase [KO:K00286] [EC:1.5.1.2]	AB00330	Arginine and proline metabolism
ABUW_RS15900	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subunit) [KO:K01962] [EC:6.4.1.2 2.1.3.15]	AB00640	Propanoate metabolism
ABUW_RS15900	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subunit) [KO:K01962] [EC:6.4.1.2 2.1.3.15]	AB00620	Pyruvate metabolism
ABUW_RS15900	acetyl-coenzyme A carboxylase carboxyl transferase (alpha subunit) [KO:K01962] [EC:6.4.1.2 2.1.3.15]	AB00061	Fatty acid biosynthesis
ABUW_RS15905	exopolyphosphatase [KO:K01524] [EC:3.6.1.11 3.6.1.40]	AB00230	Purine metabolism
ABUW_RS16005	panthoate-beta-alanine ligase [KO:K01918] [EC:6.3.2.1]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS16010	3-methyl-2-oxobutanate hydroxymethyltransferase [KO:K00606] [EC:2.1.2.11]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS16015	2-amino-4-hydroxy-6-hydroxymethylidihydropterdine pyrophosphokinase [KO:K00950] [EC:2.7.6.3]	AB00793	Folate biosynthesis
ABUW_RS16040	GTP pyrophosphokinase [KO:K00951] [EC:2.7.6.5]	AB00230	Purine metabolism
ABUW_RS16055	cysteine synthase B [KO:K12339] [EC:2.5.1.144]	AB00270	Cysteine and methionine metabolism
ABUW_RS16060	GacS-like sensor kinase protein [KO:K07678] [EC:2.7.13.3]	AB02020	Two-component system
ABUW_RS16070	putative 3-hydroxyisobutyrate dehydrogenase or 2-hydroxy-3-oxopropionate reductase [KO:K00020] [EC:1.1.1.131]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS16075	hydroxypyruvate isomerase [KO:K01816] [EC:5.3.1.22]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS16090	pyridine nucleotide transhydrogenase beta subunit [KO:K00325] [EC:1.6.1.2 7.1.1.1]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS16095	pyridine nucleotide transhydrogenase (proton pump) alpha subunit (part2) [KO:K00324] [EC:1.6.1.2 7.1.1.1]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS16100	pyridine nucleotide transhydrogenase (proton pump) alpha subunit (part1) [KO:K00324] [EC:1.6.1.2 7.1.1.1]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS16145	Heavy metal response regulator [KO:K07665]	AB02020	Two-component system
ABUW_RS16255	aconitate hydratase 1 [KO:K01681] [EC:4.2.1.3]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS16255	aconitate hydratase 1 [KO:K01681] [EC:4.2.1.3]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS16300	acetylhydroxy acid isomerase [KO:K00053] [EC:1.1.1.86]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS16305	acetylacetyl synthase isozyme III small subunit [KO:K01653] [EC:2.2.2.1.6]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS16305	acetylacetyl synthase isozyme III small subunit [KO:K01653] [EC:2.2.2.1.6]	AB00650	Butanoate metabolism
ABUW_RS16310	acetylacetyl synthase III large subunit [KO:K01652] [EC:2.2.2.1.6]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS16310	acetylacetyl synthase III large subunit [KO:K01652] [EC:2.2.2.1.6]	AB00650	Butanoate metabolism
ABUW_RS16340	macrolide transport protein [KO:K05685] [EC:7.6.2.-]	AB02010	ABC transporters
ABUW_RS16350	NADH-dependent enoyl-ACP reductase [KO:K00208] [EC:1.3.1.9 1.3.1.10]	AB00780	Biotin metabolism
ABUW_RS16350	NADH-dependent enoyl-ACP reductase [KO:K00208] [EC:1.3.1.9 1.3.1.10]	AB00061	Fatty acid biosynthesis
ABUW_RS16380	protein exporting molecular chaperone [KO:K03071]	AB03070	Bacterial secretion system
ABUW_RS16380	protein exporting molecular chaperone [KO:K03071]	AB03060	Protein export
ABUW_RS16380	protein exporting molecular chaperone [KO:K03071]	AB02024	Quorum sensing
ABUW_RS16410	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase [KO:K03526] [EC:1.17.7.1 1.17.7.3]	AB00900	Terpenoid backbone biosynthesis
ABUW_RS16430	nucleoside diphosphate kinase [KO:K00940] [EC:2.7.4.6]	AB00240	Pyrimidine metabolism
ABUW_RS16430	nucleoside diphosphate kinase [KO:K00940] [EC:2.7.4.6]	AB00230	Purine metabolism
ABUW_RS16440	putative phosphatidylglycerolphosphatase B [KO:K19302] [EC:3.6.1.27]	AB00550	Peptidoglycan biosynthesis
ABUW_RS16455	beta-N-acetyl-D-glucosaminidase [KO:K01207] [EC:3.2.1.52]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS16470	gamma-glutamyl phosphate reductase [KO:K00147] [EC:1.2.1.41]	AB00330	Arginine and proline metabolism
ABUW_RS16480	thermoresistant glucokinase [KO:K00851] [EC:2.7.1.12]	AB00030	Pentose phosphate pathway
ABUW_RS16490	hypothetical protein [KO:K01625] [EC:4.1.2.14 4.1.3.42]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS16490	hypothetical protein [KO:K01625] [EC:4.1.2.14 4.1.3.42]	AB00030	Pentose phosphate pathway
ABUW_RS16495	phosphogluconate dehydratase [KO:K01690] [EC:4.2.1.12]	AB00030	Pentose phosphate pathway
ABUW_RS16500	acetate kinase (propionate kinase) [KO:K00925] [EC:2.7.2.1]	AB00680	Methane metabolism
ABUW_RS16500	acetate kinase (propionate kinase) [KO:K00925] [EC:2.7.2.1]	AB00640	Propanoate metabolism
ABUW_RS16500	acetate kinase (propionate kinase) [KO:K00925] [EC:2.7.2.1]	AB00620	Pyruvate metabolism
ABUW_RS16505	phosphate acetyltransferase [KO:K13788] [EC:2.3.1.8]	AB00680	Methane metabolism
ABUW_RS16505	phosphate acetyltransferase [KO:K13788] [EC:2.3.1.8]	AB00640	Propanoate metabolism
ABUW_RS16505	phosphate acetyltransferase [KO:K13788] [EC:2.3.1.8]	AB00620	Pyruvate metabolism
ABUW_RS16510	fumarate hydratase [KO:K01676] [EC:4.2.1.2]	AB00620	Pyruvate metabolism
ABUW_RS16510	fumarate hydratase [KO:K01676] [EC:4.2.1.2]	AB00020	Citrate cycle (TCA cycle)
ABUW_RS16550	2-isopropylmalate synthase [KO:K01649] [EC:2.3.3.13]	AB00620	Pyruvate metabolism
ABUW_RS16555	homoserine O-acetyltransferase [KO:K00641] [EC:2.3.1.31 2.3.1.46]	AB00920	Sulfur metabolism
ABUW_RS16555	homoserine O-acetyltransferase [KO:K00641] [EC:2.3.1.31 2.3.1.46]	AB00270	Cysteine and methionine metabolism
ABUW_RS16570	hypothetical protein [KO:K02428] [EC:3.6.1.66]	AB00230	Purine metabolism
ABUW_RS16580	Sec-independent protein translocase protein [KO:K03116]	AB03070	Bacterial secretion system
ABUW_RS16580	Sec-independent protein translocase protein [KO:K03116]	AB03060	Protein export
ABUW_RS16585	Sec-independent protein translocase protein [KO:K03117]	AB03070	Bacterial secretion system
ABUW_RS16585	Sec-independent protein translocase protein [KO:K03117]	AB03060	Protein export
ABUW_RS16590	Sec-independent protein translocase protein [KO:K03118]	AB03070	Bacterial secretion system
ABUW_RS16590	Sec-independent protein translocase protein [KO:K03118]	AB03060	Protein export
ABUW_RS16625	thymidylate synthase [KO:K00560] [EC:2.1.1.45]	AB00240	Pyrimidine metabolism
ABUW_RS16630	dihydrofolate reductase [KO:K00287] [EC:1.5.1.3]	AB00795	Folate biosynthesis
ABUW_RS16660	formyltetrahydrofolate deformylase [KO:K01433] [EC:3.5.1.10]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS16760	lipid A biosynthesis lauroyl acyltransferase [KO:K02517] [EC:2.3.1.241 2.3.1.-]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS16780	aspartate-semialdehyde dehydrogenase NAD(P)-binding [KO:K00133] [EC:1.2.1.11]	AB00300	Lysine biosynthesis
ABUW_RS16780	aspartate-semialdehyde dehydrogenase NAD(P)-binding [KO:K00133] [EC:1.2.1.11]	AB00270	Cysteine and methionine metabolism
ABUW_RS16780	aspartate-semialdehyde dehydrogenase NAD(P)-binding [KO:K00133] [EC:1.2.1.11]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS16795	putative L-asparaginase I (AnsA) [KO:K01424] [EC:3.5.1.1]	AB00250	Alanine, aspartate and glutamate metabolism
ABUW_RS16870	catalase [KO:K03782] [EC:1.11.1.21]	AB00380	Tryptophan metabolism
ABUW_RS16870	catalase [KO:K03782] [EC:1.11.1.21]	AB00360	Phenylalanine metabolism
ABUW_RS16890	putative glutathione S-transferase [KO:K00799] [EC:2.5.1.18]	AB00480	Glutathione metabolism
ABUW_RS16900	putative phosphoglycolate phosphatase protein [KO:K01091] [EC:3.1.3.18]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS16950	putative membrane protein [KO:K09936]	AB02024	Quorum sensing
ABUW_RS17010	hypothetical protein [KO:K01069] [EC:3.1.2.6]	AB00620	Pyruvate metabolism
ABUW_RS17015	ferrochelatase [KO:K01772] [EC:4.99.1.1 4.99.1.9]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS17070	general secretion pathway protein G [KO:K02456]	AB03070	Bacterial secretion system

ABUW_RS17075	general secretion pathway protein F [KO:K02455]	AB03070	Bacterial secretion system
ABUW_RS17180	hypothetical protein [KO:K11755] [EC:3.5.4.19 3.6.1.31]	AB00340	Histidine metabolism
ABUW_RS17260	preprotein translocase IISF family auxiliary membrane component [KO:K03075]	AB03070	Bacterial secretion system
ABUW_RS17260	preprotein translocase IISF family auxiliary membrane component [KO:K03075]	AB03060	Protein export
ABUW_RS17260	preprotein translocase IISF family auxiliary membrane component [KO:K03075]	AB02024	Quorum sensing
ABUW_RS17265	triosephosphate isomerase [KO:K01803] [EC:5.3.1.1]	AB00010	Glycolysis / Gluconogenesis
ABUW_RS17285	dephosphocoenzyme A kinase [KO:K00859] [EC:2.7.1.24]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS17300	hypothetical protein [KO:K09913] [EC:2.4.2.1 2.4.2.2]	AB00240	Pyrimidine metabolism
ABUW_RS17300	hypothetical protein [KO:K09913] [EC:2.4.2.1 2.4.2.2]	AB00230	Purine metabolism
ABUW_RS17355	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase [KO:K00995] [EC:2.7.8.5]	AB00564	Glycerophospholipid metabolism
ABUW_RS17375	beta-hydroxylase [KO:K12879] [EC:1.14.11.-]	AB00540	Lipopolysaccharide biosynthesis
ABUW_RS17390	3-ketoacyl-CoA thiolase [KO:K00632] [EC:2.3.1.16]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS17390	3-ketoacyl-CoA thiolase [KO:K00632] [EC:2.3.1.16]	AB00071	Fatty acid degradation
ABUW_RS17505	preprotein translocase IISF family membrane subunit [KO:K03073]	AB03070	Bacterial secretion system
ABUW_RS17505	preprotein translocase IISF family membrane subunit [KO:K03073]	AB03060	Protein export
ABUW_RS17505	preprotein translocase IISF family membrane subunit [KO:K03073]	AB02024	Quorum sensing
ABUW_RS17540	anthranilate synthase component I; TrpE [KO:K01657] [EC:4.1.3.27]	AB02024	Quorum sensing
ABUW_RS17540	anthranilate synthase component I; TrpE [KO:K01657] [EC:4.1.3.27]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS17545	phosphoglycolate phosphatase [KO:K01091] [EC:3.1.3.18]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS17555	putative general secretion pathway protein [KO:K02453]	AB03070	Bacterial secretion system
ABUW_RS17560	putative general secretion pathway protein [KO:K02452]	AB03070	Bacterial secretion system
ABUW_RS17590	uroporphyrinogen-III synthase [KO:K01719] [EC:4.2.1.175]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS17595	prophobilinogen deaminase [KO:K01749] [EC:2.5.1.61]	AB00860	Porphyrin and chlorophyll metabolism
ABUW_RS17600	alginate biosynthesis regulatory protein [KO:K08083]	AB02020	Two-component system
ABUW_RS17605	alginate biosynthesis protein [KO:K08082] [EC:2.7.13.3]	AB02020	Two-component system
ABUW_RS17625	putative RND family drug transporter [KO:K12340]	AB03070	Bacterial secretion system
ABUW_RS17625	putative RND family drug transporter [KO:K12340]	AB02020	Two-component system
ABUW_RS17655	cyclic 3'-adenosine monophosphate phosphodiesterase [KO:K03651] [EC:3.1.4.53]	AB00230	Purine metabolism
ABUW_RS17675	UDP-N-acetylmuramoylalanine-D-glutamate ligase [KO:K01925] [EC:6.3.2.9]	AB00550	Peptidoglycan biosynthesis
ABUW_RS17705	homoserine dehydrogenase [KO:K00003] [EC:1.1.1.3]	AB00300	Lysine biosynthesis
ABUW_RS17705	homoserine dehydrogenase [KO:K00003] [EC:1.1.1.3]	AB00270	Cysteine and methionine metabolism
ABUW_RS17705	homoserine dehydrogenase [KO:K00003] [EC:1.1.1.3]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS17710	threonine synthase pyridoxal-5'-phosphate-dependent enzyme [KO:K01733] [EC:4.2.3.1]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS17725	sensor protein [KO:K02698] [EC:2.7.13.3]	AB02020	Two-component system
ABUW_RS17740	phosphoglycerate mutase II cofactor independent [KO:K15633] [EC:5.4.2.12]	AB00680	Methane metabolism
ABUW_RS17740	phosphoglycerate mutase II cofactor independent [KO:K15633] [EC:5.4.2.12]	AB00260	Glycine, serine and threonine metabolism
ABUW_RS17740	phosphoglycerate mutase II cofactor independent [KO:K15633] [EC:5.4.2.12]	AB00010	Glycolysis / Gluconogenesis
ABUW_RS17745	putative membrane protein [KO:K11720]	AB02010	ABC transporters
ABUW_RS17750	putative membrane protein [KO:K07091]	AB02010	ABC transporters
ABUW_RS17755	aminopeptidase A [KO:K01255] [EC:3.4.11.1]	AB00480	Glutathione metabolism
ABUW_RS17785	hypothetical protein [KO:K11752] [EC:3.5.4.26 1.1.1.193]	AB02024	Quorum sensing
ABUW_RS17945	inorganic pyrophosphatase [KO:K01507] [EC:3.6.1.1]	AB00190	Oxidative phosphorylation
ABUW_RS18050	cysteine synthase A/O-acetylserine sulfhydrylase A subunit PLP-dependent enzyme [KO:K01738] [EC:2.5.1.147]	AB00920	Sulfur metabolism
ABUW_RS18050	cysteine synthase A/O-acetylserine sulfhydrylase A subunit PLP-dependent enzyme [KO:K01738] [EC:2.5.1.147]	AB00270	Cysteine and methionine metabolism
ABUW_RS18150	glutathione peroxidase [KO:K00432] [EC:1.11.1.9]	AB00480	Glutathione metabolism
ABUW_RS18160	membrane-bound ATP synthase F1 sector, epsilon-subunit [KO:K02114]	AB00190	Oxidative phosphorylation
ABUW_RS18165	membrane-bound ATP synthase F1 sector, beta-subunit [KO:K02112] [EC:7.1.2.2 7.2.2.1]	AB00190	Oxidative phosphorylation
ABUW_RS18170	membrane-bound ATP synthase F1 sector, gamma-subunit [KO:K02115]	AB00190	Oxidative phosphorylation
ABUW_RS18175	membrane-bound ATP synthase F1 sector, alpha-subunit [KO:K02111] [EC:7.1.2.2 7.2.2.1]	AB00190	Oxidative phosphorylation
ABUW_RS18180	membrane-bound ATP synthase F1 sector, delta-subunit [KO:K02113]	AB00190	Oxidative phosphorylation
ABUW_RS18185	membrane-bound ATP synthase F0 sector, subunit b [KO:K02109]	AB00190	Oxidative phosphorylation
ABUW_RS18190	membrane-bound ATP synthase F0 sector, subunit c [KO:K02110]	AB00190	Oxidative phosphorylation
ABUW_RS18195	membrane-bound ATP synthase F0 sector, subunit a [KO:K02108]	AB00190	Oxidative phosphorylation
ABUW_RS18205	high affinity Zn transport protein [KO:K09815]	AB02010	ABC transporters
ABUW_RS18210	transcriptional repressor of Zn transport system (Fur family) [KO:K09823]	AB02024	Quorum sensing
ABUW_RS18215	high affinity Zn transport protein [KO:K09817] [EC:7.2.2.20]	AB02010	ABC transporters
ABUW_RS18220	high affinity Zn transport protein [KO:K09816]	AB02010	ABC transporters
ABUW_RS18235	NAD-linked malate dehydrogenase [KO:K00027] [EC:1.1.1.38]	AB02020	Two-component system
ABUW_RS18235	NAD-linked malate dehydrogenase [KO:K00027] [EC:1.1.1.38]	AB00620	Pyruvate metabolism
ABUW_RS18250	glutathione S-transferase [KO:K00799] [EC:2.5.1.18]	AB00480	Glutathione metabolism
ABUW_RS18280	GMP synthetase [KO:K01951] [EC:6.3.5.2]	AB00230	Purine metabolism
ABUW_RS18335	Phosphopantetheinyl-protein transferase [KO:K06133] [EC:2.7.8.-]	AB00770	Pantothenate and CoA biosynthesis
ABUW_RS18385	homoserine lactone synthase [KO:K13061] [EC:2.3.1.184]	AB02024	Quorum sensing
ABUW_RS18385	homoserine lactone synthase [KO:K13061] [EC:2.3.1.184]	AB02020	Two-component system
ABUW_RS18385	homoserine lactone synthase [KO:K13061] [EC:2.3.1.184]	AB00270	Cysteine and methionine metabolism
ABUW_RS18400	putative enoyl-CoA hydratase/isomerase [KO:K01692] [EC:4.2.1.17]	AB00650	Butanoate metabolism
ABUW_RS18400	putative enoyl-CoA hydratase/isomerase [KO:K01692] [EC:4.2.1.17]	AB00640	Propanoate metabolism
ABUW_RS18400	putative enoyl-CoA hydratase/isomerase [KO:K01692] [EC:4.2.1.17]	AB00390	Tryptophan metabolism
ABUW_RS18400	putative enoyl-CoA hydratase/isomerase [KO:K01692] [EC:4.2.1.17]	AB00360	Phenylalanine metabolism
ABUW_RS18400	putative enoyl-CoA hydratase/isomerase [KO:K01692] [EC:4.2.1.17]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS18400	putative enoyl-CoA hydratase/isomerase [KO:K01692] [EC:4.2.1.17]	AB00071	Fatty acid degradation
ABUW_RS18405	putative acyl-CoA dehydrogenase [KO:K00248] [EC:1.3.8.1]	AB00650	Butanoate metabolism
ABUW_RS18405	putative acyl-CoA dehydrogenase [KO:K00248] [EC:1.3.8.1]	AB00640	Propanoate metabolism
ABUW_RS18405	putative acyl-CoA dehydrogenase [KO:K00248] [EC:1.3.8.1]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS18405	putative acyl-CoA dehydrogenase [KO:K00248] [EC:1.3.8.1]	AB00071	Fatty acid degradation
ABUW_RS18410	putative acetyl-coA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00680	Methane metabolism
ABUW_RS18410	putative acetyl-coA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00640	Propanoate metabolism
ABUW_RS18410	putative acetyl-coA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00630	Glyoxylate and dicarboxylate metabolism
ABUW_RS18410	putative acetyl-coA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00620	Pyruvate metabolism
ABUW_RS18410	putative acetyl-coA synthetase/AMP-(fatty) acid ligase [KO:K01895] [EC:6.2.1.1]	AB00010	Glycolysis / Gluconogenesis
ABUW_RS18415	3-hydroxyisobutyrate dehydrogenase [KO:K00020] [EC:1.1.1.31]	AB00290	Valine, leucine and isoleucine degradation
ABUW_RS18450	D-amino acid dehydrogenase [KO:K00285] [EC:1.4.5.1]	AB00360	Phenylalanine metabolism
ABUW_RS18525	aconitate hydratase 1 [KO:K20459] [EC:4.2.1.117]	AB00640	Propanoate metabolism
ABUW_RS18535	putative carboxyphosphonoenolpyruvate phosphonmutase or putative methylsuccinate lyase (PtpB) [KO:K03417] [EC:4.1.3.30]	AB00640	Propanoate metabolism
ABUW_RS18545	tyrosine aminotransferase tyrosine repressible, PLP-dependent [KO:K00832] [EC:2.6.1.57]	AB00400	Phenylalanine, tyrosine and tryptophan biosynthesis
ABUW_RS18545	tyrosine aminotransferase tyrosine repressible, PLP-dependent [KO:K00832] [EC:2.6.1.57]	AB00360	Phenylalanine metabolism
ABUW_RS18545	tyrosine aminotransferase tyrosine repressible, PLP-dependent [KO:K00832] [EC:2.6.1.57]	AB00350	Tyrosine metabolism
ABUW_RS18545	tyrosine aminotransferase tyrosine repressible, PLP-dependent [KO:K00832] [EC:2.6.1.57]	AB00270	Cysteine and methionine metabolism
ABUW_RS18550	D-lactate dehydrogenase NADH independent, FAD-binding domain [KO:K03777] [EC:1.1.5.12]	AB00620	Pyruvate metabolism
ABUW_RS18555	L-lactate dehydrogenase FMN linked [KO:K00101] [EC:1.1.2.3]	AB00620	Pyruvate metabolism
ABUW_RS18570	hypothetical protein [KO:K01840] [EC:5.4.2.8]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS18575	putative UDP-glucose 4-epimerase [KO:K01784] [EC:5.1.3.2]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS18590	putative UTP-glucose-1-phosphate uridylyltransferase [KO:K00963] [EC:2.7.7.9]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS18685	nicotinate-nucleotide pyrophosphorylase [KO:K00767] [EC:2.4.2.19]	AB00760	Nicotinate and nicotinamide metabolism
ABUW_RS18695	hypothetical protein [KO:K01114] [EC:3.1.4.3]	AB02024	Quorum sensing
ABUW_RS18695	hypothetical protein [KO:K01114] [EC:3.1.4.3]	AB00564	Glycerophospholipid metabolism
ABUW_RS18735	putative phosphoglycolate phosphatase 2 (PGP 2) [KO:K22292] [EC:3.1.3.105]	AB00520	Amino sugar and nucleotide sugar metabolism
ABUW_RS18755	N-alpha-acetylglutamate synthase [KO:K14682] [EC:2.3.1.1]	AB00220	Arginine biosynthesis
ABUW_RS18760	alkanesulfonate transport protein [KO:K15553]	AB02010	ABC transporters
ABUW_RS18760	alkanesulfonate transport protein [KO:K15553]	AB00920	Sulfur metabolism

ABUW_RS18765	ABC-type nitrate/sulfonate/bicarbonate transport system [KO:K15553]	AB02010	ABC transporters
ABUW_RS18765	ABC-type nitrate/sulfonate/bicarbonate transport system [KO:K15553]	AB00920	Sulfur metabolism
ABUW_RS18770	FMNH ₂ -dependent alkanesulfonate monooxygenase [KO:K04091] [EC:1.14.14.5]	AB00920	Sulfur metabolism
ABUW_RS18775	alkanesulfonate transport protein [KO:K15554]	AB02010	ABC transporters
ABUW_RS18775	alkanesulfonate transport protein [KO:K15554]	AB00920	Sulfur metabolism
ABUW_RS18780	alkanesulfonate transport protein [KO:K15555] [EC:7.6.2.14]	AB02010	ABC transporters
ABUW_RS18780	alkanesulfonate transport protein [KO:K15555] [EC:7.6.2.14]	AB00920	Sulfur metabolism
ABUW_RS18790	putative MTA/SAH nucleosidase [KO:K01243] [EC:3.2.2.9]	AB00270	Cysteine and methionine metabolism
ABUW_RS18810	Signal peptidase II [KO:K03101] [EC:3.4.23.36]	AB03060	Protein export
ABUW_RS18915	phosphoribosylaminoimidazole carboxylase ATPase subunit [KO:K01589] [EC:6.3.4.18]	AB00230	Purine metabolism
ABUW_RS18920	phosphoribosylaminoimidazole carboxylase mutase subunit [KO:K01588] [EC:5.4.99.18]	AB00230	Purine metabolism
ABUW_RS18940	putative membrane protein [KO:K19302] [EC:3.6.1.27]	AB00550	Peptidoglycan biosynthesis
ABUW_RS18965	guanine deaminase [KO:K01487] [EC:3.5.4.3]	AB00230	Purine metabolism
ABUW_RS18975	hypoxanthine phosphoribosyltransferase [KO:K00760] [EC:2.4.2.8]	AB00230	Purine metabolism
ABUW_RS19005	hypothetical protein [KO:K03217]	AB03070	Bacterial secretion system
ABUW_RS19005	hypothetical protein [KO:K03217]	AB03060	Protein export
ABUW_RS19005	hypothetical protein [KO:K03217]	AB02024	Quorum sensing