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**Characterisation of the
alternative sigma factor SigAB in
*Acinetobacter baumannii***

MSc Microbiology, 2025

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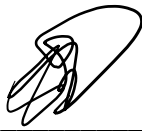
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SUMMARY

Acinetobacter baumannii is a priority pathogen and is known to be a leading cause of nosocomial infections worldwide. It is associated with a variety of illnesses including septicaemia, pneumonia, and urinary tract infections (UTIs). It readily acquires resistances to antimicrobials making it extremely difficult to treat in hospital settings. It is an opportunistic pathogen that generally infects people who already have a compromised immune system. *A. baumannii* survives in a variety of environmental conditions and readily forms biofilms which allow it to persist in hospital settings making it even more dangerous especially due to its capacity to persist on biomedical devices like catheters and ventilators.

Despite the dangers posed by *A. baumannii*, there is still relatively little known about how *A. baumannii* regulates the expression of various metabolic pathways and how it initiates various stress responses to mitigate environmental stressors. It is crucial to develop a comprehensive understanding of the mechanisms utilised by this bacteria to regulate its metabolism and physiology to adapt to its environment as well as its transcriptional changes in response to various conditions. This knowledge can then be utilised to develop novel treatments and identify drug targets for this pathogen of global concern.

One aspect of the regulatory arsenal of *A. baumannii* that up until now has been understudied are the sigma factor including the alternative sigma factor SigAB. Extra cytoplasmic function (ECF) sigma factors allow bacteria to regulate gene expression by binding to specific promoter regions of the genes in their regulon causing initiation of transcription. ECF sigma factors have been implicated in a variety of biological roles from general stress responses to virulence and antimicrobial resistance.

A conserved alternative sigma factor of *A. baumannii* is SigAB, and this conservation points towards it playing an important role. This study sought to investigate this sigma factor to elucidate its biological function as well as to identify its regulon. A series of phenotypic growth experiments were carried out that identified that a $\Delta sigAB$ deletion mutant suffered from a growth defect when exposed to osmotic stressors and detergents. These experiments also identified that the $\Delta sigAB$ mutant grew significantly better than wild-type *A. baumannii* AB5075 when exposed to sub-inhibitory concentrations of chloramphenicol. It was also established that the $\Delta sigAB$ mutant suffered no defect in biofilm formation. SigAB is present in *A. baumannii* across growth stages when grown in rich medium.

Transcriptome analysis at late stationary phase, in which SigAB is most abundant in the cell, showed that >300 genes the $\Delta sigAB$ mutant were differentially expressed compared to the wild-type AB5075 indicating that it is a global regulator of bacterial gene expression in *A. baumannii*. Pathway analysis discovered that ATP-synthase biosynthesis and histidine catabolism were significantly downregulated in the deletion mutant. The most down-regulated gene was uncovered to be the uncharacterised small RNA sRNA90 (SabS)

and the expression of sRNA90 was independently shown to be dependent on SigAB. Further work indicated that sRNA90 could play a role in regulating multiple hypothetical lipoproteins of unknown function, including ABUW_RS18870. In the heterologous *E. coli*, it was established that translation of ABUW_RS18870 mRNA was repressed through direct base-pairing with sRNA90. Taken together, an initial characterisation of the alternative SigAB factor showed that it is a global regulator of gene expression mediating resistance to environmental stress and which is directly controlling the expression of sRNA90, which is suggested to act as a post-transcriptional regulator of lipoproteins in *A. baumannii* AB5075.

INTRODUCTION

History

The genus *Acinetobacter* was established in 1968 when it was isolated from soil and water collected from the environment where it was present in all samples tested showing its ubiquity (Baumann 1968). Despite the much earlier foundation of the *Acinetobacter* genus it was not until the year 1986 that *Acinetobacter baumannii* was officially designated as a defined species (Bouvet and Grimont 1986). It appears that although not formally designated at the time infections caused by *A. baumannii* first became a problem of significance during the 1970s (Bergogne-Bérézin and Towner 1996).

Hospital acquired infections with *A. baumannii*.

A. baumannii is an opportunistic pathogen meaning it primarily infects and causes disease in patients who are already very sick (Antunes et al. 2014). It is prevalent in nosocomial settings where *A. baumannii* is transmitted and where it is of major global concern due to its capacity to resist treatment. This is largely due to its vast arsenal of antimicrobial resistance mechanisms (Perez et al. 2007). The infections caused by *A. baumannii* are diverse including ventilator associated pneumonia (VAP) and hospital acquired pneumonia (HAP) as well as urinary tract infections, bacteraemia and wound infections (Doi et al. 2015; Nasr 2020). It is thought that one of the tools *A. baumannii* utilises in particular for causing VAP is its capacity to survive on ventilators by forming biofilms (Pakharukova et al. 2018). Due to this capacity to form biofilms and survive for extended periods on medical devices, we see that it is not just in hospitals but specifically within Intensive Care Units (ICUs) where most of *A. baumannii* infections occur.

Community acquired *A. baumannii* infections.

Although far less common than nosocomial infections, *A. baumannii* community acquired infections are also found, although these are generally associated with patients with risk factors such as chronic alcoholism, smoking and chronic lung disease (Dexter et al. 2015). In community settings *A. baumannii* infection is primarily associated with pneumonia (85% of cases) as well as bacteraemia, meningitis and soft tissue infections (Falagas et al. 2007). Community acquired *A. baumannii* pneumonia is generally fulminant (death occurring within 8 days post diagnosis) as well as having a mortality rate as high as 60%, making it more serious generally than the nosocomially acquired variety (Falagas and Rafailidis 2007). In one study it was found that although 58.3% of hospital strains of *A. baumannii* were closely related to each other this value was much lower with just 16.7% of community strains being closely related seeming to indicate a far higher diversity within the community (Zeana et al. 2003).

A pathogen of global concern.

As a result of rising global concern with this treatment resistant pathogen *A. baumannii* was one of the specially designated ESKAPE organisms which are characterised as the most common and serious multidrug-resistant (MDR) pathogens these include

Enterococcus faecium, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter spp.* (Rice 2008; Howard et al. 2012). This was after previously designating antimicrobial resistance as one of the three most important problems facing global health (Bassetti et al. 2011). In fact Carbapenem Resistant *A. baumannii* (CRAB) due to carbapenem resistance being a good indicator of co-resistance with other classes of antibiotics was listed as number one priority for antibiotic research and development in 2018 by the WHO (Tacconelli et al. 2018). In patients with *A. baumannii* HAP and VAP globally ~80% are thought to be infected with multidrug resistant strains (MDR) although this varies by region. It is thought that the mortality rate could be as high as 68.2%, however globally the mortality rate is 42.6% (Mohd Sazlly Lim et al. 2019).

The contemporary model organism *A. baumannii* AB5075.

One of the main concerns with *A. baumannii* infection is the capacity of the pathogen to resist antimicrobials, however, the two model strains generally studied for *A. baumannii* are ATCC19606 and ATCC1978, both of which were isolated 50 years ago and neither of which are significantly resistant to antibiotics (Jacobs et al. 2014). Realising how dated the ATCC strains were, attempts had been made to work on clinical isolates however they were found to be genetically rigid due to multiple drug resistances present in these strains. As a result of the antiquated ATCC strains and the necessity of at least partial antibiotic susceptibility for genetic manipulation, a systemic study was carried out to identify a strain that was closer to current clinical strains in terms of resistances and virulence while retaining genetic pliability. This systemic study was carried out on strains isolated from patients in the U.S. military healthcare system. Thirty-three strains were chosen from 200 isolates and were compared against a previously well characterised clinical strain from 2004 AB0057 (Adams et al. 2008). From this analysis 3 strains were found representing international cloning complexes (ICC) AB5075 (ICC I), AB5711 (ICC II) and AB4857 (ICC III). AB5075 was isolated from a tibia osteomyelitis and it was chosen as the recommended model strain for research purposes due to its utility in animal models as well as its ability to be genetically modified by exploiting certain antibiotic susceptibilities and this is the strain that was used in this thesis (Jacobs et al. 2014).

Control of gene regulation by sigma factors.

Initiation of transcription in bacteria requires the binding of a dissociable subunit to RNA polymerase called a sigma factor, this binds to the core (subunits $\beta\beta'\alpha_2\omega$) to form the RNA polymerase holoenzyme (Paget 2015). Generally, a “housekeeping” sigma factor (σ^{70} or RpoD) will initiate transcription of all the essential genes and pathways to keep the cell functioning. On top of this housekeeping sigma factor, several alternative sigma factors are used to control gene expression in response to specific conditions (Paget 2015).

Extra cytoplasmic function ECF sigma factors.

Extra cytoplasmic function sigma factors work by binding to the core RNA polymerase (RNAP) subunits in place of the primary sigma factor to form the RNA Polymerase

holoenzyme (Ishihama 2000). These alternative sigma factors are a crucial element of how bacteria can regulate their gene expression under different conditions. The mechanism ECF sigma factors employ is altering gene expression through recognising specific promoter regions. The first sigma factors identified from the ECF group were identified 23 years ago, these were σ^E from *Escherichia coli*, AlgU from *Pseudomonas aeruginosa*, σ^E from *Streptomyces coelicolor*, CarQ from *Myxococcus xanthus*, CnrH from *Alcaligenes eutrophas*, HrpL from *Pseudomonas syringae*, SigX from *Bacillus subtilis*, and FecI from *E. coli* (Sineva et al. 2017). ECF sigma factors generally respond to signals either in the cell membrane or outside of the cell and regulated genes with extracytoplasmic function which gave rise to the name (Lonetto et al. 1994; Sineva et al. 2017). There are some members of the family however which sense intracellular signals and can regulate responses that are predominantly cytoplasmic (Sineva et al. 2017). These sigma factors contain only conserved domain 2 and 4; these conserved regions are responsible for binding the core RNA polymerase and promoter recognition. Conserved domains found in other types of sigma factors are absent (Feklistov et al. 2014).

ECF sigma factors are ubiquitous and are found across both Gram-positive and -negative bacterial species. Generally, bacterial genomes encode for multiple ECF sigma factors and the size of the genome typically correlates with the number of ECFs, however the average bacterial genome encodes for six ECF sigma factors (Huang et al. 2015; Li et al. 2019). They have been identified as a major pillar of bacterial signal transduction (Staroń et al. 2009). Generally, ECF sigma factors are often co-transcribed with their anti-sigma factor which is found in the same operon downstream. They usually autoregulate their expression. ECF sigma factors are sequestered by their membrane anchored anti-sigma factor until the activation signal is detected. Upon detection of the signal, the sigma factor is released either by Regulated Intramembrane Proteolysis (RIP) of the anti-sigma factor or by conformational changes in redox sensitive anti- σ switches (Campbell et al. 2007; Brooks and Buchanan 2008; Ho and Ellermeier 2012). While within an ECF family individual sigma factors can recognise the same set promoters, there can be overlap of regulons. There appears to be very little crosstalk between families of ECF sigma factors and it seems that there is evolutionary pressure to insulate individual ECF signalling systems. As a result of this, bacteria with multiple ECF sigma factors tend to have more sigma factors from non-cross-talking families (Rhodius et al. 2013).

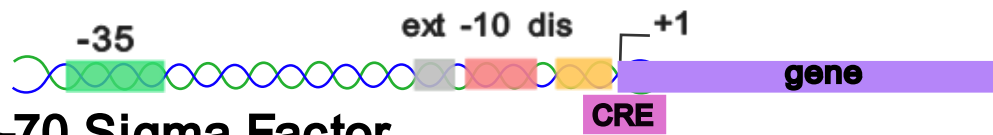
Mechanism of action.

ECF sigma factors only have two conserved domains; the $\sigma 2$ and $\sigma 4$ domain, which contain a non-conserved linker. The $\sigma 4$ domain recognises the -35 motif through a canonical helix-turn-helix DNA binding domain within $\sigma 4$ (Lane and Darst 2006). Throughout initiation the -35 motif remains as double-stranded DNA and recognising it in this form is essential for initiation (Feklistov et al. 2006). This binding is thought to anchor the holoenzyme to allow the -10 motif to be recognised by $\sigma 2$ as non-template single stranded DNA upon separation (Roberts and Roberts 1996). The $\sigma 2$ domain is thought to occupy a cleft

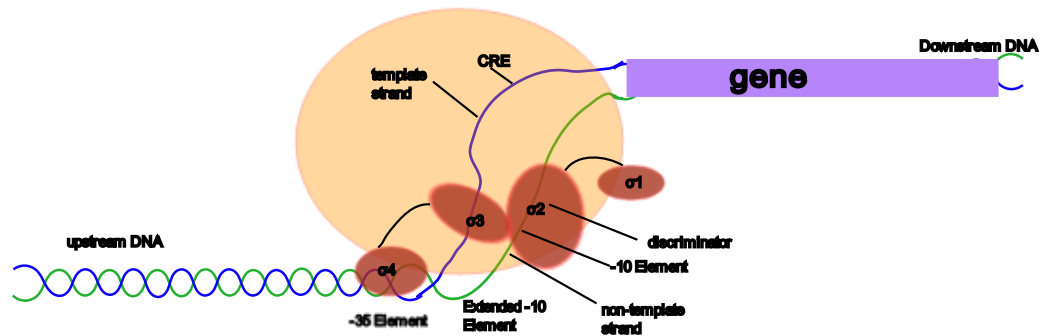
between the RNAP- β lobe and the RNAP- β' coiled-coil (β' CC). Here, $\sigma 2$ and the RNAP- β' CC make extensive electrostatic interactions (Li et al. 2019). The residues in contact here are conserved amongst primary sigma factors and ECF sigma factors suggesting that it serves as an anchor. The $\sigma 4$ domain enfolds the flap-tip helix of the RNAP- β subunit it also utilises a unique anchor point not seen in primary sigma factors which is on a C-terminal helix of the RNAP- β subunit (Li et al. 2019). The linker region appears to interact with the core RNAP core enzyme inserting into the active centre cleft and exiting through the RNA exit channel. In this way it behaves in a similar manner to the $\sigma 3.2$ region to type 1 sigma factors and this linker region is also thought to make direct interactions with ssDNA (Vassylyev et al. 2002; Lin et al. 2019).

Unlike the housekeeping sigma factor, it seems that ECF sigma factors have very low tolerance to sequence variation at the -35 and -10 promoter elements, and they also have stringent requirements for the spacer length (Campagne et al. 2015). It is also thought that the means by which ECF sigma factors recognise the -35 and -10 promoter elements is unique and not the same as the primary sigma factor (Lane and Darst 2006; Campagne et al. 2014). Sigma factors are not involved in elongation and once the RNA reaches 12-15 nt it generally is released from the transcription complex (Vassylyev et al. 2007). While this is most often the case it is not always true and there are mechanisms where the sigma factor is retained throughout elongation this is especially true at stationary phase (Bar-Nahum and Nudler 2001; Wade and Struhl 2004).

A Promoter Region



B $\sigma 70$ Sigma Factor



C ECF Sigma Factor

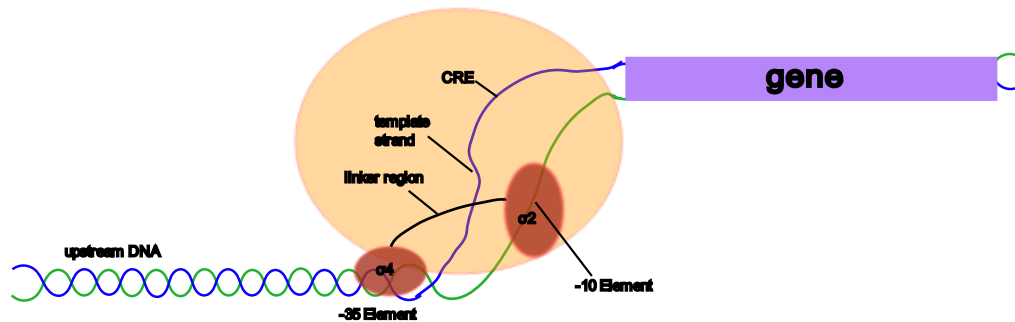


Figure 1.1 Bacterial promoter regions as well as the binding mechanism leading to transcription initiation by the RNA polymerase holoenzyme with both housekeeping sigma factors and ECF sigma factors. (A) The promoter region of bacteria is shown with the regions involved in sigma factor binding, they are noted in relation to +1 and are shown as coloured rectangular boxes. The -35 hexamer element, -10 hexamer element, extended -10 element, discriminator element, and the core recognition element are all highlighted. (B) Shows the interaction between the RNAP holoenzyme (housekeeping sigma factor) and different promoter elements. The RNA polymerase is shown as an orange oval with the subunits of the sigma factor being shown as red ovals. (C) Shows in the same convention the binding between promoter elements and RNAP holoenzyme (ECF sigma factor) (Busby and Browning 2024).

The *Acinetobacter*-specific alternative factor SigAB.

Very little is known on sigma factors in *A. baumannii*. A first study suggested that *A. baumannii* possesses five sigma factors (Casella et al. 2017). In this work, SigAB was suggested to be a RpoE homologue, however, a pre-print article published while this work was carried out identified SigAB as an *Acinetobacter*-specific sigma factor (Bacon et al. 2024). While it is structurally similar to other ECF sigma factors, its evolutionary relationship to these is unclear. There are proposed -10 and -35 binding sites for SigAB (Bacon et al. 2024). It has also been implicated in stress response to certain transition metals, most prominently copper, where copper sensitivity was increased upon deletion of *sigAB*. The regulon of SigAB was shown to consist of *sigAB* itself, *relA*, and the small RNA SabS (sRNA90). Also, the two genes *aabA* and *aabB* downstream of *sigAB* were identified to have anti-sigma activity. As a pre-print, the work is preliminary so far and was carried out in the strain ATCC17978.

Alternative sigma factor-dependent small, regulatory RNAs.

Bacterial ability to respond to change and adapt to its environment hinges upon diverse interconnected regulatory networks to control the expression of genes. Already discussed is the importance of sigma factors for the control of gene expression on a transcriptional level. Another useful tool in the arsenal of bacteria is small regulatory RNAs or sRNAs which are a key aspect to how bacteria can adapt to a wide range of environments and control their diverse and intricate network of regulatory pathways. Small RNAs convey this adaptability due to their role in post-transcriptional regulation (Waters and Storz 2009). Small RNAs are generally between 50-400 nt in length sRNAs and are particularly useful due to their capacity to act quickly and their low metabolic cost (Beisel and Storz 2010). Post transcriptional regulation involves regulation that occurs after the mRNA is produced impacting its elongation, stability and/or translation (Menendez-Gil and Toledo-Arana 2021).

There are two groups that sRNAs can be divided into *cis*-encoded and *trans*-encoded. While *cis*-encoded sRNAs are transcribed from the complementary strand of their mRNA target, *trans*-encoded sRNAs are situated at a different location on the bacterial genome than the elements they regulate. *Trans*-encoded sRNAs are also known to imperfectly bind their target mRNA often with an RNA binding protein (RBP) facilitating the interaction and acting as a chaperone (Wagner and Romby 2015). *Trans*-encoded sRNAs can be found in intergenic regions (IGR) (Argaman et al. 2001). In what has been referred to as parallel transcriptional output it has also been found that sRNAs can be generated from the 5' and 3' ends of mRNA that encode for genes (Vogel et al. 2003). The expression of some small RNAs is controlled by alternative sigma factors forming intricate regulatory networks to respond to environmental stress. The RpoE-dependent sRNAs MicA and RybB of enteric bacteria are expressed upon envelope stress, and the expression of sRNA SdrS depends on the general stress alternative sigma factor RpoS responsible for preventing translation

of a large set of outer membrane proteins to relieve envelope stress (Papenfort et al. 2006; Johansen et al. 2006; Fröhlich et al. 2012).

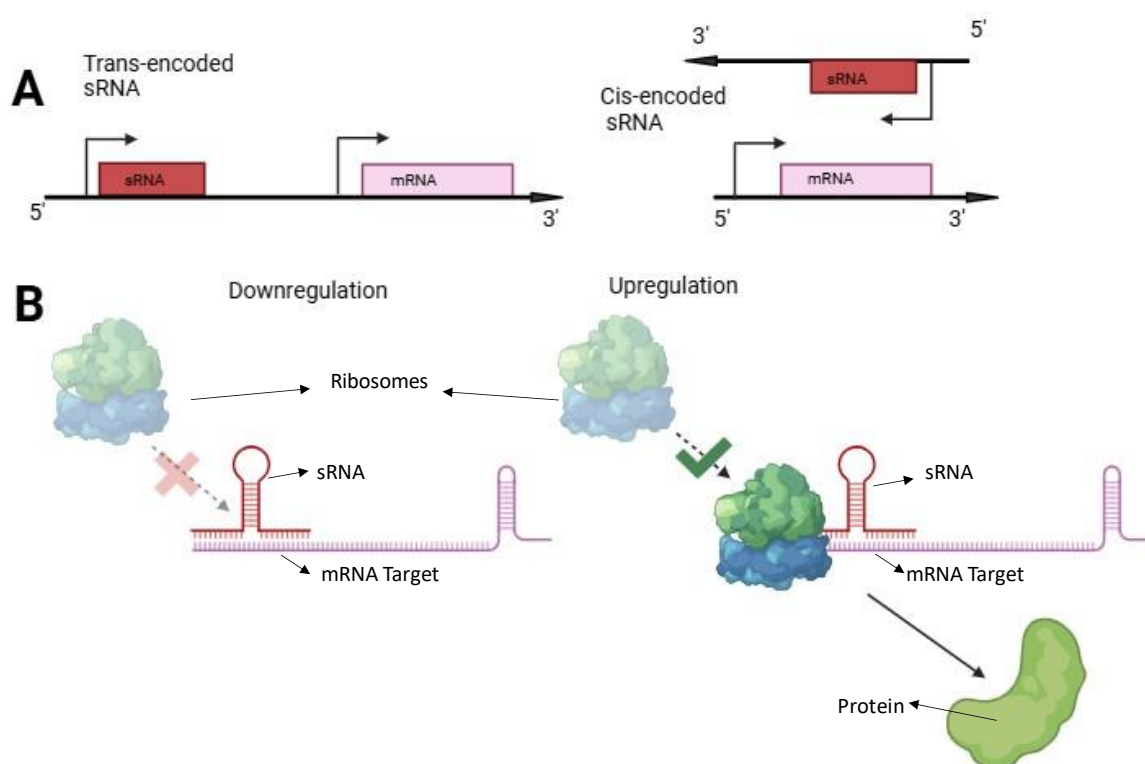


Figure 1.2 Trans and cis-encoded sRNAs and sRNA mechanisms of action. (A) cis and trans-encoded sRNAs showing how they occur on the chromosome. (B) Mechanisms of gene regulation by sRNAs. The sRNA binds to the target mRNA either repressing translation by preventing ribosomes from binding or inducing translation by causing conformational changes that allow ribosomes to bind more effectively.

The RNA binding protein Hfq.

Hfq is an RNA-binding protein that acts as a chaperone to allow for sRNAs to effectively function by binding to their target molecules. The Hfq protein is therefore a pillar of the global post-transcriptional network in its function as a chaperone. Hfq has a ring architecture being made up of six identical protomers in a hexameric configuration. Despite having a lot of variation in sequence the structure of the hexamer is highly conserved (Vogel and Luisi 2011). Due to its hexameric structure the Hfq has two exposed faces that can interact with nucleic acids, the two faces however interact in a different manner with RNA and are referred to as the proximal face (amino-terminal α -helix is exposed) and the distal face (the opposite side). The proximal side favours single stranded U rich sequences and the distal side favours single stranded ARN, ARNN or AAN rich

sequences, the third distinct RNA binding surface in Hfq is the rim which favours UA- rich sequences (Mikulecky et al. 2004; Faigenbaum-Romm et al. 2020). The sRNAs that bind Hfq are split generally into two classes depending on the Hfq faces they bind. Class I sRNAs bind to the proximal face through a U rich sequence and bind the rim via a UA binding motif and Class I sRNAs targets have ARN- or AAN- rich sequences thereby binding the distal face of Hfq (Schu et al. 2015). Class II sRNAs have a U rich sequence to facilitate binding the proximal face of Hfq and to bind the distal face possess an ARN- rich sequence motif the targets of sRNA II contain a UA motif that binds the rim of Hfq (Schu et al. 2015). It is interesting that the targets of class I sRNAs GcvB, MicA, ArcZ and RyhB lack a distinct ARN- binding motif, this is also true of the class II targets of CyaR which lack a UA rich motif (Holmqvist et al. 2016; Faigenbaum-Romm et al. 2020). This would seem to indicate that perhaps there are also more complicated mechanisms of interaction between Hfq and RNA at least under certain conditions.

The role of Hfq in *A. baumannii* is poorly understood despite the important role established in other bacteria. There is a Hfq homologue in *A. baumannii*, which has an unusual glycine-rich domain at the C terminal of the protein (Schilling and Gerischer 2009). Hfq deletion mutants in *A. baumannii* have showed that the deletion strain exhibited retarded growth and higher susceptibility to environmental stresses among a host of other aberrant phenotypes (Kuo et al. 2017). Another paper found that for high affinity binding of RNA the glycine tail is essential, it was also demonstrated that the *A. baumannii* Hfq formed complexes *in vitro* with *E. coli* sRNAs (MicA and DsrA) as well as with *A. baumannii* native sRNA Abs25. It was also shown that *A. baumannii* native Hfq can facilitate the regulation of SodB expression via facilitating the interaction with *E. coli* RyhB (Sharma et al. 2018). Hfq in *A. baumannii* appears to function as a chaperone as it does in other bacteria, however, the glycine rich tails may be acting as an additional surface for RNA binding.

sRNAs in *A. baumannii*.

Identifying sRNAs in bacterial genome sequences is notoriously difficult. A global transcriptomic analysis in *A. baumannii* has identified 88 sRNA candidates in AB5075 with six of these having been validated by northern blotting (Weiss et al. 2016). For the strain ATCC17978 another global transcriptomic analysis identified 110 sRNA candidates and seven have been validated by northern blotting of these 110 candidates only 7 sRNAs are conserved across *Pseudomonadales* (Kröger et al. 2018). Despite having identified many candidates and validating several sRNAs the role of sRNAs in regulating gene expression in *A. baumannii* is not very well understood.

AIMS OF THIS STUDY

Alternative sigma factors of RNA polymerase possess vital functions for bacterial cells. In *A. baumannii* the role of sigma factors had not been studied at the start of this work. Nothing was known on the *Acinetobacter*-specific SigAB, which was thought to be a homologue of the envelope stress response sigma factor RpoE. The goal was to investigate the biological role of the alternative sigma factor SigAB in *A. baumannii* AB5075 and its regulon.

MATERIAL AND METHODS

Culture Conditions.

L-broth and L-agar plates (Table 2.1) were incubated at 37°C for 16-18 hours. Overnight cultures were inoculated in 5 ml of L-broth from a single colony on a plate 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, 30 µg/ml apramycin, 250 µg/ml zeocin (*A. baumannii*), 25-50 µg/ml (*E. coli*), 25 µg/ml chloramphenicol) and cultivated 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. Strains were stored at -80°C as cryostocks by combining overnight culture with 30% (v/v) sterile glycerol. Strains were streaked for single colonies from these cryostocks on L- plates with the appropriate antibiotics and incubated at 37°C overnight. Plates were stored at 4°C for not longer than 10 days.

Table 2.1: Media compositions.

Media	Reagents
Lennox broth (L Broth)	Bacto-Tryptone 10g/l NaCl 5g/l Bacto-Yeast extract 5g/l
Lennox agar (L Agar)	Lennox broth Bacto-Agar 1.5%(w/v) Agar
Tryptic Soy Broth (TSB)	Tryptone (Pancreatic Digest of Casein) 17g/l Soytone (Peptic Digest of Soybean) 3g/l Glucose (= Dextrose) 2.5g/l Sodium Chloride 5.0g/l Dipotassium Phosphate 2.5g/l
Motility Media solid	Agarose – D3 20g/l Tryptone 5g/l
Transformation Media liquid	Tryptone 5g/l CaCl ₂ 680mM 0.1% (v/v) MgCl ₂ 680mM 0.1% (v/v)
M9 medium	0.1 mM CaCl ₂ 1 mM MgSO ₄ 1% pyruvate

Table 2.2: List of bacterial strains used in this study.

Species	Strain	Genotype	Resistance	Source
<i>A. baumannii</i>	AB5075	Wild-Type (WT)		Salcedo Lab (U Madison-Wisconsin)
<i>E. coli</i>	Top10	F ⁻ <i>mcrA</i> , Δ (<i>mrr-hsdRMS mcrBC</i>) ϕ 80 <i>lacZ</i> Δ M15, Δ <i>lacX74</i> , <i>nupG</i> <i>recA1 araD139</i> , Δ (<i>ara-leu</i>)7697 <i>galE15 galK16</i> , <i>rpsL</i> (StrR) <i>endA1</i> λ		Invitrogen
<i>A. baumannii</i>	AB5075	Δ <i>sigAB</i> (ABUW_RS04845)		This study
<i>A. baumannii</i>	AB5075	Δ ABUW_RS04840:: <i>aacC4-sacB</i>	Apramycin	This study
<i>A. baumannii</i>	AB5075	Δ sRNA90:: <i>aacC4-sacB</i>	Apramycin	This study
<i>A. baumannii</i>	AB5075	<i>sigAB</i> ::3XFLAG:: <i>aacC4-sacB</i>	Apramycin	This study
<i>A. baumannii</i>	AB5075	ABUW_RS18870::3XFLAG:: <i>aacC4-sacB</i>	Apramycin	This study
<i>A. baumannii</i>	AB5075	Δ <i>sigAB</i> , ABUW_RS18870::3XFLAG	Apramycin	This study

Table 2.3: List of plasmids used in this study.

Plasmid	Description	Resistance	Source
pVRL2Z	pVRL1b carrying the <i>araC</i> - <i>P_{BAD}</i> arabinose-inducible expression cassette. OriAb and ColE1-like origin of replication	Zeocin	Visca lab (Rome, Italy)(Lucidi et al. 2018).
pXG10sf	pXG10 containing <i>sfgfp</i> expressed from <i>P_{LtetO-1}</i> promoter. pSC101* origin of replication.	Chloramphenicol	Vogel lab (Würzburg, Germany)(Corcoran et al. 2012).
pVRL2Z-SigAB	<i>sigAB</i> cloned under control of <i>P_{BAD}</i> of pVRL2Z	Zeocin	This study
pVRL2Z-SigAB::3XFLAG	<i>sigAB</i> -3XFLAG cloned under control of <i>P_{BAD}</i> of pVRL2Z	Zeocin	This study
pVRL2Z-sRNA90	sRNA90 cloned under control of <i>P_{BAD}</i> of pVRL2Z	Zeocin	This study
pVRL2Z-sRNA90M	Mutated sRNA90 cloned under control of <i>P_{BAD}</i> of pVRL2Z	Zeocin	This study

pVRL2Z- ABUW_RS04840	ABUW_RS18870 cloned under control of P_{BAD} of pVRL2Z	Zeocin	This study
pXG10sf- ABUW_RS18870	ABUW_RS18870 cloned under control of $P_{LtetO-1}$ of pXG10sf	Chloramphenicol	This study

Table 2.4: List of oligonucleotides used in this study.

Name	(Primer sequence 5'-3')
RpoE_up_F	ACTCATTTTGATGCTTGCGC
RpoE_up_R	GGCCAATTCGCCCTATAGTGAGTCGGGAGATGGAAAATCCTGTCATTGG
RpoE_d_F	GGGTTTGCTCGGGTCGGTGGCATATGTGATTTCACTAAAAAGGTGACATCC
RpoE_d_R	CATTGAATAACACCTCATCTCC
RpoE_p7	GGAGATGGAAAATCCTGTCATTGG
RpoE_P8	CCAATGACAGGATTTCCATCTCC TGATTTCACTAAAAAGGTGACATCC
RpoE del test F	AGATAAGGTGGGTACGTCC
RpoE del test R	TGGGCCAACTATCGAGTTTGG
RpoE_up_FLAG_F	CTAACCAACGCCATTGGG
RpoE_up_FLAG_R	CCGTCATGGTCTTTGTAGTC TGATTCATTGGAACCTCCC
RpoE_down_F	GGGTTTGCTCGGGTCGGTGGCATATG TGATTTCACTAAAAAGGTGACATCC
RpoE_d_R	CATTGAATAACACCTCATCTCC
pVRL2Z_backbone_forward_RpoE_GFP	GAGGCATCAATAAAACGAAAGGC
pVRL2Z_backbone_reverse_RpoE_GFP	AACTAGTGGATCCCCCG
RpoE Insert reverse	GCCTTTCGTTTTATTTGATGCCTCTAGATCATGATTCATTGGAACCTCCC
RpoE Insert forward	CCTGCAGCCCGGGGATCCACTAGTTATGGATTAGCACCGAAAAAGTC
RpoE Flag insert primer	GCCTTTCGTTTTATTTGATGCCTCTAGAACTTCGAAGCAGCTCCAGC
18870 down R	AATCCTGGAATGACACGGTG
18870 down F	GGGTTTGCTCGGGTCGGTGGCATATG TTTGCTGCTAAAAATAAGAGATATGAG
18870 up R	CCGTCATGGTCTTTGTAGTC CTGAGCAGTTGCAGAACCTG
18870 up F	AGTAGGGGACTGTGCTGTTT
ABUW_RS0480 pVRL2Z reverse	GCCTTTCGTTTTATTTGATGCCTCTAGATTAGCTACCATGTTGAAC
ABUW_RS0480 pVRL2Z forward	CCGGGGGATCCACTAGTTATGAATCATGATGATTTAC
up f ABUW_RS04840	GCAGATACTCAAGAATTTGC
up r ABUW_RS04840	GGGTTTGCTCGGGTCGGTGGCATATG GGCCAACTATCGAGTTTG
down r ABUW_RS04840	CGTTCCTGGAAGTACAACCTA
Down F ABUW_RS04840	GGCCAATTCGCCCTATAGTGAGTCG TAGAAATGCTTATGGTGTTG
p7 ABUW_RS04840	GGCCAACTATCGAGTTTG
p8 ABUW_RS04840	CAAACCTCGATAGTTTGGCC TAGAAATGCTTATGGTGTTG
Riboprobe sRNA 90 Forward	AACAAGGTCGCAGCAACC
Riboprobe sRNA 90 Reverse	GAATTAATACGACTCACTATA ATAAAAACCGACGATTCGAGTG
ribo reverse 106	GAATTAATACGACTCACTATA TGTCAAGGGAAAACATCTATGG

ribo forward 106	AAGGGTGTGATAGGGATC
e coli 5s forward	TGGTCCCACCTGACCCCATG
e coli 5s reverse	GAATTAATACGACTCACTATA GTTCCTACTCTCGCATGG
RP_5S_Abau_R	GAATTAATACGACTCACTATAATGACTTACTCTCACATGG
pWH1266-min-bla_F	CCATATAAACCTGTCATAGCGCTTTTCTGTGACTGGTGAG
sRNA90 pVRL2Z IF	GCAACTCTCTACTGTTTCTCCATAACAAGGTCGCAGCAACC
sRNA90 pVRL2Z IR	CCGTCGACCTCGAGATTCGCCACGAAAGCATTATTGTG
pVRL2Z_SLiCE_F	ATGGAGAAACAGTAGAGAGTTGC
pVRL2Z_SLiCE_R	GAATCTCGAGGTCGACGG
sRNA90 mutant downstream	CTGGTAATAGTGCTGCAATC
sRNA mutant Upstream	AGGGTTGAAGACTGGATT
sRNA mutant forward	GGTTTGATTACGACTCTTTC
sRNA mutant reverse	CAAACCTCACCGAAACAATT

Monitoring Growth.

The Biomate 3S spectrophotometer (Thermo Scientific), was used to measure the optical density of cultures at a wavelength of 600 nm (OD₆₀₀). Medium containing cells was measured against a cuvette with just the appropriate medium without bacteria. If cultures had an OD₆₀₀ greater than approximately 0.5, they were diluted 10-fold in the appropriate medium to get an accurate reading.

Growth Experiments.

Growth experiments were carried out in 96 well plates using the Synergy HTX multimode reader (BioTek). Unless stated otherwise each well was made up to 100 µl. The concentration of the stressor indicated was made up to this total. Each well was set to a cell density equal to OD₆₀₀ of 0.005 of bacterial culture from an overnight culture.

Gene deletions and FLAG-tagging of proteins.

Gene deletions were created by homologous recombination as described in Godeux *et al.* (Godeux *et al.*, 2020). Briefly, ~2,000 bp up- and downstream regions of the sequence to be deleted were amplified by PCR from genomic DNA of *A. baumannii* AB5075. Overlap extension PCR with two selection genes (*aacC4*, *sacB*) amplified from pMHL-2 created a linear DNA fragment with which *A. baumannii* AB5075 was transformed with by natural transformation (Godeux *et al.*, 2020). Colonies growing on L-agar with apramycin and displaying no growth on L-agar containing 20% (w/v) sucrose were verified by colony PCR. This method was also used to add a sequence encoding for three copies of the FLAG (3x DYKDDDDK) tag of *sigAB* and *ABUW_RS18870* on the chromosome. This was achieved by fusing *sacB-aacC4* genes amplified from pMHL2 plasmid by extension overlap to a 3XFLAG-encoding sequence which was then inserted at the C-terminus of *sigAB* on the chromosome *via* homologous recombination. Oligonucleotides used in this study are listed in Table 2.4.

Measurement of fluorescence.

To monitor sfGFP-mediated fluorescence of *E. coli* strains carrying the translational fusion of ABUW_RS18870-sfGFP, bacteria were streaked out from cryostocks onto L- plates supplemented with 25 µg/ml chloramphenicol and 50 µg/ml zeocin. These were grown overnight at 37°C and single colonies were inoculated into 5ml L- broth supplemented with the same concentration of antibiotics and grown overnight at 37°C and 220 rpm. Twenty-five µl of this overnight culture was used to inoculate 25 ml of supplemented L- broth in a 250 ml Erlenmeyer flask at 37°C 220rpm until it reached an OD₆₀₀ of 0.3. The samples were aliquoted in 96-well plates (100 µl per well) and a fluorescence reading was obtained (measurement prior to induction of gene expression by addition of the inducer L-arabinose). The pre-induced culture in the flasks then were adjusted to 100 mM L-arabinose to induce gene expression and allowed to incubate at 37°C 220rpm for 1 hour. An uninduced (no addition of L-arabinose) control sample was allowed to grow for an hour after reaching an OD₆₀₀ of 0.3. After this, 100 µl of each culture was aliquoted into 96-well plates and a fluorescence reading was obtained. Fluorescence (arbitrary units; excitation at 480 nm/emission at 520 nm) and optical density at 600 nm (OD₆₀₀) were measured using a Synergy HTX multimode reader (BioTek). Fluorescence and OD₆₀₀nm values were adjusted by subtracting the background values generated by uninoculated L broth medium. Fluorescence units (RFU) were normalized by quantifying the fluorescence observed relative to optical density OD₆₀₀nm (fluorescence/OD₆₀₀nm). All experiments were performed with a minimum of three biological replicates.

Isolation of RNA from *A. baumannii* and *E. coli*

Overnight cultures were set up in 5 ml L broth containing the necessary antibiotics as already described. Following this, a 25 ml flask was inoculated (1:1000) and the flasks were allowed to grow to the desired OD₆₀₀ at 37°C and 220rpm. Once the desired OD₆₀₀ was reached, a volume containing 4-5 OD₆₀₀ units of culture were added to a 50 ml centrifuge tube and mixed with 2/5 of the volume of ice-cold stop solution (95% ethanol, 5% phenol, pH4.3) (Tedin and Bläsi 1996). This solution was allowed to stand on ice for 30 min. Next, the solution was centrifuged at 4°C at 3220 x g for 10 min. Most of the supernatant was discarded and the pellet was resuspended in residual media and transferred to a 2 ml Eppendorf tube. This was then spun at 21,000 x g for 1 minute and the supernatant was discarded. The pellet was stored at -80°C overnight. The next day, the cell pellet was resuspended in 1 ml of TRIzol and then transferred into a heavy phase lock tube. The phase lock tubes were prepped by a 15 min centrifugation step at 21,000 x g. Four-hundred µl of chloroform was added to the phase lock tube and it was vigorously mixed by shaking until the solution reached a milky pink colour after 10 seconds. The solution was incubated at room temperature for 2 min before being centrifuged at 21,000 x g for 15 min. The upper phase (~500 µl) was transferred to a new Eppendorf tube, 450 µl of 100% isopropanol was added and the suspension was incubated at room

temperature for 30 min after briefly mixing by inverting. The solution was centrifuged for 30 minutes at 21,000 x g to pellet the RNA. The supernatant was discarded. Next, the pellet was carefully washed with 75% ethanol prepared with DEPC treated water. This was centrifuged again at 21,000 x g for 10 min. The supernatant was carefully discarded, and the pellet was allowed to dry at room temperature. The pellet was then resuspended in DEPC treated water by 5 min incubation at 65°C in a heat block as well as vortexing 3 times after 1-, 3- and 5-min incubation. The RNA quality was measured using the Agilent Bioanalyser 2100.

RNA-sequencing.

Total RNA was sent to Azenta (Leipzig, Germany) for RNA-sequencing (strand-specific RNA-seq). Azenta carried out DNase digestion and rRNA depletion of samples before preparing cDNA libraries for RNA-seq. The obtained fastq files were subjected to further bioinformatic analysis assisted by Dr. Karsten Hokamp (Genetics Department, TCD) and Dr Anna Ershova (Microbiology Department, TCD). High quality mapped reads were aggregated using featureCounts (Liao et al. 2014). DESeq2 was used to calculate differential gene expression and transcripts per million (TPM) were calculated by the method of Li *et al.* (Li et al. 2010; Love et al. 2015). Batch processing was used using the tool RUVseq (Risso et al. 2014).

Biofilm Formation Assay.

The biofilm formation assay was carried out by growing overnight cultures as previously mentioned. A second culture was then prepared by adding 100 µl of overnight culture to 5ml of L broth or L broth with 2% (v/v) glucose. These cultures were then incubated at 37°C and 220 rpm for 1-2 h to reach the OD₆₀₀ of 0.5-1. The OD₆₀₀ was then set to exactly 0.5. A 1:20 dilution was made with either L broth or L broth with 2% (w/v) glucose. One hundred µl of this dilution was transferred into different wells of a 96 well plate. One hundred µl of media was added as a negative control. This 96 well plate was incubated statically for 24 h at 37°C. To prevent evaporation, the plate was placed in a plastic box with paper tissue and ca. 15 ml of deionised water. After 24 h, the supernatant was discarded using the multi-channel pipette and the biofilm was washed three times with sterile PBS. The plate was then left to dry at 60°C for 10 min without the lid. One-hundred-twenty-five µl of diluted crystal violet solution (1:1 dilution of saturated crystal violet and deionised water) was added to stain at room temperature for 10 min. The biofilm was washed five more times with deionised water. The plate was dried at 60 °C with no lid for 5 min. Two-hundred µl of 95% ethanol was added to each well. The OD₅₇₀ was measured using a Synergy HTX multimode reader (BioTek).

Plasmid isolation.

All plasmids were extracted from plasmid-containing *E. coli* or *A. baumannii* using the E.Z.N.A.® Plasmid DNA Mini Kit 1 (Omega Bio-Tek). Plasmids were isolated from 5 ml

overnight L-broth cultures supplemented with the desired antibiotic. Cultures were then pelleted by centrifugation at max speed then plasmids were isolated and purified following manufacturer's description (Omega Bio-Tek, 2018). Plasmid concentration and isolation was quantified using the Nanodrop spectrophotometer.

Isolation of genomic DNA.

Genomic DNA was isolated from wild-type *A. baumannii* AB5075 as well as the strains AB5075 *sigAB::3xFLAG* and AB5075 *ABUW_RS18870::3xFLAG*. Four-hundred µl of overnight culture grown in L broth was centrifuged (21,100 x g for 1 min) in an Eppendorf tube. The supernatant was decanted, and the pellet was then resuspended in 200 µl of deionised water, the sample was then boiled at 100°C for 5 min then briefly vortexed. After a centrifugation step 21,100 x g for 5 min, the supernatant was transferred to a new Eppendorf tube. Two-hundred µl of chloroform was added, then briefly vortexed, and the sample was centrifuged (21,100 x g for 10 min at 4°C). The upper, aqueous phase was then removed, and the DNA concentration was measured using the Nanodrop spectrophotometer. This was stored at -20°C.

Polymerase Chain Reaction (PCR).

PCRs in this study were carried out using VeriFi™ polymerase (PCRBIO systems). The primers used can be found in Table 2.4. As a template typically 100 ng of chromosomal DNA, 0.1 ng of plasmid DNA or a single colony resuspended in 20 µl of dH₂O was used. The conditions and reagents used in these reactions are shown Table 2.5.

Agarose Gel Electrophoresis.

Linear PCR fragment sizes were determined by agarose gel electrophoresis. A 1% (w/v) agarose gel was made by adding 1 g of agarose powder per 100 ml TAE (40 mM Tris-acetate, 1 mM EDTA). The powder was melted into solution by boiling and inverting until fully solubilised. Bands were visualised through incubating the gel after electrophoresis in a water-bath containing 1x SYBR™ Safe (Thermo Fisher Scientific) DNA gel stain. The molten 1% agarose is poured into a mould with a comb making wells for sample to be loaded. The sample (typically 5 µl) is mixed with 1 µl 6 x DNA loading dye and then added to a well of the solidified 1% gel that had been submerged fully in 1x TAE. Two-and-a-half µl of Thermo Scientific GeneRuler Ready-to-use 1kb DNA Ladder was also added to a well to compare the fragment sizes. Gels were run for 30 min at 100 V to separate the fragments. The gels were then removed and imaged under blue light (400–525 nm).

PCR purification.

Electrophoresis verified PCR products were purified using the Monarch PCR Cleanup Kit (New England BioLabs) to remove PCR reactants and other impurities. PCR replicates were

pooled and purified using DNA spin columns as specified in the manufacturer's instructions.

Sanger sequencing.

All plasmids constructed in this study were sent to Eurofins Genomics for Sanger sequencing. The results were analysed using a EMBOSS Water pairwise local alignment programme (Madeira et al. 2024).

***DpnI* restriction digest.**

Restriction enzymes were purchased from Thermo Scientific and used according to the manufacturers' specifications. *DpnI* is used to digest the methylated parental DNA (e.g., plasmids). 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), 10x CutSmart Buffer (5 µl) and dH₂O (39 µl) at 37°C for 5 min. The incubation was run for up to 8 hours at 37°C.

Sequence and ligation independent cloning (SLiCE).

The SLiCE cloning procedure used recombination to integrate DNA inserts into linearised 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 2.6. These mixtures were then incubated at 37°C for 1 h. The SLiCE extract was prepared prior to the start of this project. This was accomplished by lysing *E. coli* cells that are overexpressing prophage protein λ Red system from pKD46 (Datsenko and Wanner 2000).

Transformation-competent *E. coli* (CaCl₂ method).

E. coli TOP10 was made competent for heat-shock transformation with plasmid DNA using CaCl₂. An overnight culture was prepared by inoculating in 5 ml L broth one colony of *E. coli* TOP10. Fifty µl of this culture was then added to a flask with 50 ml of L broth which was then incubated at 37°C and 220 rpm until it reached exponential phase (OD₆₀₀ 0.4-0.8). This culture was then centrifuged (2,000 x g for 10 min at 4°C). The supernatant was decanted, the pellet was resuspended in 40 ml of ice cold CaCl₂ (100 mM) and incubated on ice for 20 minutes. It was centrifuged again at the same settings, the supernatant decanted and resuspended in 10 ml CaCl₂, and 1.25ml glycerol (85%). This was aliquoted (100 µl) into separate Eppendorf tubes and stored at -80°C.

Transformation of Calcium Competent *E. coli*.

An aliquoted sample of CaCl₂-competent *E. coli* TOP10 was removed from -80°C storage and thawed on ice. Once thawed, 100 ng of plasmid DNA or 5 µl of a SLiCE reaction was added, and the solution was briefly vortexed. This mixture was left to incubate on ice for 20 min. Next, it was incubated at 42°C in a water bath for 2 min before putting the tubes

back on ice for 2 min. Next, 800 µl of L broth was added to the solution, and this was left to incubate at 37°C for 90 min at 220 rpm. This solution was then plated on L agar plates containing the appropriate antibiotics. These were then left to grow overnight at 37°C.

Natural Transformation (solid media).

Two ml of L- broth was inoculated with a single colony and incubated at 37°C and 220 rpm until it reached an OD₆₀₀ of 0.1. The culture is diluted to an OD₆₀₀ of 0.01 with sterile PBS. Next, 5 µl of diluted cells are mixed with 5 µl of DNA (100-500 ng/µl). Next, 2.5 µl of the cell/DNA mix are spotted on the motility agar described in Table 2.1. The cells were incubated at 37°C overnight. The next day, 100µl of sterile PBS was added and after vortexing to mix, the solution was plated on L agar plates supplemented with the necessary antibiotics and incubated at 37°C.

Natural Transformation (liquid media).

An overnight culture is set up from a single colony of the strain to be transformed in 2 ml of L broth without NaCl. The next day, 100 µl of transformation media is added to a sterile Eppendorf the liquid transformation medium is prepared as described in Table 2.1. Overnights are added to the Eppendorf of media to make an OD₆₀₀ of 0.01. One hundred ng of DNA to be transformed is added. One tube is left without DNA to act as a negative control. The tubes are left to incubate for 5 h or overnight at 37°C without shaking. The culture is then plated on L agar plates supplemented with the appropriate antibiotics and incubated at 37°C.

Creating gene deletions in *A. baumannii* AB5075.

Deletion mutants were constructed using the scarless gene removal protocol (Godeux et al. 2020). This is a PCR-based genome editing method utilising naturally transformable *A. baumannii*. It involves amplification of a 2 kb upstream and downstream sequence from the gene desired to be deleted to allow for homologous recombination. During the PCR, short overhangs are included that contain complementary sequences to allow overlap-extension PCR (see below). These regions are amplified by PCR and the amplicon size was confirmed by agarose gel electrophoresis. After confirming the fragments are the correct sizes, the samples were purified by the PCR purification protocol described above. The selection genes *sacB* and *aacC4* are amplified by PCR from the plasmid pMHL2. An overlap-extension was carried out to create a linear DNA fragment from the up- and downstream fragments and the selection genes on the order of: Upstream fragment-Selection cassette-Downstream fragment. This produces an ca. 8 kb long product which is validated by agarose gel electrophoresis. The two 2 kb regions homologous to the recipient genome allow for recombination of the chimeric product into the recipient genome by natural transformation which is catalysed by endogenous recombinases. Insertion mutants could be selected for as they carry the dual phenotypes of apramycin resistance (L agar with 60 µg/ml apramycin) and sucrose sensitivity (L agar plates without

NaCl, 20% sucrose). The selection genes are then removed by the creation of linear DNA fragment fused from the up- and down-stream fragments and transformation of the insertion mutant. Removal of *sacB* and *aacC4* genes is tested by selecting cells for sucrose resistance and apramycin sensitivity (as above), when transformants are plated on L agar without NaCl and with 20% sucrose, L agar with apramycin and incubated overnight at 30°C. Arising colonies are tested by colony PCR with primers listed in Table 2.4.

Creation of pVRL2Z-sRNA90M.

Primers were designed to create a mutation region of sRNA90 implicated with forming an sRNA-mRNA duplex with ABUW_RS18870 mRNA. A forward primer 500 nt upstream of sRNA90 and a reverse primer located at the binding site designed with three bp substitutions were used to amplify the 'upstream' fragment. The same base pair substitutions were also made in a forward primer at the binding site which was used with a reverse primer 500 nt downstream of the sRNA90 to make the 'downstream' fragment as above. These PCR products were validated by agarose gel electrophoresis and purified according to the protocol described above. An overlap-extension PCR was prepared by combined 100 ng of each of these 'upstream' and 'downstream' fragments to create a template piece of DNA with the three point mutations at the binding site incorporated. This PCR product was again purified and used as template DNA for PCR to amplify the sRNA90 mutant. This PCR product was purified and cloned into the pVRL2Z plasmid using the SLiCE cloning method as before to create the pVRL2Z-sRNA90M plasmid. A two-plasmid system in *E. coli* was created again using pXG10-ABUW_RS18870 to examine the impact of disrupting the sRNA-mRNA interaction.

Northern blotting.

Non-radioactive northern blotting was carried out as described earlier (Kröger et al. 2018). To detect a specific RNA species, digoxigenin (DIG)-labelled single stranded RNA molecules ("riboprobes") are generated by *in vitro* transcription using T7 RNA polymerase and the DIG northern starter kit (Roche). The DNA template of the required riboprobe was prepared by PCR using the primers listed in Table 2.4. These templates include the sequence of the T7 RNA polymerase promoter (5'-GAATTAATACGACTCACTATA-3'). The PCR products were purified as already discussed and eluted in DEPC-treated water. Two-hundred ng of purified PCR product was used as template for the *in vitro* transcription. Labelling efficiency was tested by spotting 1 µl of riboprobe on a nylon membrane and developed according to the manufacturer's instructions. The riboprobes were then stored at -20°C. Total RNA from the required conditions was tested by electrophoresis on a 7% acrylamide, 8.3 M urea, 1x TBE gel. Either 5 or 10 µg of total RNA was mixed with 2x RNA loading dye and 5 µl of RiboRuler Low Range RNA Ladder (Fisher) was also mixed with 2x RNA loading dye. All samples were then heated at 65°C for 10 minutes and cooled on ice before gel loading. The gel was run in autoclaved 1x TBE at 100V for 2 hours at room temperature. The RNA is then blotted onto a positively charged nylon membrane (Roche)

in ice-cold 1x TBE using the Biometra Fastblot B43 semi-dry blotting apparatus at 125 mA for 30 min at 10°C. Then the RNA was UV crosslinked using a Peqlab UV-crosslinker at 120 mJ. The ladder was cut from the membrane and stained in methylene blue solution (2% w/v) for 5 minutes before being destained with dH₂O and stored for imaging. The membrane was hybridised in the ProBlot12 hybridization oven using the rotating function at 62°C for 1 hour in pre-warmed DIG easy Hyb buffer (Merck). Five µl of the riboprobe of interest was boiled at 95°C for 5 min before a 5 min incubation on ice, then it was added to the membrane in the Hybridisation buffer. This was incubated overnight at 62°C. The following day membranes were washed twice for 10 min each using stringency washing buffer I which had been prewarmed to 62°C, this was followed by two washes for 30 min each in stringency washing buffer II also preheated to 62°C. The membrane was then incubated in 1x blocking buffer at room temperature for 2 h, subsequently the membrane was incubated in a 1:10,000 dilution of the Anti-digoxigenin AP Fab fragments in 1x blocking buffer for 30 min. Following this, the membrane was washed twice for 10 min each using northern wash buffer. Following a 5 min equilibration in detection buffer. The membrane was then placed in a plastic sleeve with the ladder cut out from earlier, it was next covered with CDP-star (Applied Biosystems). Chemiluminescence was detected using the ImageQuant™ LAS 4000 (GE Healthcare Life Sciences). Membranes were stripped by rinsing twice in DEPC treated water for 5 minutes. The membrane is incubated twice for 60 minutes each in stripping buffer in the hybridisation oven at 72°C. The membrane is rinsed twice with 2x SSC buffer for 5 min each at room temperature. The membrane was then re-probed with a 1:100 diluted riboprobe detecting 5S rRNA to determine that RNA samples had been loaded equivalently. Buffers and solutions are described in Table 2.10.

Whole cell lysates for western blotting.

An overnight of the culture was made as described previously for the strain being investigated. Twenty-five µl of this culture was then used to inoculate 25 ml of L broth in a 250 ml Erlenmeyer flask, which was incubated to the growth phase required and with the correct antibiotics where appropriate. Once the desired conditions were fulfilled, a sample was collected and set to an OD₆₀₀ of 0.01 in an Eppendorf tube. Next the sample was spun down at 3,200 x g for 5 min at 4°C and the supernatant was discarded. The pellet washed in 1 ml PBS and the sample was resuspended in 25 µl of PBS and 25 µl of 2 x Lämmli buffer (0.5 M Tris- HCl pH 6.8, 15% (w/v) SDS, 80% (v/v) glycerol, 1% (w/v) bromophenol blue, 200 mM dithiothreitol (DTT)). The samples were boiled for 10 minutes at 100°C and centrifuged at 21,000 x g for 1 min. The samples were then stored at -20°C.

SDS Polyacrylamide Gel Electrophoresis (PAGE) and western blotting.

Protein samples were separated by SDS PAGE (12.5% (v/v) acrylamide). The Polyacrylamide gel was prepared in two layers: the separating and stacking layers were made according to Table 2.8. Fifteen μl of whole cell lysate (approximately 0.03 OD₆₀₀) sample was loaded and 5 μl of EZ-Run™ Prestained Rec Protein Ladder was used as a size comparison. The gel was run submerged in 1x SDS running buffer at 100 V for ca. 2.5 h. The Proteins were then transferred to a nitrocellulose membrane by submerging the gel and membrane in blotting buffer 25 mM Tris, 192 mM glycine surrounded by 3x Whatman paper on either side an electric charge of 125 mA for 2 h. After the transfer, the membrane was briefly soaked in Ponceau Stain to ensure a successful transfer occurred and to assess equal loading of protein samples. The membrane was incubated with 1x blocking buffer for 3 h. The membrane was then washed twice for 10 min each using antibody wash buffer (0.5% (w/v) skim milk powder, 0.9% (w/v) NaCl, 0.1% (v/v) Tween 20, 10 mM Tris/HCl pH7.5). The membrane was probed overnight at 4°C with monoclonal mouse anti-FLAG (1:10,000, Merck) and monoclonal mouse anti-DnaK antibody (1:3,000, Enzo Life Sciences) diluted in antibody wash solution. The membrane was washed 4 times (10 min each) using antibody wash solution before probing for 1.5 h at room temperature with the secondary antibody (monoclonal rabbit antibody anti-mouse IgG (H+L) horseradish peroxidase (HRP), (1:10,000, Millipore)) diluted in antibody wash solution. The membrane was washed three times (10 min each wash) with PBS-T (PBS, 0.05% (v/v) Tween 20). The membrane was then put in a plastic membrane to prepare for imaging. Chemiluminescent signal was visualized using the ImageQuant LAS4000 (GE) with ECL chemiluminescent HRP substrate containing luminol and peroxide in a 1:1 ratio. Buffers and solutions are described in Table 2.9

Table 2.5: Conditions for PCR.

Components	Standard PCR	Control
VeriFi	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	50 μl	50 μl

Table 2.6: Conditions for SliCE

Components	Standard	Control
10x Ligation buffer	1µl	1µl
Insert	100ng	0µl
SliCE extract	1µl	1µL
dH ₂ O	To 10µl total	8µl

Table 2.7: PCR cycle settings.

Step	Temperature	Time	No. of cycles
Denaturation	95°C	2 minutes	1x
Denaturation	95°C	15 seconds	35x
Annealing	Variable	30 seconds	
Extension	72°C	Variable	
Extension	72°C	5 minutes	1x

Table 2.8: SDS gel composition for PAGE.

12.5% Separating Gel 15ml		Stacking Gel 5ml	
Volume (ml)	Reagent	Volume (ml)	Reagent
4.69	Acrylamide:Bisacrylamide (40%)	0.825	Acrylamide: Bisacrylamide (40%)
3.75	1.5M Tris/HCl pH 8.8	0.6	0.5M Tris/HCl pH 6.8
0.1	SDS (15%)	0.05	SDS (15%)
1.42	Glycerol (87%)	3.47	dH ₂ O
4.875	dH ₂ O	0.005	TEMED
0.015	TEMED	0.05	APS (10%)
0.15	APS (10%)		

Table 2.9: Solutions for western blotting.

Name	Reagent	Concentration
SDS run buffer 1x	Tris	25mM
	Glycine	192mM
	SDS	0.1% (v/v)
	H ₂ O	
Blotting buffer 1x	Tris	25mM
	Glycine	192mM
	H ₂ O	
Blocking buffer 1x	Skimmed milk powder	5% (w/v)
	NaCl	0.9% (w/v)
	Tris/HCl pH7.5	10mM
Antibody wash buffer1x	Skimmed milk powder	0.5% (w/v)
	NaCl	0.9% (w/v)
	Tween 20	0.1% (v/v)
	Tris/HCl pH7.5	10mM
PBS-T	Tween 20	0.05% (v/v)
	PBS	

Table 2.10: Solutions for northern blotting.

Name	Reagent	Concentration
2x RNA loading dye	Xylene cyanol FF	0.25% (w/v)
	Bromophenol blue	0.25% (w/v)
	EDTA pH8.0	18 mM
	SDS	0.025% (w/v)
	Formamide	95% (v/v)
20x SSC	NaCl	3 M
	Sodium citrate	0.3 M
	H ₂ O	
Stringency wash I	SSC	2x
	SDS	0.1%(w/v)
	H ₂ O	

Stringency wash II	SSC	0.5x
	SDS	0.1% (w/v)
	H ₂ O	
Maleic acid buffer pH 7.5	Maleic acid	0.1 M
	NaCl	0.15 M
Northern wash buffer	Maleic acid buffer	1x
	Tween-20	0.3% (v/v)
1x Blocking buffer	Casein blocking solution (Roche)	0.1x
	Maleic acid buffer	0.9x
Detection buffer pH 9.5	Tris-HCl	0.1 M
	NaCl	0.1 M
Stripping buffer	Formamide	50% (v/v)
	Tris-HCl (pH7.5)	50 mM
	SDS	5% (w/v)
	<u>H₂O</u>	

RESULTS

Sequence comparison of SigAB with other well-studied alternative sigma factors.

A previous study had identified ABUW_RS048545 (now referred to as SigAB) as an RpoE homologue (Casella et al. 2017). To test this prediction, a multiple sequence alignment was performed comparing SigAB against other ECF sigma factors, primarily RpoE homologues, in other Gram-negative species, as well as the ECF sigma factor SigW from *B. subtilis*. The percent identity matrix (amino acids) identified that SigW as the closest match with 20.43% and found that AlgU had the lowest percent identity with 17.89% (Table 3.1 and Table 3.2). In Figure 3.1, the two highlighted boxes represent the σ 2.2 and σ 4.2 subregions, which identify SigAB as an ECF sigma factor. The low sequence similarity indicates that, although SigAB is a sigma factor, it is not closely related to the other sigma factors that were used for comparison, especially RpoE from *E. coli* and *S. enterica*.

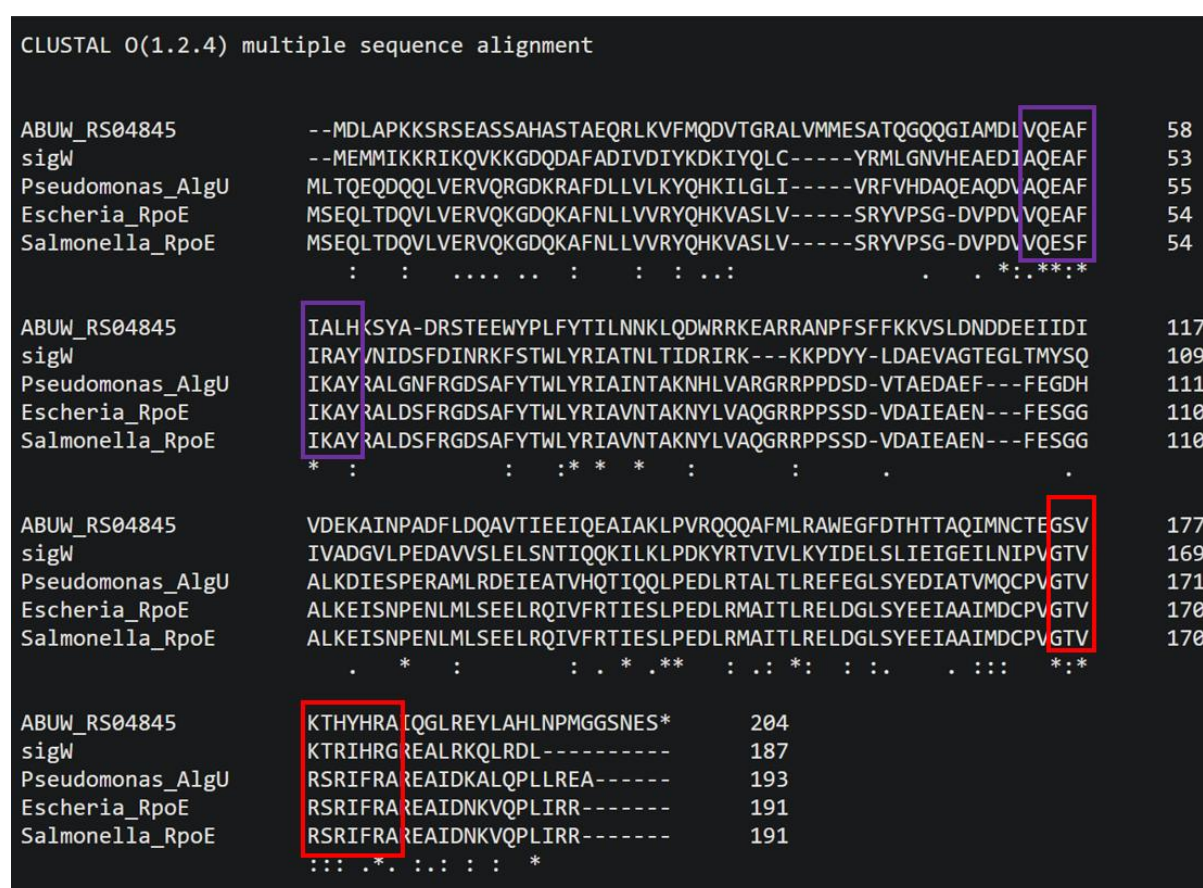


Fig 3.1: Multiple sequence alignment of ABUW_RS04845 (SigAB) against other ECF sigma factors using CLUSTAL Omega. Amino acid sequences from SigAB (*A. baumannii*), SigW (*B. subtilis*), AlgU (*P. aeruginosa*) and RpoE (*E. coli* and *S. enterica*) were compared. The purple box indicates the subregion 2.2 and the red box indicates subregion 4.2. A variety of sigma factors were compared, mainly RpoE homologues.

Table 3.1: Amino acid sequence identity matrix generated with CLUSTAL Omega.

	SigAB	SigW	AlgU	RpoE <i>E. coli</i>	RpoE <i>S. enterica</i>
SigAB	100%	20.43%	17.89%	19.15%	18.62%
SigW	20.43%	100%	36.41%	35.52%	34.97%
AlgU	17.89%	36.41%	100%	65.97%	99.48%
RpoE <i>E. coli</i>	19.15%	35.52%	65.97%	100%	65.45%
RpoE <i>S. enterica</i>	18.62%	34.97%	65.45%	99.48%	100%

Table 3.2: Amino acid percent identity with SigAB using CLUSTAL Omega.

Sigma Factor	Percent Identity
SigW <i>B. subtilis</i>	20.43%
AlgU <i>P. aeruginosa</i>	17.89%
RpoE <i>E. coli</i>	19.15%
RpoE <i>S. enterica</i>	18.62%

Growth Experiments.

Sigma factors have been extensively implicated as regulators of stress responses. When SigAB was first identified, it was predicted to be an RpoE homologue in *A. baumannii* (Casella et al. 2017). To investigate whether deletion of $\Delta sigAB$ affected growth in rich medium and when exposed to a number of stress conditions, growth experiments were carried out (Figure 3.2). As sigma factors have also been shown to play a role in regulating diverse metabolic pathways, it was also tested how the $\Delta sigAB$ deletion mutants growth would compare to the wild-type strain in different media (Figure 3.2).

Table 3.3: Description of growth conditions.

Condition name	Medium composition
EtOH	L-broth with 1.25%(v/v) ethanol
EDTA	L-broth containing 0.02mM EDTA pH 8.0
NaCl 200 mM	L-broth containing 200 mM NaCl
NaCl 500 mM	L-broth containing 500 mM NaCl
SDS	L-broth containing 0.03% (v/v) SDS
Triton	L-broth containing 0.03%(v/v) Triton-X

Polymyxin B	L-broth containing 100 µg/l polymyxin B
Chloramphenicol	L-broth containing 50 µg/ml chloramphenicol
TSB-D	TSB, 8.3% (w/v) chelex, 10 mM nitrilotriacetic acid pH 7.0
Dipyridyl	L-broth containing 0.02 mM 2,2'-dipyridyl

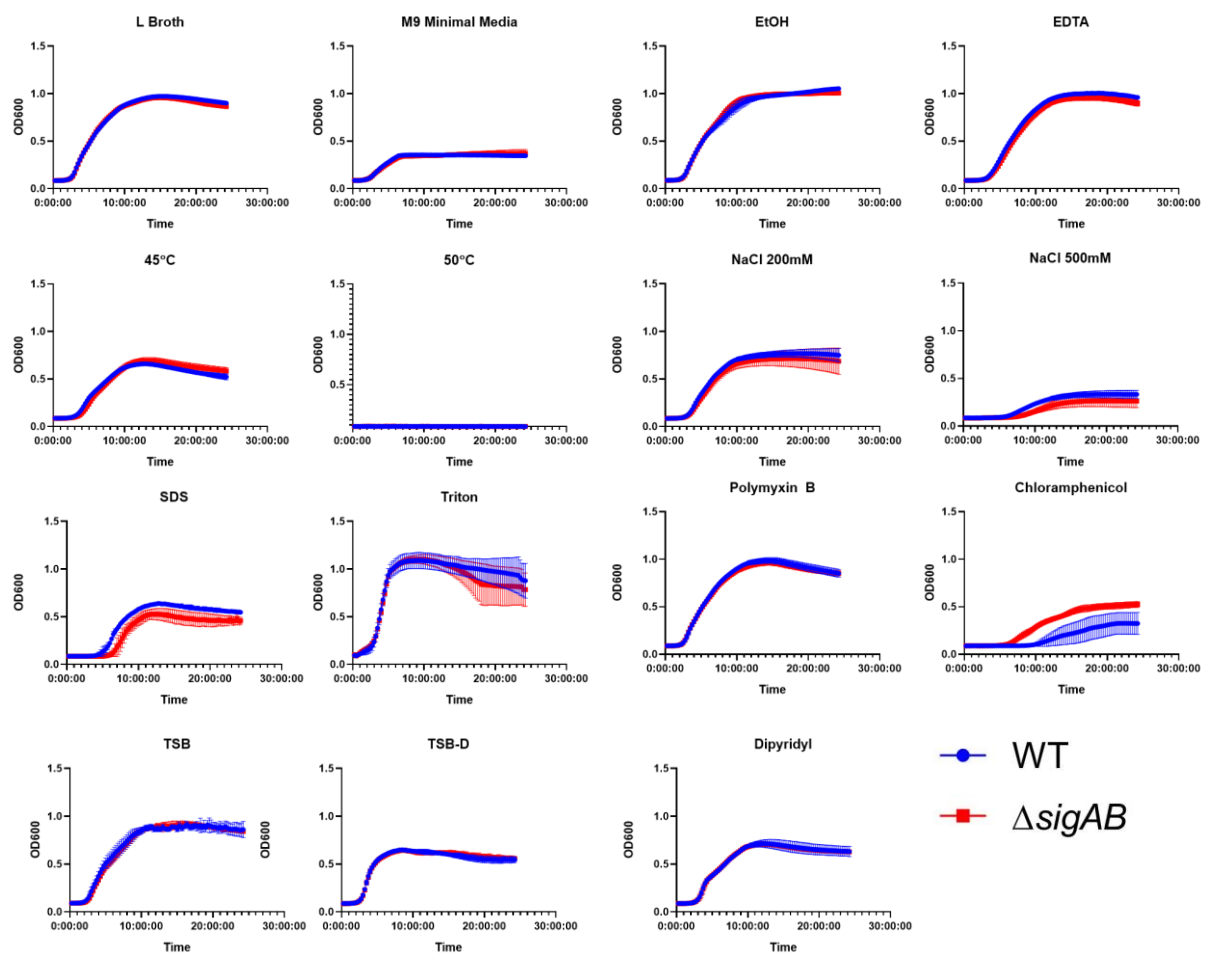


Figure 3.2. Growth experiments carried out using *A. baumannii* AB5075 (WT) and AB5075 $\Delta sigAB$ across a variety of conditions. Experiments were carried out using three biological replicates and a minimum of 3 technical replicates for each biological replicate in 96 well plates on a Synergy HTX multimode reader (BioTek). Growth conditions are depicted in Table 3.3. values were calculated using an unpaired T test by comparing means of the area under the curve (AUC)

The growth of the $\Delta sigAB$ mutant was compared to the wild-type strain in rich media TSB and L-broth (Figure 3.2). In these media, the mutant grew almost identically to the wildtype showing no apparent loss of fitness. When grown in nutrient poor media (M9 minimal media supplemented with pyruvate as the sole carbon source), there was also no difference between the wildtype and the deletion mutant. Due to the role that ECF sigma factors play in mediating responses to stress conditions, multiple stress conditions were tested.

As SigAB was initially described as an RpoE homologue, therefore growth in the presence of polymyxin B (100 $\mu\text{g/L}$) in L-broth was tested. Polymyxin B has been established to induce the envelope stress response in other bacteria such as *S. enterica* (Humphreys et al. 1999). However, as seen in Figure 3.2, there was no significant growth defect in the $\Delta sigAB$ strain compared to the wildtype. Following this result, as well as the sequence alignment, it appeared that SigAB was unlikely to be an RpoE homologue and may not have been involved in regulating the envelope stress response. Therefore, other stress conditions were tested to see if the deletion of *sigAB* is involved a response to other stress conditions.

The maximum temperature *A. baumannii* can grow in is 45°C, which is higher than for other *Acinetobacter spp.* (Antunes et al. 2011). Two temperatures were tested using nutrient rich L-broth (45°C and 50°C) investigating whether SigAB might be involved in mediating heat stress response. No difference in growth was observed, indicating that the ability of *A. baumannii* $\Delta sigAB$ to grow at higher temperature was not altered compared to the wild-type strain.

To test if the osmotic stress response is controlled by SigAB, the growth of the mutant was tested against the wildtype in a variety of concentrations of NaCl in L-broth (Zeidler et al. 2017). There was no significant defect in growth for 200 mM of added NaCl. A growth defect in the mutant when compared to the wildtype AB5075 was observed at 500mM NaCl, this defect was found to be significant ($P < 0.0001$).

The addition of ethanol was shown to induce the expression of virulence factors in *A. baumannii* (Camarena et al. 2010). However, growth in the presence of ethanol (1.25%) did not result in a difference in growth between wild-type and $\Delta sigAB$ mutant strains. The addition of the chelator agent EDTA (0.25 mM) also showed no significant difference in growth between the wild-type and deletion mutant.

The deletion mutant and the wildtype strain were exposed to further stressors including iron limiting conditions (addition of 0.2 mM 2,2'-dipyridyl in L-broth and iron-limited TBS-D medium), detergents SDS and Triton-X and the antibiotic chloramphenicol. There was no growth difference upon addition of 2,2'-dipyridyl or in TBS-D between wild-type and mutant strains. In the presences of SDS and Triton-X, the cells in the Triton-X condition appeared to show a slight growth defect as LSP ($P = 0.0169$) and in the SDS condition a stronger impaired growth in the deletion mutant ($P < 0.0001$). In the chloramphenicol

condition, surprisingly, the mutant $\Delta sigAB$ strain showed a significant increase ($P < 0.0001$) in fitness compared to the wildtype strain.

The impact of SigAB on biofilm formation of *A. baumannii* AB5075.

The ability of *A. baumannii* to form a biofilm is crucial to survive in the hospital settings (Howard et al. 2012). Alternative sigma factors such as SigB of *Bacillus subtilis* have also been implicated in regulating biofilm formation and maturation (Bartolini et al. 2019). Consequently, the ability of the *sigAB* deletion to form a biofilm was compared to the AB5075 wild-type strain in either L-broth or L-broth supplemented with 2% (w/v) glucose at 37°C (Figure 3.3). There was no statistically significant difference between the wild-type strain and the deletion mutant (Figure 3.3).

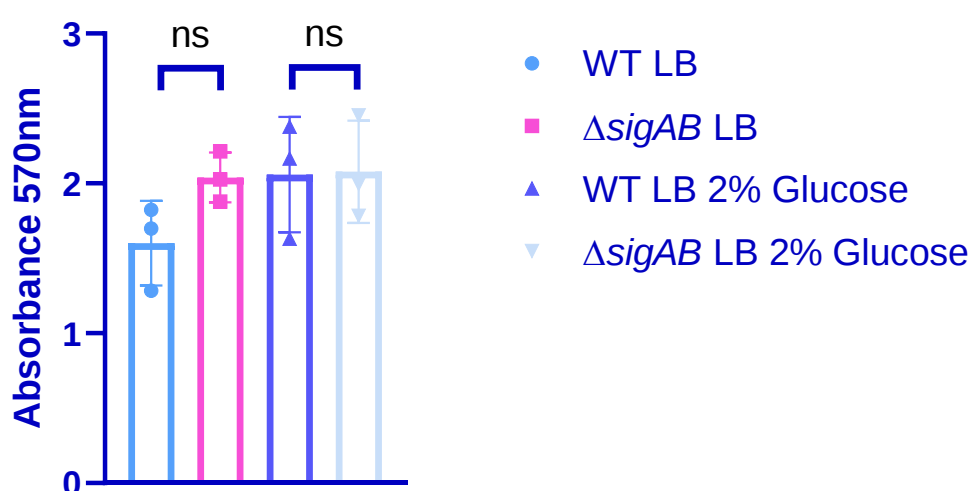


Fig 3.3: Biofilm formation analysis of wild-type AB5075 and AB5075 $\Delta sigAB$. Biofilm formation assay was assessed in L-broth and L-broth with 2% glucose after 24 h of static incubation at 37°C. Statistical significance was determined by Student's T tests (ns = $p > 0.05$). An unpaired T-test gave a P value = 0.2472 giving no significant difference between the wild-type and $\Delta sigAB$ in L-broth. The error bars are showing the standard deviation for each sample. 5 technical replicates were obtained.

Table 3.4: Environmental conditions RNA was isolated from (Bakheet 2024).

Abbreviation	Condition	Growth Set-up
EEP	Early exponential phase	L-broth, OD ₆₀₀ 0.1
MEP	Mid exponential phase	L-broth, OD ₆₀₀ 0.3
LEP	Late exponential phase	L-broth, OD ₆₀₀ 1

ESP	Early stationary phase	L-broth, OD ₆₀₀ 2
LSP	Late stationary phase	L-broth, 16 h overnight
Cm	Chloramphenicol shock	L-broth, OD ₆₀₀ 0.3, then chloramphenicol added (32 µg/ml) for 15 min
Tet	Tetracycline shock	L-broth OD ₆₀₀ 0.3, then tetracycline added (1 µg/ml) for 15 min
CS	Cold shock	L-broth, OD ₆₀₀ 0.3 at 37°C, then 15 min at 22°C
Low Fe	Iron limitation	L-broth, OD ₆₀₀ 0.3, then 0.22 mM 2,2'-dipyridyl added for 15 min
NaCl	Osmotic shock	L-broth, OD ₆₀₀ 0.3 then NaCl added (300 mM) for 15 min
22C	Ambient temperature	L-broth, OD ₆₀₀ 0.3 at 22°C
TS	Temperature shift	L-broth, OD ₆₀₀ 0.3 at 22°C then 15 minutes at 37°C

Table 3.5: Transcripts per million for genes of interest across the project (Bakheet 2024).

Gene name	EEP	MEP	LEP	ESP	LSP	cm	Tet	CS	Low Fe	NaCl	22C	TS
<i>sigAB</i>	209	185	514	706	2,954	130	91	61	193	182	173	707
<i>sRNA90</i>	432	318	1,553	1,456	8,925	2,604	274	577	358	370	466	1,591
<i>ABUW_RS18870</i>	43	51	745	285	124	389	747	96	172	144	1,398	940
<i>sRNA106</i>	10	10	10	10	15	12	10	10	10	10	10	10

Analysis of SigAB Expression in *A. baumannii* AB5075.

To measure protein abundance of SigAB, the protein was FLAG-tagged at the C-terminus. Transcriptomic data showed that *sigAB* was expressed across the different growth stages in L-broth with increasing level of expression towards late stationary phase this is seen in Tables 3.4 and 3.5, however, it was important to validate this data experimentally (Bakheet 2024). Whole cell lysates were prepared from different growth conditions (MEP, ESP and LSP) and the protein abundance was measured by western blotting. Figure 3.4 shows a band at the expected size of 26.2 kDa for SigAB in the LSP condition. This validates the RNA-seq data generated previously (Bakheet 2024).

Given that SigAB was predicted to be a sigma factor and possibly involved in regulating a large number of genes, the large-scale changes in protein abundance were assessed by SDS PAGE when overexpressing SigAB from a plasmid. It was expected that there might be a large difference in protein abundance on a global protein level. However, Figure 3.6 shows that there is no obvious difference in global protein abundance between the induced and uninduced samples. Either the pVRL2Z system was not functioning as expected despite correct plasmid sequence as confirmed by Sanger sequencing, or that the system is working as intended, however the quantity of protein produced was insufficient. Overexpression did not appear to be very strong (or there is no expression at all), as a band at the expected size for SigAB was not apparent on the protein gel.

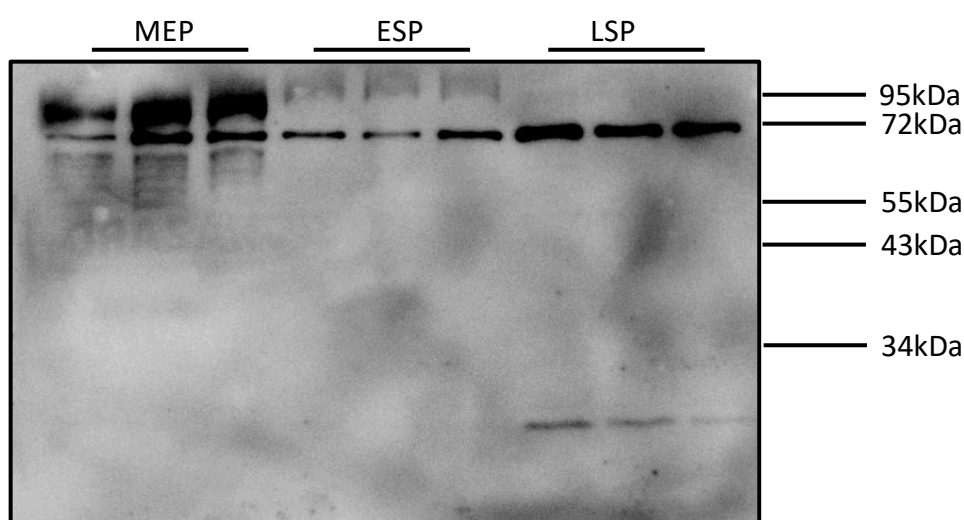


Fig 3.4: Protein abundance of *A. baumannii* SigAB-3xFLAG in different stages of growth. *A. baumannii* AB5075 *sigAB::3xFLAG* was grown to a variety of growth phases in L-broth at 37°C (MEP: OD₆₀₀ = 0.3, ESP: OD₆₀₀ = 2, LSP: Growth for 16 h. Whole cell lysates were separated by SDS PAGE and subjected to Western blotting using a anti-FLAG antibody. Fifteen µl of a culture set to OD₆₀₀ = 0.1 was loaded into each well. Three biological replicates are shown per condition. The expected molecular weight of SigAB-3xFLAG is 26.2 kDa. DnaK is used as a loading control (69.4 kDa).

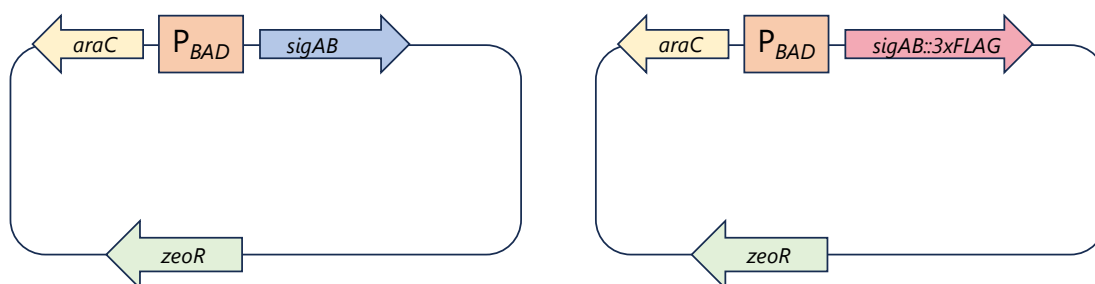


Figure 3.5: Plasmids for complementing $\Delta sigAB$. SigAb and SigAB:3XFLAG encoding genes were expressed from the L-arabinose-inducible pVRL2Z plasmid via the P_{BAD} promoter. The *zeoR* gene confers resistance gene to zeocin (250 μ g/ml). The *araC*-P_{BAD} regulatory region from *P. aeruginosa* which has an altered RBS that allows for arabinose dependent expression of the gene downstream of the promoter (Lucidi et al. 2018).

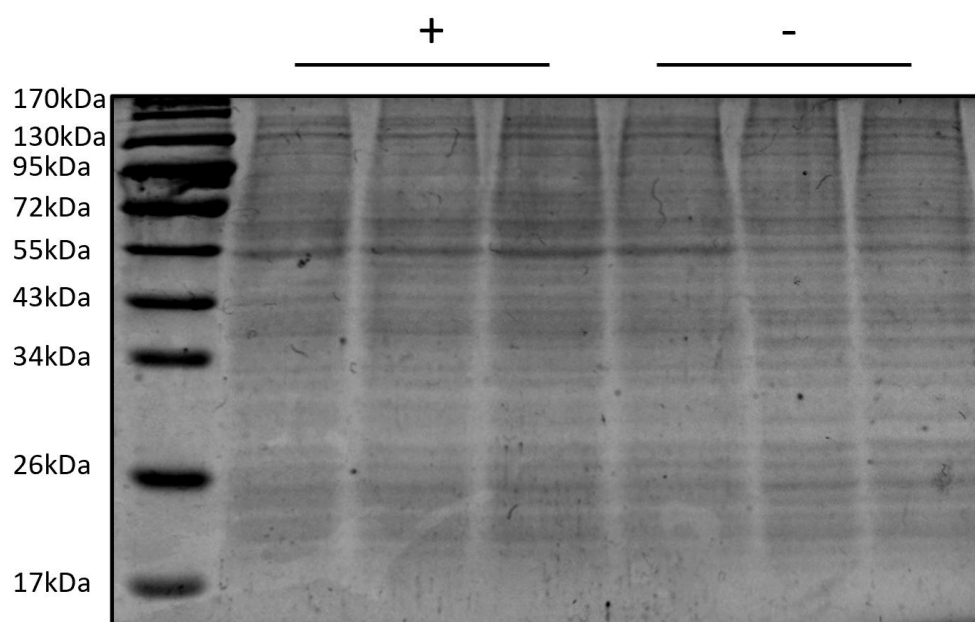


Figure 3.6: Protein analysis by SDS PAGE stained with coomassiw blue of *A. baumannii* AB5075 $\Delta sigAB$ pVRL2Z-*sigAB*. Cultures were grown to OD₆₀₀ = 0.3 in L-broth without NaCl. Upon reaching OD₆₀₀ = 0.3, expression of *sigAB* was induced by the addition of 100 mM L-arabinose (+). Non-induced samples served as a control (-). Whole cell lysates were loaded into each well (10 μ l of a culture set to OD₆₀₀ = 0.3). Three biological replicates for induced (+) and non-induced (-) are shown.

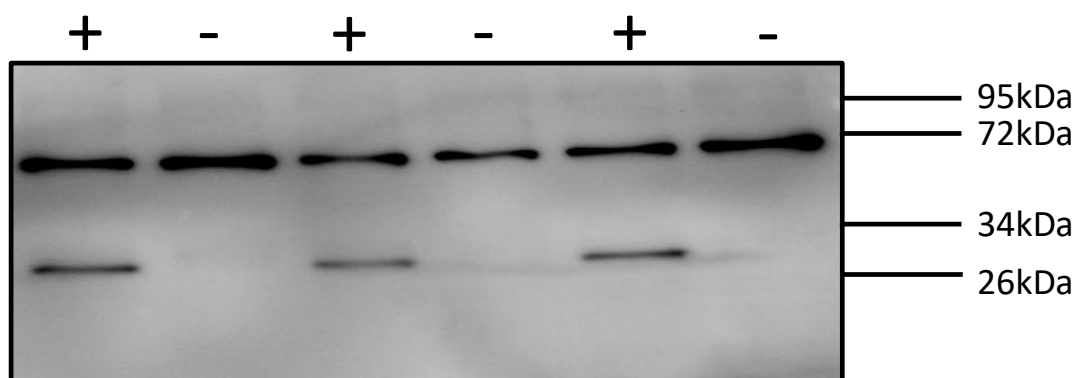


Figure 3.7: Protein abundance of SigAB-3xFLAG of *A. baumannii* AB5075 $\Delta sigAB$ when overexpressed from pVRL2Z-. Cultures were grown to $OD_{600} = 0.3$ at 37°C in L-broth without NaCl. Once the samples reached $OD_{600} = 0.3$, gene expression of *sigAB* was induced by the addition of 100 mM of L-arabinose for 1 h (+). Non-induced samples served as a control (-). Whole cell lysates were prepared and 15 μ l of whole cell lysate of a culture set to $OD_{600} = 0.1$ were loaded into each well. Three biological replicates for induced (+) and non-induced (-) are shown. DnaK is used as a loading control (69.4 kDa).

To test the level of expression of *sigAB* from the pVRL2Z plasmid, a plasmid-encoded FLAG-tagged version of pVRL2Z-*sigAB* (i.e., pVRL2Z-*sigAB*::3xFLAG) was constructed (Figure 3.5). This was done to see if any of the desired protein was expressed following the induction of the pBAD promoter by the addition of L-Arabinose. This was tested by Western Blot in Figure 3.7, this shows that the expression of *sigAB* from the pVRL2Z-inducible system is functional in AB5075. The addition of L-arabinose results in a marked increase in SigAB:3xFLAG protein abundance. The system does not show any basal expression in the non-induced samples. The DnaK bands also show that the samples of whole cell lysates were equally loaded.

Overexpression of SigAB might be detrimental for *A. baumannii* AB5075.

To complement the deletion of *sigAB*, a plasmid was constructed to express *sigAB* under the control of the P_{BAD} promoter (pVRL2Z-*sigAB*). The growth of *A. baumannii* AB5075 $\Delta sigAB$ in L-broth was monitored with different amounts of the inducer L-arabinose (0-100 mM, Figure 3.8). Only one experiment was conducted, but suggests that, at lower concentrations of L-arabinose (5 mM and 12.5 mM) the bacteria grow better than the strains without the addition of L-arabinose. Addition of higher concentrations of L-arabinose (25, 50 or 100 mM) resulted in poorer growth compared to the no-arabinose control. This suggests that overproduction SigAB in the $\Delta sigAB$ background that is deleterious for the cells. However, from this experiment it cannot be ruled out that the growth differences are caused by the different levels of added L-arabinose. To test whether the addition of arabinose has an effect on cell growth, a growth experiment was

carried out in a condition where it was previously seen that the $\Delta sigAB$ mutant has a growth defect compared to the wild-type strain (i.e., L-broth with 500 mM NaCl, Figure 3.2 and whether over-expression of *sigAB* can rescue the growth phenotype.

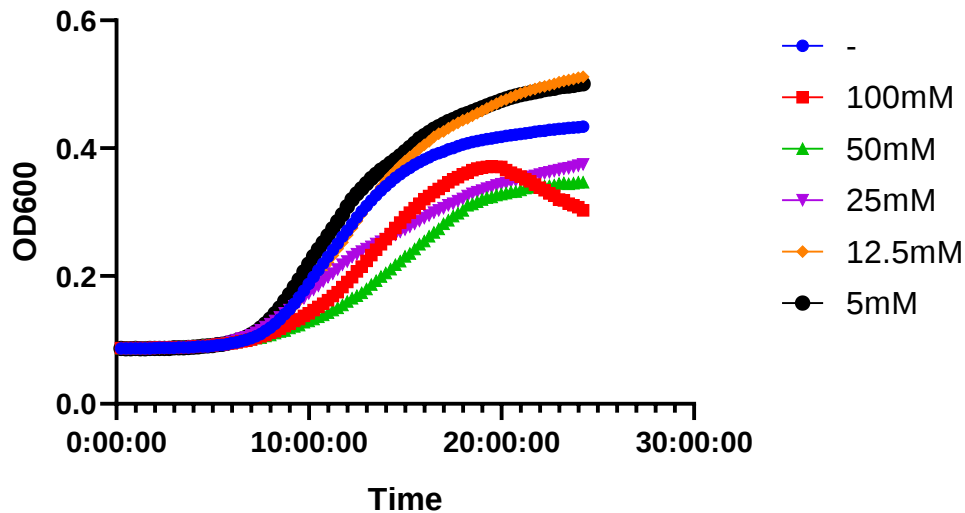


Figure 3.8: Growth experiment in L-broth with different amounts of L-arabinose of *A. baumannii* AB5075 $\Delta sigAB$ pVRL2Z-*sigAB*. Cells were grown in the presence of the indicated concentrations of L-arabinose. A control was set up (-) where no L-arabinose was added.

As seen in Figure 3.2, the *sigAB* mutant grows worse in L-broth in the presence of 500 mM NaCl. The growth experiment was repeated with wild-type and $\Delta sigAB$ mutant strains carrying the pVRL2Z “empty” plasmid or pVRL2Z-*sigAB* and without (Figure 3.9A) or with (Figure 3.9B) the addition of 100 mM L-arabinose. Without the addition of L-arabinose, wild-type and $\Delta sigAB$ mutant carrying the empty plasmid showed the expected result, where the $\Delta sigAB$ mutant has impaired growth. Addition of pVRL2Z-*sigAB* in the mutant strain partially rescued the growth defect. This could be due to a low basal expression of *sigAB* from the P_{BAD} promoter, which is not very tightly repressed (Hamrock et al. 2024). Therefore, even low levels of expression (a protein band is not visible on Figure 3.4) appears to be sufficient for partial rescue of the growth defect in the presence of 500 mM of NaCl. Conversely, strong overexpression of *sigAB* resulted in a pronounced growth defect compared to wild-type and $\Delta sigAB$ mutant strains (Figure 3.9B). This shows that it is not the addition of L-arabinose that is causing the growth defect but rather the overexpression of *sigAB* and that mild expression of *sigAB* can phenotypically compensate for the chromosomal deletion.

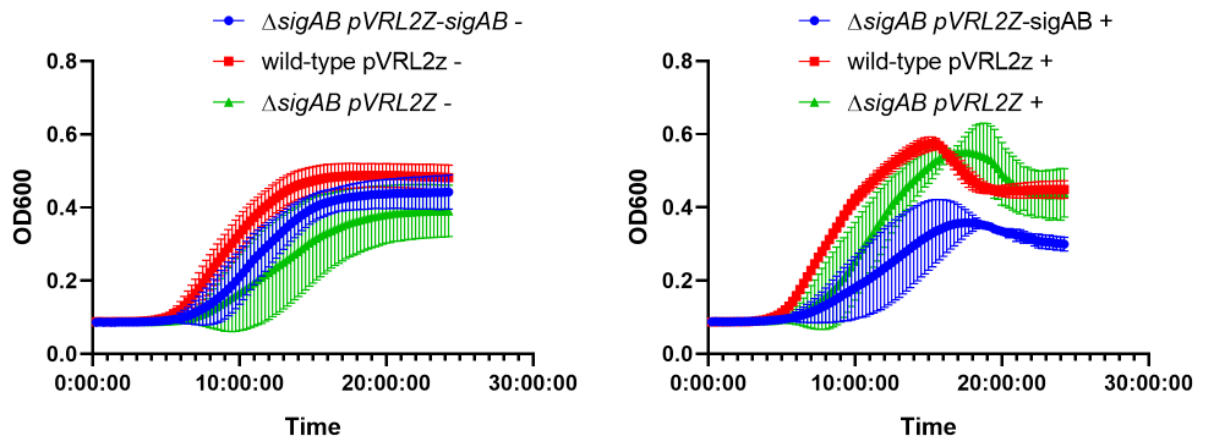


Figure 3.9: Growth experiment of *A. baumannii* AB5075 WT pVRL2Z, $\Delta sigAB$ pVRL2Z and $\Delta sigAB$ pVRL2Z-sigAB in L-broth with 500mM NaCl. Media was supplemented with 250 μ g/ml zeocin. (A) Growth with (-) L-arabinose. (B) Prior to the start of the growth experiment, 100 mM L-arabinose was added (+). The error bars depict the standard deviation of three biological replicates.

Transcriptomic analysis of the *A. baumannii* AB5075 $\Delta sigAB$ mutant.

To investigate which genes SigAB regulates, a transcriptomic experiment was carried out using RNA-seq comparing the transcriptomes of AB5075 wild-type and $\Delta sigAB$ mutant strains. Cells were grown to late stationary phase because this is the growth phase where *sigAB* was most highly expressed as can be seen in Figure 3.4. The RNA-seq data identified transcripts from a total of 3190 genes 142 genes were more than 2.8-fold up-regulated and 163 genes were 2.8-fold down-regulated in *A. baumannii* AB5075 $\Delta sigAB$ vs wild-type AB5075. This gives a total of 4.45% of the transcriptome being up-regulated as opposed to 5.1% being down-regulated (~10% of the transcriptome is affected by the deletion of *sigAB*) indicating that the sigma factor either directly or indirectly controls a large set of genes at LSP.

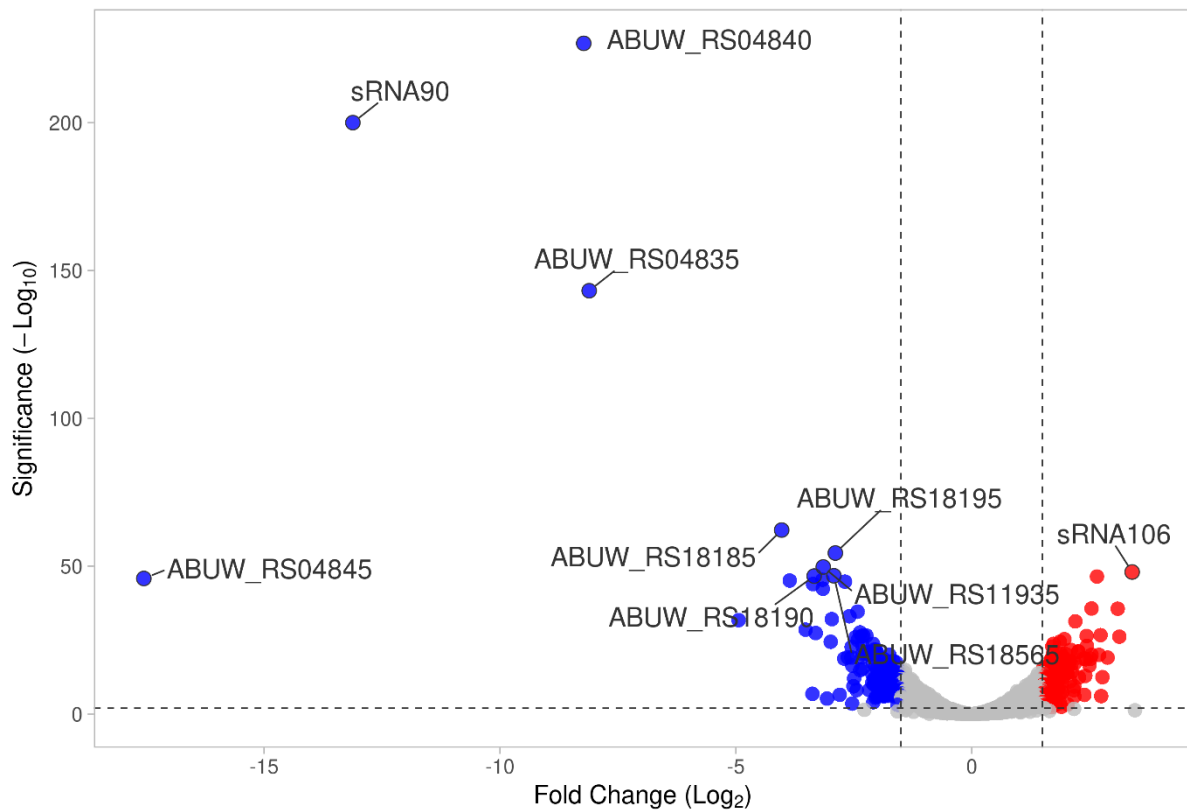


Figure 3.10: Volcano plot showing genes up- and downregulated at LSP in *A. baumannii* AB5075 Δ *sigAB* vs. wild-type AB5075 (x-axis) and statistical analysis (y-axis). The dashed vertical lines indicate two-fold up- and down-regulated cutoffs. The dashed horizontal line is set to an adjusted P value (P_{adj}) of 0.05. The blue dots indicate genes down-regulated in the mutant compared to the wild-type strain more than 2-fold and a $P_{adj} < 0.05$. The red dots indicate genes up-regulated more than 2-fold in the mutant compared to the wild-type strain and a $P_{adj} < 0.05$.

Analysis of differentially expressed gene sets.

To investigate biological functions of differentially expressed genes, the programme FUNAGE-Pro was used to identify if amongst the significantly up- or down-regulated genes there were any enriched sets of functionally related genes (de Jong et al. 2022). Genes contributing to ATP synthase activity made up almost 5% of the significantly down-regulated genes in the Δ *sigAB* mutant (Table 3.6). These genes are all in the same operon starting at *ABUW_RS18200* which encodes for ATP synthase subunit I, however this gene does not appear to be significantly downregulated just 1.3 times downregulated. In fact, *ABUW_RS18200* is the only gene in the operon that isn't significantly downregulated. The predicted binding site of SigAB was not found upstream of any of these genes TSS (Bacon et al. 2024). Table 3.7 shows another enriched group of genes all found in the same operon. This operon starts with *ABUW_RS00380* (*hutU*), all of these genes are implicated in the catabolic process of L-histidine. The operon was again examined for the binding motif identified in previous work but no matches were found (Bacon et al. 2024). There were only very few genes of similar function enriched in the significant upregulated genes, however, no full pathway stood out as being up-regulated.

Table 3.6: Downregulated genes involved with ATP synthase activity in *A. baumannii* 5075 $\Delta sigAB$ mutant compared to the wildtype at LSP.

Annotation	Product	log2fold change
ABUW_RS18160	FOF1 ATP synthase subunit epsilon	-2.24
ABUW_RS18165	FOF1 ATP synthase subunit beta	-2.33
ABUW_RS18170	FOF1 STP synthase subunit gamma	-2.41
ABUW_RS18175	FOF1 ATP synthase subunit alpha	-2.03
ABUW_RS18180	FOF1 ATP synthase subunit delta	-2.37
ABUW_RS18185	FOF1 ATP synthase subunit B	-4.03
ABUW_RS18190	FOF1 ATP synthase subunit C	-3.34
ABUW_RS18195	FOF1 ATP synthase subunit A	-2.89

Table 3.7: Downregulated genes involved with histidine catabolism in *A. baumannii* 5075 $\Delta sigAB$ mutant compared to the wildtype at LSP.

Annotation	Product	log2fold change
ABUW_RS00380	urocanate hydratase	-3.16
ABUW_RS00385	histidine ammonia-lyase	-2.22
ABUW_RS00390	amino acid permease	-2.55
ABUW_RS00395	imidazolonepropionase	-2.53
ABUW_RS00400	formimidoylglutamase	-1.67

Table 3.8: Down-regulated genes in the *A. baumannii* 5075 $\Delta sigAB$ mutant compared to the wildtype at LSP.

log2FoldChange	Annotation	Product
-17.55	ABUW_RS04845	RNA polymerase sigma factor
-13.12	sRNA90	
-8.22	ABUW_RS04840	hypothetical protein
-8.11	ABUW_RS04835	DUF3106 domain-containing protein
-4.94	ABUW_RS20020	TniB family NTP-binding protein
-4.03	ABUW_RS18185	FOF1 ATP synthase subunit B
-3.86	ABUW_RS19255	GNAT family N-acetyltransferase
-3.52	ABUW_RS01870	DEAD/DEAH box helicase
-3.38	ABUW_RS12675	hypothetical protein
-3.36	ABUW_RS11930	isovaleryl-CoA dehydrogenase
-3.34	ABUW_RS18190	FOF1 ATP synthase subunit C
-3.31	ABUW_RS19260	sulfonamide-resistant dihydropteroate synthase Sul1
-3.16	ABUW_RS00995	amino acid permease
-3.16	ABUW_RS00380	urocanate hydratase
-3.15	ABUW_RS11935	methylcrotonoyl-CoA carboxylase
-3.07	ABUW_RS08150	chlorhexidine efflux PACE transporter AceI
-2.99	ABUW_RS19270	trimethoprim-resistant dihydrofolate reductase DfrA7
-2.96	ABUW_RS01495	pilin
-2.92	ABUW_RS18565	L-lactate permease
-2.89	ABUW_RS18195	FOF1 ATP synthase subunit A
-2.80	ABUW_RS19275	aminoglycoside N-acetyltransferase AAC(6')-Ib3
-2.70	ABUW_RS02620	tRNA guanosine(34) transglycosylase Tgt
-2.69	ABUW_RS15580	FAD-dependent tricarballylate dehydrogenase TcuA
-2.63	ABUW_RS19265	quaternary ammonium compound efflux SMR transporter QacE delta 1
-2.59	ABUW_RS01005	4-aminobutyrate--2-oxoglutarate transaminase
-2.55	ABUW_RS00390	amino acid permease

-2.54	ABUW_RS12665	divalent metal cation transporter
-2.53	sRNA61	
-2.53	ABUW_RS00395	imidazolonepropionase
-2.51	ABUW_RS19295	APH(6)-I family aminoglycoside O-phosphotransferase
-2.49	ABUW_RS10350	alpha-ketoacid dehydrogenase subunit beta
-2.46	ABUW_RS11940	enoyl-CoA hydratase/isomerase family protein
-2.44	ABUW_RS19355	hypothetical protein
-2.42	ABUW_RS08740	cytochrome bd oxidase subunit I
-2.41	ABUW_RS18170	F0F1 ATP synthase subunit gamma
-2.37	ABUW_RS18180	F0F1 ATP synthase subunit delta
-2.36	ABUW_RS17200	Na ⁺ /H ⁺ antiporter subunit C
-2.33	ABUW_RS18165	F0F1 ATP synthase subunit beta
-2.32	ABUW_RS10585	acetyltransferase
-2.32	ABUW_RS17645	phosphomethylpyrimidine synthase ThiC
-2.32	ABUW_RS04480	phosphoenolpyruvate carboxykinase (GTP)
-2.31	ABUW_RS16495	phosphogluconate dehydratase
-2.30	ABUW_RS01265	RNA-binding transcriptional accessory protein
-2.28	ABUW_RS07925	iron-containing alcohol dehydrogenase
-2.24	ABUW_RS18160	F0F1 ATP synthase subunit epsilon
-2.23	ABUW_RS02105	30S ribosomal protein S13
-2.22	ABUW_RS00385	histidine ammonia-lyase
-2.17	ABUW_RS19010	membrane protein insertion efficiency factor YidD
-2.12	ABUW_RS01250	acetyl-CoA hydrolase/transferase family protein
-2.11	ABUW_RS12330	phenylacetic acid degradation bifunctional protein PaaZ
-2.10	ABUW_RS12650	5-oxoprolinase/urea amidolyase family protein
-2.10	ABUW_RS15950	50S ribosomal protein L20
-2.09	ABUW_RS16475	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
-2.09	sRNA60	
-2.08	ABUW_RS05720	acinetobactin non-ribosomal peptide synthetase subunit BasB
-2.08	ABUW_RS13735	ribonuclease T
-2.07	ABUW_RS12825	type I secretion system permease/ATPase
-2.07	ABUW_RS16425	23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN
-2.06	ABUW_RS15585	tricarballoylate utilization 4Fe-4S protein TcuB
-2.06	ABUW_RS10355	thiamine pyrophosphate-dependent dehydrogenase E1 component subunit alpha
-2.05	ABUW_RS02110	30S ribosomal protein S11
-2.04	ABUW_RS01400	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
-2.04	ABUW_RS05770	histidine decarboxylase
-2.04	ABUW_RS08745	hypothetical protein
-2.03	ABUW_RS18175	F0F1 ATP synthase subunit alpha
-2.02	ABUW_RS02115	30S ribosomal protein S4
-2.02	ABUW_RS05765	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF
-2.01	ABUW_RS17835	signal peptidase II
-2.01	ABUW_RS16490	bifunctional 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxy-phosphogluconate aldolase
-2.00	ABUW_RS19280	class A extended-spectrum beta-lactamase GES-11
-1.98	ABUW_RS10525	hypothetical protein
-1.97	ABUW_RS04970	7-carboxy-7-deazaguanine synthase QueE
-1.95	ABUW_RS15525	DUF1852 domain-containing protein
-1.94	ABUW_RS01730	succinylglutamate-semialdehyde dehydrogenase
-1.93	ABUW_RS15410	NADH-quinone oxidoreductase subunit NuoF
-1.93	ABUW_RS04385	glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit
-1.92	sRNA6	
-1.90	ABUW_RS03530	rod shape-determining protein MreD
-1.90	ABUW_RS11945	acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha
-1.89	ABUW_RS16555	homoserine O-acetyltransferase
-1.87	ABUW_RS16105	DMT family transporter
-1.87	ABUW_RS04135	multidrug efflux RND transporter periplasmic adaptor subunit Adel
-1.87	ABUW_RS03125	patatin family protein
-1.87	ABUW_RS00920	BCCT family transporter
-1.86	ABUW_RS03525	rod shape-determining protein MreC
-1.85	ABUW_RS14490	hypothetical protein
-1.85	ABUW_RS11950	hydroxymethylglutaryl-CoA lyase
-1.84	ABUW_RS13190	ATP-dependent RNA helicase HrpA
-1.84	ABUW_RS04130	multidrug efflux RND transporter permease subunit AdeJ
-1.84	ABUW_RS16485	permease
-1.84	ABUW_RS05750	putative histamine N-monooxygenase

-1.84	ABUW_RS16840	3-isopropylmalate dehydratase large subunit
-1.83	ABUW_RS12820	HlyD family type I secretion periplasmic adaptor subunit
-1.83	ABUW_RS14475	heme oxygenase
-1.83	ABUW_RS13300	OsmC family protein
-1.82	sRNA84	
-1.82	ABUW_RS01735	N-succinylarginine dihydrolase
-1.82	ABUW_RS17840	sodium:proton antiporter
-1.82	ABUW_RS11170	methionine adenosyltransferase
-1.82	ABUW_RS05760	(2%2C3-dihydroxybenzoyl)adenylate synthase
-1.81	ABUW_RS08405	D-amino acid dehydrogenase
-1.80	ABUW_RS01800	glycine--tRNA ligase subunit alpha
-1.77	ABUW_RS16420	type IV pilus biogenesis/stability protein PilW
-1.77	ABUW_RS01440	hypothetical protein
-1.77	ABUW_RS01405	phospho-N-acetylmuramoyl-pentapeptide-transferase
-1.76	ABUW_RS09965	type 1 fimbrial protein
-1.76	ABUW_RS12655	putative hydro-lyase
-1.76	ABUW_RS11680	triphosphoribosyl-dephospho-CoA synthase
-1.75	ABUW_RS15900	acetyl-CoA carboxylase carboxyltransferase subunit alpha
-1.75	ABUW_RS01220	imidazole glycerol phosphate synthase subunit HisH
-1.75	ABUW_RS17475	DNA-directed RNA polymerase subunit beta
-1.75	ABUW_RS15035	ribose-phosphate pyrophosphokinase
-1.74	ABUW_RS02425	50S ribosomal protein L13
-1.74	ABUW_RS19130	SAM-dependent DNA methyltransferase
-1.74	ABUW_RS02940	aspartate--tRNA ligase
-1.74	ABUW_RS04380	carbamoyl-phosphate synthase large subunit
-1.73	ABUW_RS15400	NADH-quinone oxidoreductase subunit NuoH
-1.73	ABUW_RS05890	MFS transporter
-1.72	ABUW_RS00765	M23 family metalloproteinase
-1.71	ABUW_RS18555	alpha-hydroxy-acid oxidizing protein
-1.71	ABUW_RS19140	ParA family protein
-1.69	ABUW_RS01140	hypothetical protein
-1.69	ABUW_RS17205	monovalent cation/H+ antiporter subunit D
-1.69	ABUW_RS00065	anhydro-N-acetylmuramic acid kinase
-1.68	ABUW_RS15375	NADH-quinone oxidoreductase subunit M
-1.68	ABUW_RS15570	ABC transporter substrate-binding protein
-1.67	ABUW_RS00400	formimidoylglutamase
-1.66	ABUW_RS15415	NADH-quinone oxidoreductase subunit NuoE
-1.66	ABUW_RS15405	NADH-quinone oxidoreductase subunit NuoG
-1.66	ABUW_RS02295	malate dehydrogenase
-1.65	ABUW_RS12660	LamB/YcsF family protein
-1.65	ABUW_RS15370	NADH-quinone oxidoreductase subunit NuoN
-1.65	ABUW_RS17115	polyribonucleotide nucleotidyltransferase
-1.64	ABUW_RS08735	cytochrome d ubiquinol oxidase subunit II
-1.63	ABUW_RS19015	ribonuclease P protein component
-1.63	ABUW_RS16910	hypothetical protein
-1.61	ABUW_RS04095	valine--tRNA ligase
-1.61	ABUW_RS13375	NCS2 family permease
-1.60	ABUW_RS16915	Rne/Rng family ribonuclease
-1.60	ABUW_RS17210	Na+/H+ antiporter subunit E
-1.60	ABUW_RS08465	phosphatidate cytidyltransferase
-1.60	ABUW_RS15385	NADH-quinone oxidoreductase subunit NuoK
-1.59	ABUW_RS01795	glycine--tRNA ligase subunit beta
-1.58	ABUW_RS00925	carbapenem susceptibility porin CarO
-1.58	ABUW_RS10620	lucA/lucC family siderophore biosynthesis protein
-1.57	ABUW_RS19020	50S ribosomal protein L34
-1.57	ABUW_RS18615	glycosyltransferase family 4 protein
-1.57	ABUW_RS16405	histidine--tRNA ligase
-1.56	ABUW_RS10060	polyphosphate kinase 1
-1.56	ABUW_RS15390	NADH-quinone oxidoreductase subunit J
-1.56	ABUW_RS02060	30S ribosomal protein S14
-1.56	ABUW_RS03510	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA
-1.55	ABUW_RS15420	NADH-quinone oxidoreductase subunit C/D
-1.55	ABUW_RS02280	tRNA (N6-isopentenyl adenosine(37)-C2)-methylthiotransferase MiaB
-1.54	ABUW_RS00910	cation acetate symporter
-1.54	ABUW_RS10345	diaminohydroxyphosphoribosylaminopyrimidine deaminase
-1.53	ABUW_RS01580	ribosome maturation factor RimM
-1.53	ABUW_RS01585	tRNA (guanosine(37)-N1)-methyltransferase TrmD

-1.53	ABUW_RS01380	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH
-1.51	ABUW_RS02080	30S ribosomal protein S5
-1.51	ABUW_RS11855	catalase HPII
-1.51	ABUW_RS09465	methylenetetrahydrofolate reductase
-1.50	ABUW_RS18610	sugar transferase

Table 3.9: Up-regulated genes in the *A. baumannii* 5075 $\Delta sigAB$ mutant compared to the wildtype at LSP.

log2FoldChange	annotation	Product
3.40	sRNA106	
3.13	ABUW_RS14395	hypothetical protein
3.09	ABUW_RS09540	endonuclease/exonuclease/phosphatase family protein
2.88	ABUW_RS08240	TetR/AcrR family transcriptional regulator
2.77	ABUW_RS03985	hypothetical protein
2.74	ABUW_RS06275	hypothetical protein
2.73	ABUW_RS16285	TetR/AcrR family transcriptional regulator
2.70	ABUW_RS11305	TetR/AcrR family transcriptional regulator
2.66	ABUW_RS08610	MarR family transcriptional regulator
2.54	ABUW_RS07820	hypothetical protein
2.54	ABUW_RS11270	hypothetical protein
2.52	ABUW_RS13775	hypothetical protein
2.50	ABUW_RS13915	5-formyltetrahydrofolate cyclo-ligase
2.44	ABUW_RS03380	entericidin A/B family lipoprotein
2.44	ABUW_RS13765	hypothetical protein
2.42	ABUW_RS00205	2%2C5-didehydrogluconate reductase DkgB
2.41	ABUW_RS16210	hypothetical protein
2.39	ABUW_RS02710	hypothetical protein
2.37	ABUW_RS11175	hypothetical protein
2.27	ABUW_RS01120	AraC family transcriptional regulator
2.26	ABUW_RS18520	hypothetical protein
2.26	ABUW_RS05685	hypothetical protein
2.20	ABUW_RS06425	hypothetical protein
2.19	ABUW_RS03365	radical SAM protein
2.18	sRNA71	
2.17	ABUW_RS05675	TetR/AcrR family transcriptional regulator
2.17	sRNA105	
2.16	ABUW_RS02355	GFA family protein
2.12	ABUW_RS10675	AraC family transcriptional regulator
2.11	ABUW_RS06430	hypothetical protein
2.10	ABUW_RS10890	DUF1049 domain-containing protein
2.08	ABUW_RS11140	hypothetical protein
2.08	ABUW_RS01690	hypothetical protein
2.05	ABUW_RS05330	DUF962 domain-containing protein
2.03	ABUW_RS15455	hypothetical protein
2.03	ABUW_RS08045	hypothetical protein
2.03	ABUW_RS14830	arginyltransferase
2.01	ABUW_RS09205	MerR family transcriptional regulator
2.00	ABUW_RS08690	DUF2750 domain-containing protein
1.99	ABUW_RS15335	hypothetical protein
1.98	ABUW_RS02985	hypothetical protein
1.97	ABUW_RS08700	hypothetical protein
1.94	ABUW_RS13220	hypothetical protein
1.94	ABUW_RS15290	hypothetical protein
1.91	ABUW_RS01165	AraC family transcriptional regulator
1.91	ABUW_RS09960	hypothetical protein
1.91	ABUW_RS16880	DNA-binding transcriptional regulator HcaR
1.90	ABUW_RS11230	hypothetical protein

1.89	ABUW_RS04825	rhombotarget A
1.88	ABUW_RS10895	integration host factor subunit beta
1.87	ABUW_RS18820	NAD(P)H-dependent oxidoreductase
1.87	ABUW_RS11530	metalloregulator ArsR/SmtB family transcription factor
1.87	ABUW_RS07290	hypothetical protein
1.86	ABUW_RS14680	hypothetical protein
1.86	ABUW_RS10155	AraC family transcriptional regulator
1.86	ABUW_RS08590	universal stress protein
1.84	ABUW_RS18485	DUF1003 domain-containing protein
1.82	ABUW_RS13480	MarR family transcriptional regulator
1.82	ABUW_RS12910	right-handed parallel beta-helix repeat-containing protein
1.82	ABUW_RS04760	hypothetical protein
1.82	ABUW_RS08110	RDD family protein
1.81	ABUW_RS15790	ribosome-associated translation inhibitor RaiA
1.80	ABUW_RS08410	hypothetical protein
1.80	ABUW_RS18030	MerR family transcriptional regulator
1.78	ABUW_RS07635	hypothetical protein
1.77	ABUW_RS17410	hypothetical protein
1.76	ABUW_RS10315	MBL fold metallo-hydrolase
1.76	ABUW_RS08650	hypothetical protein
1.74	ABUW_RS06270	hypothetical protein
1.74	ABUW_RS08530	hypothetical protein
1.74	ABUW_RS09645	hypothetical protein
1.74	ABUW_RS18865	hypothetical protein
1.74	ABUW_RS11345	amino acid ABC transporter substrate-binding protein
1.73	ABUW_RS07490	DUF3426 domain-containing protein
1.72	ABUW_RS10925	uracil-DNA glycosylase
1.71	ABUW_RS18720	TetR/AcrR family transcriptional regulator
1.71	ABUW_RS07440	TetR/AcrR family transcriptional regulator
1.71	ABUW_RS07450	hypothetical protein
1.71	ABUW_RS00410	HAD family hydrolase
1.71	ABUW_RS03915	Arc family DNA-binding protein
1.70	ABUW_RS02360	DUF4256 domain-containing protein
1.70	ABUW_RS12775	Lrp/AsnC family transcriptional regulator
1.70	ABUW_RS16110	RidA family protein
1.70	ABUW_RS11155	polyisoprenoid-binding protein
1.70	ABUW_RS11830	translesion error-prone DNA polymerase V autoproteolytic subunit
1.69	ABUW_RS07410	N-acetyltransferase
1.69	ABUW_RS04360	MGMT family protein
1.69	ABUW_RS12540	hypothetical protein
1.69	ABUW_RS02790	alkaline phosphatase
1.69	ABUW_RS08685	CBS domain-containing protein
1.68	ABUW_RS14745	class II glutamine amidotransferase
1.68	ABUW_RS11400	Crp/Fnr family transcriptional regulator
1.68	ABUW_RS14810	threonine export protein RhtC
1.68	ABUW_RS06065	DUF962 domain-containing protein
1.67	ABUW_RS19055	hypothetical protein
1.67	ABUW_RS07835	type II toxin-antitoxin system RelB/DinJ family antitoxin
1.66	ABUW_RS13910	hypothetical protein
1.66	sRNA87	
1.65	ABUW_RS19450	hypothetical protein
1.65	ABUW_RS10420	hypothetical protein
1.64	ABUW_RS17640	hypothetical protein
1.64	ABUW_RS10885	orotidine-5'-phosphate decarboxylase
1.64	ABUW_RS19510	hypothetical protein
1.64	ABUW_RS05285	hypothetical protein
1.64	ABUW_RS03310	DUF1508 domain-containing protein
1.63	ABUW_RS13380	hypothetical protein
1.63	ABUW_RS02965	hypothetical protein
1.62	ABUW_RS09470	LuxR family transcriptional regulator
1.61	ABUW_RS19620	DIP1984 family protein
1.60	ABUW_RS15940	hypothetical protein
1.60	ABUW_RS04500	co-chaperone GroES
1.59	ABUW_RS06595	NirD/YgiW/YdeI family stress tolerance protein
1.58	ABUW_RS09535	hypothetical protein

1.58	ABUW_RS13205	O-methyltransferase
1.58	ABUW_RS11070	helix-turn-helix transcriptional regulator
1.57	ABUW_RS12715	serine hydrolase
1.57	ABUW_RS12880	hypothetical protein
1.57	ABUW_RS13035	hypothetical protein
1.57	ABUW_RS07785	hypothetical protein
1.56	ABUW_RS11290	integrase
1.56	ABUW_RS14025	copper resistance protein NlpE
1.56	ABUW_RS03850	hypothetical protein
1.55	ABUW_RS08695	hypothetical protein
1.54	ABUW_RS01615	hemerythrin
1.54	ABUW_RS12260	DUF2813 domain-containing protein
1.54	ABUW_RS11410	hypothetical protein
1.54	ABUW_RS03385	DUF1853 family protein
1.54	sRNA28	
1.54	ABUW_RS13210	DUF1653 domain-containing protein
1.54	ABUW_RS05115	GFA family protein
1.53	ABUW_RS17270	type IV-A pilus assembly ATPase PilB
1.53	ABUW_RS09425	fumarylacetoacetate hydrolase
1.52	ABUW_RS10790	hypothetical protein
1.52	ABUW_RS06670	hypothetical protein
1.52	ABUW_RS04830	CSLREA domain-containing protein
1.51	ABUW_RS11885	hypothetical protein
1.51	ABUW_RS15920	hypothetical protein
1.51	ABUW_RS04550	hypothetical protein
1.51	ABUW_RS10930	6-carboxytetrahydropterin synthase
1.51	ABUW_RS12115	FMN-dependent NADH-azoreductase

Analysis of genes under direct control of SigAB.

To verify whether the effect of the deletion on the transcriptome was direct or indirect, it is important to identify the SigAB binding motif. During the preparation of this work, a preprint identified the binding motif of *sigAB* in *A. baumannii* ATCC17978 by chromatin immunoprecipitation sequencing (ChIP-seq) (Bacon et al. 2024). This found the consensus motif to be CGTT at the –10 region and GTCAAC at the –35 region of SigAB-dependent promoters. Promoters that have this motif were identified including for the genes *sigAB*, *sRNA90* (*sabS*), *relA* and *cysT* and these were analysed in *A. baumannii* AB5075. A strong down-regulation of *sigAB* (the gene is deleted) and *sRNA90* in the mutant was observed, which agrees with previous work (Bacon et al. 2024). However, the *relA* gene is only slightly down-regulated (1.5-fold) in the $\Delta sigAB$ mutant in this study and the binding of SigAB is not near the transcriptional start site (*relA*) (Kröger et al. 2018). questioning whether there is a direct effect on transcription of *relA* through SigAB in *A. baumannii* AB5075. The gene *cysT* is not expressed; therefore, we cannot assess whether the expression is affected (Bakheet 2024). The *relA* gene is also only slightly down-regulated (1.5-fold) in the $\Delta sigAB$ mutant in our data questioning whether there is a direct effect on transcription of *relA* through SigAB.

Table 3.10: Differential gene expression of genes directly regulated SigAB (Bacon et al. 2024).

Gene name	Relative gene expression (log2 fold-change) WT vs. $\Delta sigAB$ at LSP
<i>ABUW_RS04845 (sigAB)</i>	-17.55
sRNA90	-13.12
<i>ABUW_RS16040 (relA)</i>	-0.62
<i>ABUW_RS05000 (cysT)</i>	n/a

The expression of sRNA90 is controlled by SigAB.

The transcriptomic data suggests that SigAB is tightly regulating sRNA90 in LSP (Figure 3.10 and Table 3.8). To validate this result, a northern blot was carried out to test the abundance of sRNA90 in wild-type and mutant strains. Total RNA was isolated from *A. baumannii* AB5075 $\Delta sigAB$ and wild-type AB5075 grown in L-broth until LSP and subjected to northern blotting (Figure 3.11). The predicted size of sRNA90 is 176 nt as discovered by dRNA-seq (Kröger et al. 2018). A band was visible on the northern blot at a slightly lower than the 200 nt band of the single-stranded RNA ladder, which was absent in the $\Delta sigAB$ mutant. A few less abundant bands were also visible, which might be processed or degrading sRNA90. A riboprobe detecting 5S rRNA was used as a loading control (Figure 3.11B). Therefore, the expression of sRNA90 is dependent on the presence of *sigAB* in LSP.

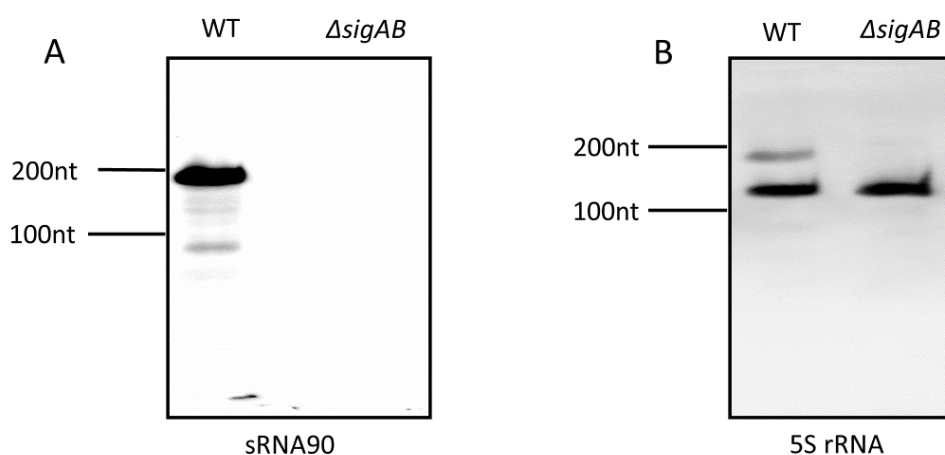


Figure 3.11: Northern Blot analysis of sRNA90 for *A. baumannii* AB5075 Wildtype and $\Delta sigAB$ at LSP. Panel A shows a northern blot using the sRNA90 riboprobe. Panel B shows the same blot re-probed for 5S rRNA which serves as a loading control. Five μ g of total RNA was loaded into each well. Three biological replicates were run for each sample and one representative blot is shown.

Overexpression of SigAB induces the expression of sRNA90.

To test whether the expression of sRNA90 could be induced by ectopic expression of SigAB, *sigAB* was cloned under the control of the arabinose-inducible P_{BAD} promoter of pVRL2Z (pVRL2Z-*sigAB*). *A. baumannii* AB5075 $\Delta sigAB$ was transformed with pVRL2Z-*sigAB* and the expression of *sigAB* was induced for one hour at MEP with 100 mM L-arabinose to recover expression of sRNA90. Figure 3.12 shows that expression of sRNA90 was restored upon *sigAB* expression further confirming that *sigAB* expression is essential for sRNA90 expression.

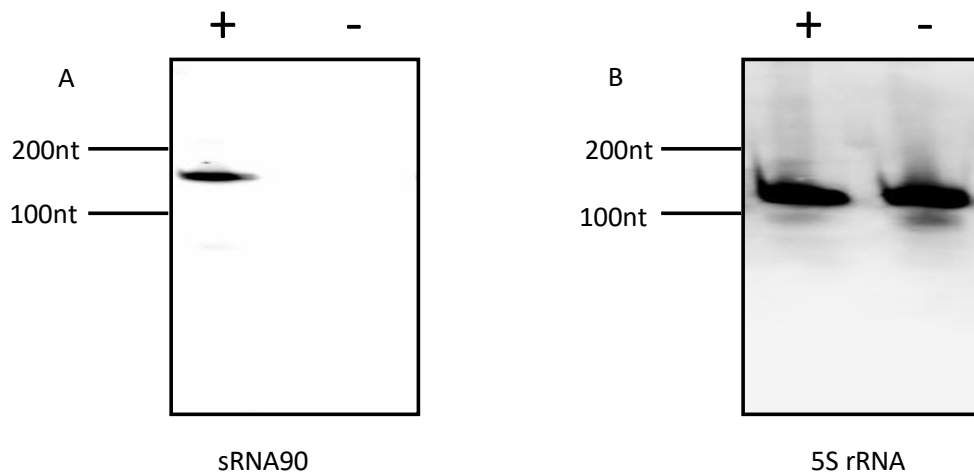


Figure 3.12: Northern Blot analysis of sRNA90 showing overexpression of *sigAB* in *A. baumannii* AB5075 $\Delta sigAB$ pVRL2Z-*sigAB*. Cultures were grown to $OD_{600} = 0.3$ at 37°C in L-broth without NaCl. Once the samples reached $OD_{600} = 0.3$, gene expression of *sigAB* was induced by the addition of 100 mM of L-arabinose for 1 h (+). Non-induced samples served as a control (-). Panel A shows the northern blot probed with the sRNA90 riboprobe and panel B shows the 5S rRNA loading control. Ten μ g of total RNA was loaded into each well. Three biological replicates were run for each sample and one representative blot is shown.

Functional characterisation of sRNA90.

Having identified that activation of SigAB induces the expression of sRNA90, the biological role of sRNA90 was characterised and whether it may act as a regulatory sRNA. Previous Hi-GRIL-seq data had identified several potential target molecules of sRNA90 (Hamrock et al. 2024). Of these predicted targets, the most promising was gene encoding for a hypothetical protein (ABUW_RS18870, Table 3.11), which had 8705 ligation events with sRNA90. As all genes are annotated to encode hypothetical proteins, a more detailed sequence analysis was carried out. Closer inspection of the amino acid sequences of ABUW_RS18870 and ABUW_RS15920 suggested that these hypothetical proteins might be a lipoproteins, because the sequences contain a “lipobox” motif (Huang et al. 2022). BLAST analysis predicted that ABUW_RS13220 might be *tolA*. This is shown in Figure 3.13, where the amino acid sequences of ABUW_RS18870 and ABUW_RS15920 are compared with the known lipoproteins TolA (ABUW_RS13220) and LirL.

Table 3.11: Potential target molecules of sRNA90 from Hi-GRIL-seq data (Hamrock et al. 2024). Only potential target genes with >50 ligation events with sRNA90 are depicted.

Interaction partner	Annotation	Total number of chimeric reads with sRNA90
<i>ABUW_RS18870</i>	hypothetical protein	8705
<i>tolA (ABUW_RS13220)</i>	hypothetical protein	969
<i>ABUW_RS15920</i>	hypothetical protein	360
<i>ABUW_RS00045</i>	hypothetical protein	81
<i>ABUW_RS13040</i>	hypothetical protein	80

The lipoprotein LirL, which was identified in *A. baumannii* ATCC19606 and ATCC17978, showed a high level of sequence identity (82.72%) with ABUW_RS15920 (Table 3.12) (Huang et al. 2022). Further functional analyses will be required to confirm the biological role of ABUW_RS18870, however that presence of the lipobox would suggest that ABUW_RS18870 is a lipoprotein.

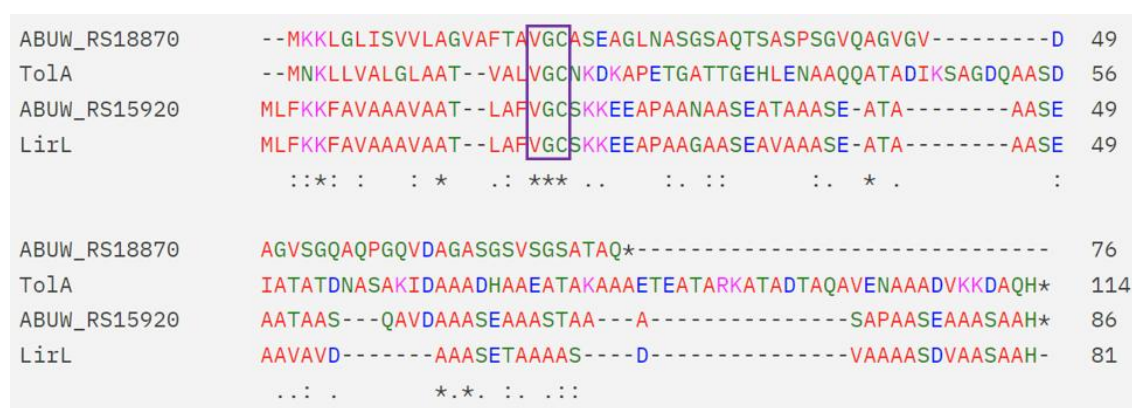


Figure 3.13: Multiple sequence alignment of ABUW_RS18870 and lipoproteins TolA, ABUW_RS15920 and LirL using CLUSTAL O (1.2.4). The amino acid sequences from *A. baumannii* AB5075 ABUW_RS18870, TolA and ABUW_RS15920 and *A. baumannii* ATCC17978 LirL are aligned. The Lipobox is highlighted in purple.

Table 3.12: Percent amino acid sequence identity matrix of multiple sequence alignment shown in Figure 3.13.

	ABUW_RS18870	ToIA ABUW_RS13220)	ABUW_RS15920	LirL
ABUW_RS18870	100%	20.27%	25.76%	26.23%
ToIA (ABUW_RS13220)	20.27%	100%	40.48%	43.04%
ABUW_RS15920	25.76%	40.48%	100%	82.72%
LirL	26.23%	43.04%	82.72%	100%

Characterisation of the hypothetical lipoprotein ABUW_RS18870.

To investigate when ABUW_RS18870 is expressed across growth stages, a FLAG-tagged strain was created. The sequence encoding the 3xFLAG tag was inserted at the end of the *ABUW_RS18870* open reading frame to create a C-terminally tagged ABUW_RS18870-3xFLAG protein. The predicted size of ABUW_RS18870-3xFLAG was expected to be 9.8 kDa. However, western blotting appeared to show a molecular weight of >26 kDa. This aberrant migration has occurred with lipoproteins studied in *A. baumannii* before and might be the case for ABUW_RS18870-3xFLAG (Huang et al. 2022). ABUW_RS18870-3xFLAG was more abundant in ESP and LSP compared to MEP, which agreed with transcriptional data (Bakheet 2024). Transcriptional data showed that ABUW_RS18870 was more highly expressed at ambient temperature (22°C) compared to 37°C (Bakheet 2024). To test this, LSP samples obtained from LSP at the two temperatures were compared for the relative abundance of ABUW_RS18870. No major difference at the protein level was observed, potentially ABUW_RS18870 was more abundant at ambient temperature, however, poor blot quality prevented quantification. Further experiments will be required to elucidate if the observed band is indeed ABUW_RS18870-3xFLAG.

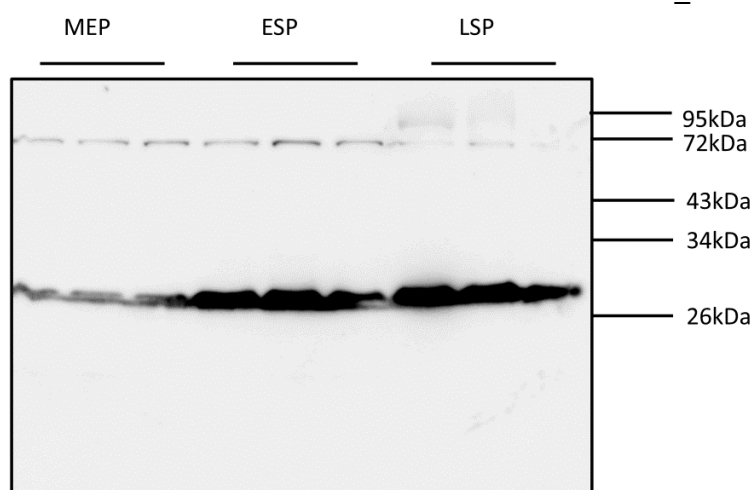


Figure 3.14: Protein abundance of *A. baumannii* ABUW_RS18870-3xFLAG in different stages of growth. *A. baumannii* AB5075 ABUW_RS18870::3xFLAG was grown to a variety of growth phases in L-broth at 37°C (MEP: OD₆₀₀ = 0.3, ESP: OD₆₀₀ = 2, LSP: Growth for 16 h. Whole cell lysates were separated by SDS-PAGE and subjected to western blotting using an anti-FLAG antibody. Fifteen µl of a culture set to OD₆₀₀ = 0.1 was loaded into each well.

Three biological replicates are shown for each condition. The expected molecular weight of the ABUW_RS18870-3xFLAG is 9.8 kDa. DnaK is used as a loading control (69.4 kDa).

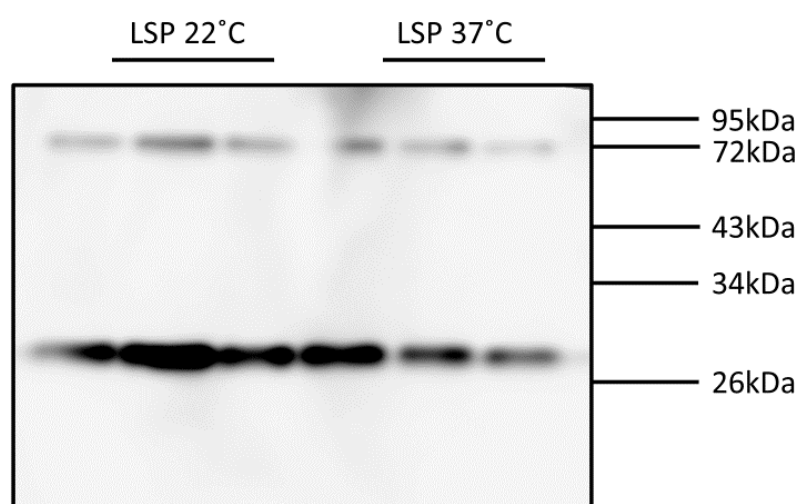


Figure 3.15: Protein abundance of *A. baumannii* ABUW_RS18870-3xFLAG after 16 h growth (LSP) at ambient temperature and 37°C. *A. baumannii* AB5075 ABUW_RS18870::3xFLAG was grown for 16 h at 22 and 37°C (LSP) in L-broth. Whole cell lysates were separated by SDS-PAGE and subjected to western blotting using an anti-FLAG antibody. Fifteen μ l of a culture set to OD₆₀₀ = 0.1 was loaded into each well. Three biological replicates are shown for each condition. The expected molecular weight of the ABUW_RS18870-3xFLAG is 9.8 kDa. DnaK is used as a loading control (69.4 kDa).

Is sRNA90 a post-transcriptional regulator of ABUW_RS18870?

Following the identification by Hi-GRIL-seq that sRNA90 might bind to ABUW_RS18870 mRNA, it was necessary to experimentally validate this interaction (Hamrock et al. 2024). The experimental strategy of the well-established two-plasmid translational reporter system in *E. coli*, where the effect of expression of an sRNA from one plasmid on a translational reporter consisting of a fusion of the target gene and *sfGFP* is assessed, was adapted and used which previously identified the interaction between Aar and *carO* mRNA in *A. baumannii* (Urban and Vogel 2007; Hamrock et al. 2024). It was not feasible to carry out this experiment *in vivo* in *A. baumannii* as it lacks two suitable plasmids capable of replicating.

To construct the two plasmids, sRNA90 was cloned into the pVRL2Z plasmid under the control of the *P_{BAD}* arabinose-inducible promoter (Lucidi et al. 2018). The pXG10sf-ABUW_RS18870 had been constructed earlier in the host lab and was available. It was made by cloning the 5'UTR and four amino acids of ABUW_RS18870 into the pXG10sf

plasmid (Corcoran et al. 2012). Expression of sRNA90 upon addition of the inducer L-arabinose was validated by northern blotting (Figure 3.16).

Prediction of a potential RNA-RNA duplex was carried out using IntaRNA (Mann et al. 2017). This identified a likely binding site of sRNA90 (5'-CCUUUCAUUACGAC-3') with the target ABUW_RS18870 mRNA (5'-GUCGUAAUGAAAGG-3') (Figure 3.17A). Using this prediction, a sRNA90 mutant (sRNA90M) was designed to specifically interrupt this binding (5'-GGUUUGAUUACGAC-3', changes highlighted in red) (Figure 3.17B). The mutations introduced into sRNA90M drastically weaken the interaction reducing the hybridization energy with ABUW_RS18870 mRNA from -21.89 kcal/mol for the wildtype sRNA90 to -10.97 kcal/mol for the sRNA90M mutant. There was also a predicted dramatic shift in the predicted secondary structure of the interaction (Figure 3.17C and 3.17D), which might affect sRNA stability, which should be assessed in future experimentation.

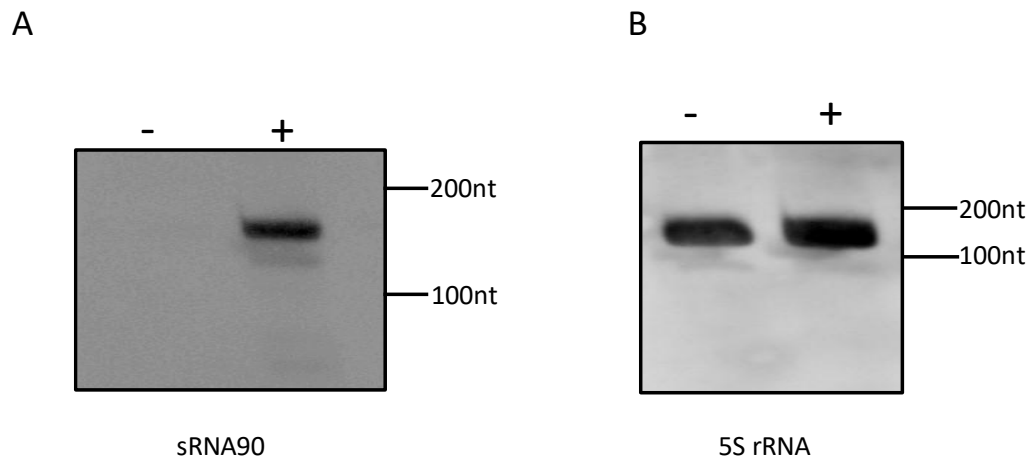


Fig 3.16: Induction of sRNA90 of *E. coli* pVRL2Z:sRNA90. Northern blot using a sRNA90 riboprobe. Cultures were grown in 25 ml flasks in L-broth and RNA was isolated after the samples were grown to OD₆₀₀ of 0.3. The strains also contained pXG10sf-ABUW_RS18870. The induced samples (+) were then adjusted to 100 mM L-arabinose and RNA was isolated from these samples 1 h after the addition of the L-arabinose. Non-induced samples (-) were grown to OD₆₀₀ of 0.3 and were allowed to continue to grow for an additional hour before RNA was isolated. Blot A shows the induced and uninduced samples after probing with the sRNA90 riboprobe. Blot B shows induced and uninduced samples after probing with the *E. coli* 5S rRNA riboprobe. Each well was loaded with 10 µg of total RNA.

To establish experimentally the interaction between sRNA90, sRNA90M and ABUW_RS18870 using the two plasmid reporter system, fluorescence of *E. coli* equipped with pXG10sf-ABUW_RS18870 and either pVRL2Z-sRNA90, pVRL2Z-sRNA90M or the pVRL2Z empty plasmid was measured and compared between pre-induction with L-arabinose (P.I.), induction (+) and no induction (-) (Figure 3.18). This two plasmid system functions as the inducible plasmid pVRL2Z can be used to control the expression of

sRNA90, the effect of this on ABUW_RS18870 can be measured using the translational fusion, i.e. the more fluorescence measured the more protein being produced. This can be used to measure the effect of sRNA90 on ABUW_RS18870 translation. Fluorescence levels pre-induction (Figure 3.18A), were already significantly reduced for the strain expressing sRNA90 indicating that leaky expression from PBAD repressed translation of ABUW_RS18870. This effect was much less pronounced ($p > 0.05$) when the cells carried pVRL2Z-sRNA90M. (Figure 3.18B) Further incubation without the inducer L-arabinose exacerbated the effect and the difference between the strains with empty plasmid and pVRL2Z was now statistically significant. This indicates that the interaction is much weaker, but not fully disrupted as predicted by IntaRNA (Figure 3.17). The difference in fluorescence between strains carrying pVRL2Z-sRNA90 and the two other strains became much more pronounced upon overexpression of sRNA90 (Figure 3.18C). Overall, fluorescence levels did not change significantly for *E. coli* carrying the empty plasmid or pVRL2Z-sRNA90M irrespective of the three conditions tested (Figure 3.18D and 3.18E), while induction of sRNA90 reduced the level of fluorescence compared to the pre-induced and non-induced samples. Taken together, expression of sRNA90 might not only repress translation but could also accelerate degradation of ABUW_RS18870 mRNA and this interaction is significantly weakened with mutant sRNA90M.

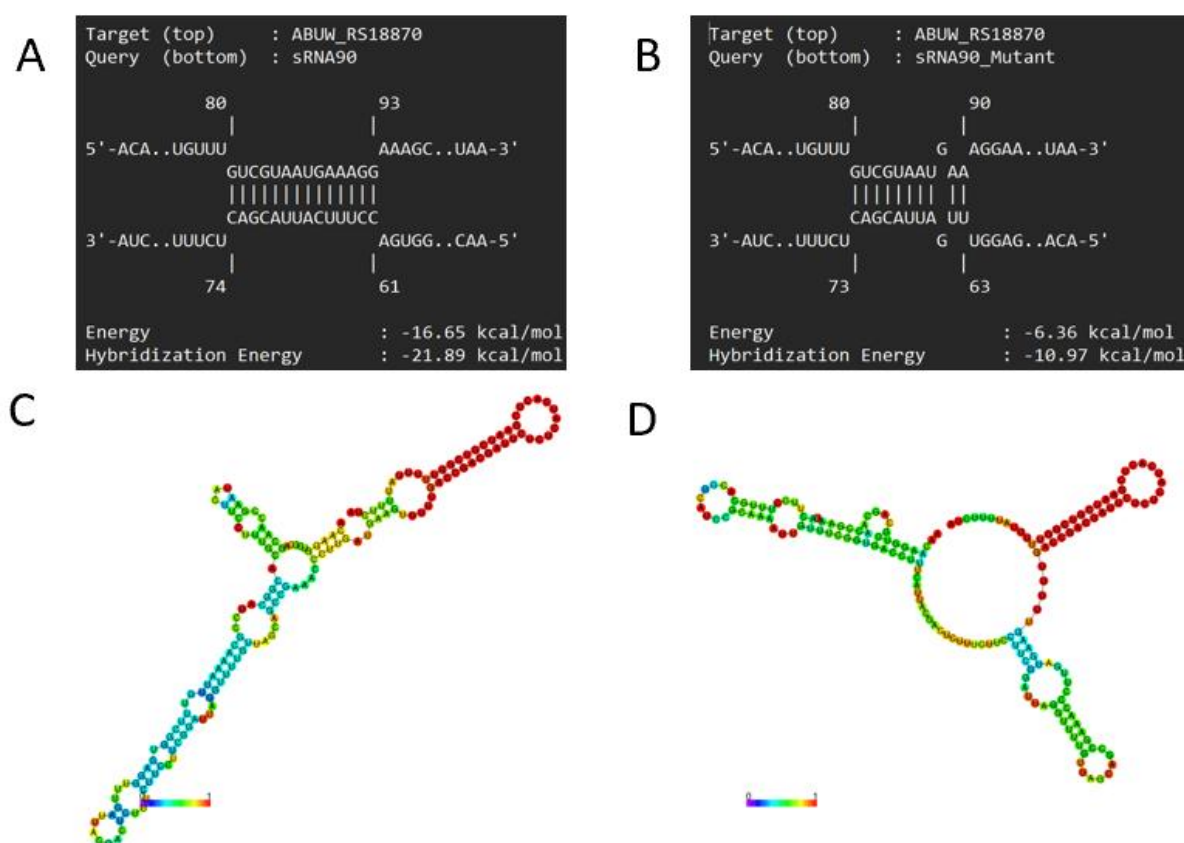


Figure 3.17: Predicted sRNA-mRNA interactions and secondary structures. Panels A and B show the mRNA-sRNA interaction predicted by IntaRNA for both sRNA90 and the sRNA90M when binding to the ABUW_RS18870 mRNA. Panels C and D show the predicted

secondary structure of both sRNA90 and the sRNA90M as found by RNAfold (Hofacker and Stadler 2006).

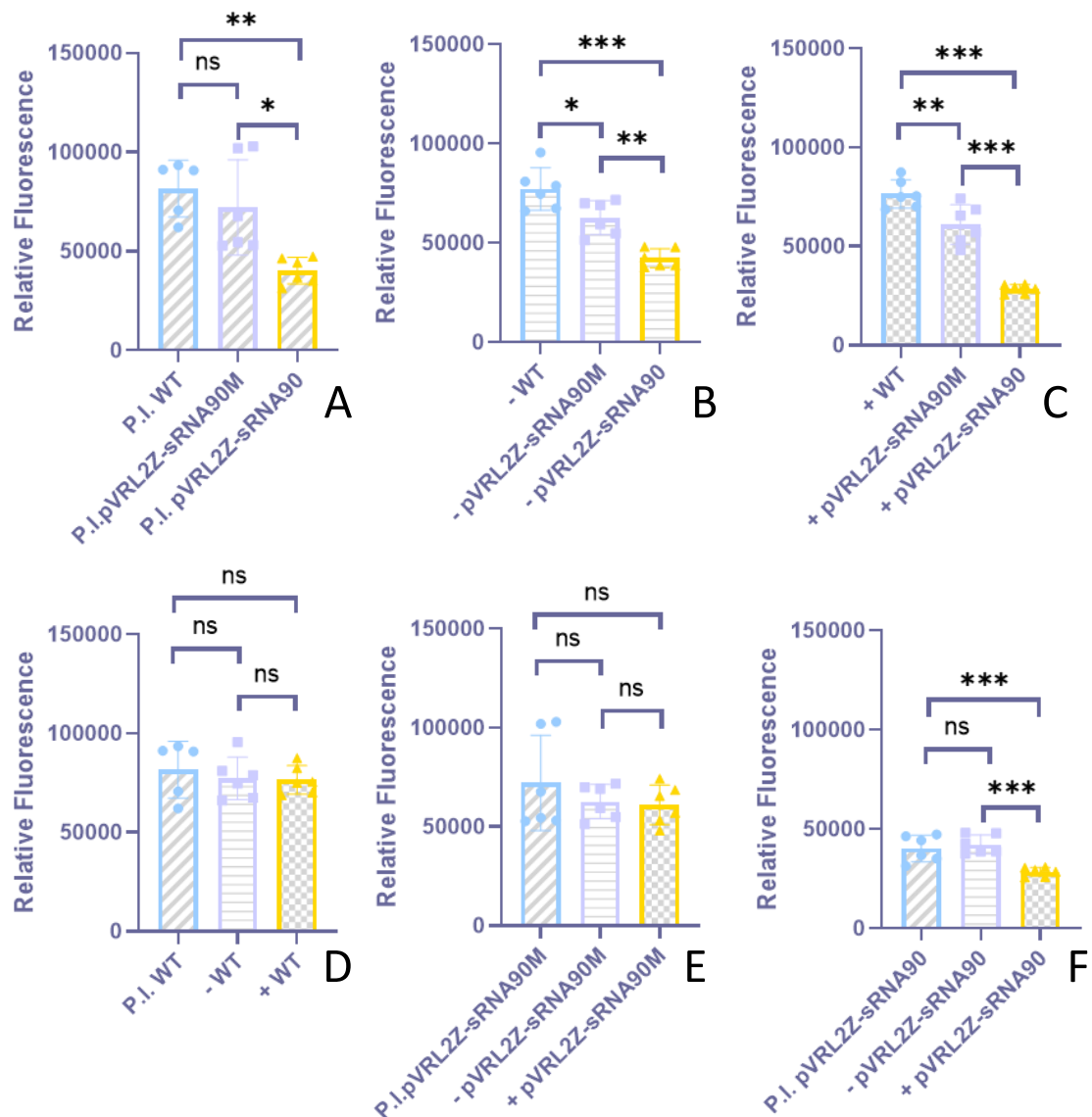


Figure 3.18: Two plasmid translation reporter system in *E. coli* with pXG10-ABUW_RS18870-sfGFP co-equipped with pVRL2Z, pVRL2Z-sRNA90 or pVRL2Z-sRNA90M. The measured relative fluorescence is in arbitrary units per OD₆₀₀. Error bars depict standard deviation of at least five biological replicates. Statistically significant differences were assessed by One-way ANOVA with Tukey's multiple comparisons post-test (ns = $p > 0.05$, * = $p < 0.05$, ** = $p < 0.01$, *** = $p < 0.001$).

Does sRNA90 regulate other mRNA target molecules?

As shown in Table 3.11, other mRNA were ligated to sRNA90 in the Hi-GRIL-seq experiments (Hamrock et al. 2024). IntaRNA was used again to predict possible duplex

structures. The likeliest duplexes of sRNA90 and the mRNAs of potential lipoproteins ABUW_RS15920 and ABUW_RS13220 are depicted in Figure 3.19 . Further analysis will be required to assess if these interactions occur *in vivo*.

Interestingly Figure 3.20 shows that the best characterised sRNA-mRNA interaction which is its regulation of ABUW_RS18870 has a unique binding site compared to the other predicted targets. It is possible that the seed sequence for sRNA90 is either very short, e.g. the GGC nucleotides located at 36 nt or there is no conserved seed sequence for sRNA90. This is uncertain however as the ABUW_RS18870 interaction is the most well established and it is unclear whether the predicted binding sites of the other target genes are functional.

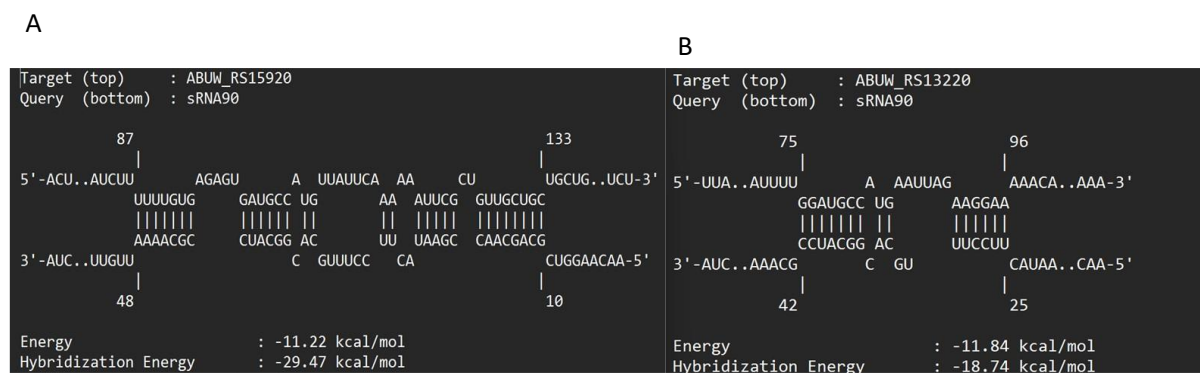


Figure 3.19: sRNA-mRNA interactions between sRNA90 and ABUW_RS15920 & ABUW_RS13320. These are the two other top targets of sRNA 90 according to the Hi-GRIL seq data (Hamrock et al. 2024). Both are also lipoproteins shown in Figure 3.13.

DISCUSSION

Identifying the mechanisms by which bacteria regulate their physiology can provide valuable targets and weaknesses which can then be utilised to develop new treatments. This is especially important in the case of *A. baumannii* due to the rapidity with which it can adapt to and neutralise our current treatment methods. Key to adapting to stressful environments are regulons controlled by alternative sigma factors. By investigating the function of SigAB a clearer picture will be painted of the global regulation of *A. baumannii*. From the results in this study, *sigAB* is playing an important role in *A. baumannii* AB5075 however that role is still not fully clear. Work from a pre-print that was published while this study was carried out shows that it is involved in mediating the response to certain transition metals in *A. baumannii* ATCC19798, especially in copper resistance (Bacon et al. 2024). This study also showed that SigAB is not homologous to the envelope stress response alternative sigma factor RpoE from *E. coli* or *S. enterica* but is an *Acinetobacter*-specific alternative sigma factor (Casella et al. 2017; Bacon et al. 2024). Crucially Polymyxin B which is a known and well characterised inducer of the envelope stress response in other Gram-negative bacteria did not affect growth at all in the deletion mutant compared to the wild-type (Figure 3.1) (Zeng et al. 2023a). Deletion of *sigAB* resulted in impaired growth at high osmotic pressure (500 mM NaCl) and this phenotype was rescued by mild overexpression of SigAB from a plasmid. Surprisingly, the *sigAB* mutant grew better than the wild-type strain when sub-inhibitory concentration of chloramphenicol was added to the growth medium. The reason for these phenotypes is unclear and should be studied in more detail in the future. The copper sensitivity phenotype reported by Bacon et al. in *A. baumannii* ATCC19798 was not tested in *A. baumannii* AB5075 because of time constraints, but this should be assessed in *A. baumannii* AB5075 whether the phenotype is conserved (Bacon et al. 2024). This makes *A. baumannii* quite distinct and unusual amongst other Gram-negative bacteria lacking both two critical stress response ECFs RpoE and RpoS (Maharjan et al. 2023). It has been suggested that the role as a general stress response may be undertaken by DksA or RelA in *A. baumannii*, however it appears in AB5075 at least that the binding motif is absent from the promoter region of RelA and there is no indication that RelA expression is controlled by SigAB at least in AB5075 (Pérez-Varela et al. 2020; Maharjan et al. 2023; Bacon et al. 2024). The only characterised ECF sigma factor is SigAB, however, there is another predicted ECF sigma factor in AB5075 encoded by the gene *ABUW_RS14505*. The role of this sigma factor is still uncharacterised and work needs to be done to identify a potential role for it in regulating the transcriptional landscape of *A. baumannii* (Casella et al. 2017; Geisinger et al. 2018). Genes that are regulated by RpoE in other Gram-negative bacteria are conserved in *A. baumannii*, therefore work is necessary to identify how these genes are regulated in *A. baumannii*.

In this work, previous transcriptional data of the expression pattern of *sigAB* was confirmed at the protein level (Bakheet 2024). SigAB being most strongly expressed in LSP, and this also was found to be true for the expression pattern of *ABUW_RS18870* (Figure 3.14 and Figure 3.15). Consequently, the transcriptomic experiment comparing wild-type and $\Delta sigAB$ mutant

strains was carried out at LSP. Although the direct regulon of *sigAB* is small, its deletion has far-reaching consequences for the transcriptome of the bacteria. Due to the absence of the identified SigAB binding motifs in the identified differentially regulated genes, this effect is largely indirect. The small RNA sRNA90 is the only convincing candidate that appears to be directly regulated and the results from Figure 3.12 imply that it may be solely regulated by *SigAB* and has the binding motif for SigAB within its promoter sequence.

It has been established that sRNA90 has a lot of candidate targets from previous work (Hamrock et al. 2024). It could be that at least part of the effect of the deletion of *sigAB* on the transcriptome of *A. baumannii* is in fact a consequence of the impeded expression of sRNA90. Pathway analysis using FUNAGE-Pro suggested that histidine catabolism into glutamate and formamide and ATP biosynthesis were down-regulated in the *sigAB* mutant at LSP.

Histidine catabolism is well-conserved in bacteria and due to the importance of histidine as an amino acid, the regulation of this pathway is tightly regulated (Bender 2012). This pathway is also referred to as the Hut pathway and allows cells to use histidine as a source of carbon energy and nitrogen. Histidine is amongst the most energetically expensive amino acids to synthesise requiring an input of twenty high-energy phosphate bonds (Akashi and Gojobori 2002). As a result of this, the Hut pathway is only upregulated in very specific conditions, i.e. when there are high levels of exogenous histidine, when there is a biological need for a product of histidine catabolism and when protein synthesis will not be disrupted by the draining of internal pools of histidine (Bender 2012). To follow on from this result a growth experiment could be carried out using histidine as the sole carbon source to identify if there is a loss of fitness in the deletion mutant.

The synthesis of ATP is amongst the most important chemical reactions in all of biology and is essential to all life. ATP synthase is a multicomponent enzyme that is largely conserved not just amongst bacteria but across all kingdoms of life (Von Ballmoos et al. 2009). There are eight genes that make up *A. baumannii* F₀F₁ATP synthase, all of these genes are downregulated in the *A. baumannii* AB5075 Δ *sigAB* compared to the wild-type at LSP. The F₀ membrane embedded domain consists of subunits α , β , γ , σ and ϵ (ABUW_RS18175, ABUW_RS18165, ABUW_RS18170, ABUW_RS18180, ABUW_RS18160 respectively). These proteins form a superstructure which translocate protons across a membrane and then using the energy potential from the electrochemical gradient converting it to rotational energy by utilising protons flowing along the gradient to generate adenosine triphosphate (ATP) from adenosine diphosphate (ADP) and inorganic phosphate (Pi) (Vestergaard et al. 2022). ATP synthase is crucial for many bacterial pathogens but especially *A. baumannii* as it is an obligate aerobe and ATP synthase is essential for growth even in rich medium as well as essential for persistence in the mouse lung (Wang et al. 2014). ATP synthase is so important that oxidative phosphorylation has been targeted in a strategy to develop anti-infective agents (Rubin et al. 2015). As it is clear that the mutant is expressing less ATP synthase in LSP, perhaps growth experiments should be done past 24 hours to identify if this is deleterious to the cell in long

term. Alternatively, the mutant and the wild-type could be grown to stationary phase, then inoculated into fresh media where it would be expected that the wild-type would have a potential fitness advantage during outgrowth.

Although FUNAGE-Pro was unable to identify any significantly enriched ontologies in the genes upregulated at LSP *A. baumannii* AB5075 $\Delta sigAB$ vs wild-type AB5075, it appears that four genes in the TetR/AcrR family of transcriptional repressors are upregulated and are amongst the most upregulated genes identified. TetR-like regulators are widespread amongst not only bacteria but also archaea have a conserved helix-turn-helix DNA-binding domain as well as a C-terminal ligand regulatory domain (Ramos et al. 2005). The founding member of TetR was identified in *E. coli* and regulates genes that encode for a tetracycline resistance. TetR represses gene expression by binding the promoter region of TetA as a homodimer, once tetracycline is present in the cell it chelates Mg^{2+} which forms the complex $[MgTc]^+$ this binds the $(TetR)_2$ homodimer which induces conformational changes that allow the expression of TetA which then confers tetracycline resistance to the cell (Saenger et al. 2000). The TetR/AcrR family regulate a wide range of cellular activities including osmotic stress, antibiotic resistance and virulence (Deng et al. 2013). Although there are a variety of genes regulated by the TetR family generally they are implicated in the regulation of efflux pumps and transporters involved in antibiotic resistance and tolerance to toxic compounds (Deng et al. 2013). This implies that the family could serve as targets for new treatments. In *A. baumannii* the TetR family regulator AdeN has been showed to be involved in regulation the expression of the efflux system AdeIJK which contributes to intrinsic resistance to various drugs, it has also been shown to play a role in virulence (Rosenfeld et al. 2012; Saranathan et al. 2017). Stochastic expression of several TetR type regulators is also involved in switching between virulent opaque (VIR-O) and avirulent translucent (AV-T) colony types in *A. baumannii* AB5075 (Pérez-Varela et al. 2022). Whether SigAB is involved in these processes could be investigated in the future.

The small RNA sRNA106 is the most strongly upregulated gene in the *A. baumannii* AB5075 $\Delta sigAB$ vs wild-type AB5075. It is assumed that this is an indirect effect of the deletion of *sigAB*. There are no predicted targets of sRNA106 in the Hi-GRIL-seq data (Hamrock et al. 2024). Due to this it is difficult to ascertain the biological function of sRNA106. It also seems that sRNA106 is not transcribed at high levels in wild-type AB5075 in any conditions previously tested (Bakheet 2024).

A complication with this study is that in the creation of the *A. baumannii* AB5075 $\Delta sigAB$ mutant the start codon from the downstream gene *aabA* (ABUW_RS04840) was also deleted. The mutant is effectively a double deletion with *aabA* which is one of the proposed anti-sigma factors of *sigAB*. It is thought that *aabA* works alongside the other gene in the operon *aabB* (ABUW_RS04835) through an unknown mechanism to function as *sigAB*s anti-sigma factors (Bacon et al. 2024). RpoE has a similar dual system of anti-sigma factors RseA and RseB however here RseA binds RpoE and anchors it to the membrane sequestering it and RseB stabilises RseA by binding to it (De Las Peñas et al. 1997; Chaba et al. 2011). However results

show that *aabB* functions as an anti-sigma factor in its own right and can suppress *sigAB* expression (Bacon et al. 2024).

Overexpression of *sigAB* from the induction of the P_{BAD} promoter by addition of L-arabinose in the AB5075 Δ *sigAB* background has been shown in Figure 3.9 to have a drastic impact on growth. Perhaps absence of the *aabA* anti-sigma factor that typically sequesters SigAB results in accumulation of SigAB to toxic levels within the cell (Paget 2015). However due to the previously discussed anti-sigma factor activity of *aabB* it may be that this can partially make up for the deletion of *aabB* (Bacon et al. 2024). In Figure 3.8 you can also see that the defect in growth could possibly be mitigated by reducing the amount of L-arabinose used in the induction, the growth defect was recovered using 12.5 mM and 5mM L-arabinose respectively. More work needs to be done on this as only one biological replicate was obtained.

There is a conserved sequence amongst lipoproteins it consists of a four amino acid sequence [LVI], [ASTI],[GAS],C this is commonly referred to as the lipobox and is recognised by lipoprotein modification factors (Babu et al. 2006). This conserved lipobox sequence is present in the top three predicted targets of sRNA90 shown in Table 3.11 and Figure 3.13. This indicates that ABUW_RS18870 and the other top targets are lipoproteins. Lipoproteins are a family of proteins that are secreted then quickly acylated once translocated across the plasma membrane (Selvan and Sankaran 2008; Buddelmeijer 2015). Lipoproteins are known to perform a variety of roles including in peptidoglycan biosynthesis, signal transduction, antimicrobial resistance and virulence (Paradis-Bleau et al. 2010; Kovacs-Simon et al. 2011). In *A. baumannii* peptidoglycan associated protein (Pal) is important for growth and has been implicated as an important virulence factor, deletion of Pal drastically reduced virulence in a mouse infection model and increased susceptibility to detergents and serum killing (Zeng et al. 2023b). Pal is hypothesised to be a promising vaccine candidate. It remains unclear the biological role of ABUW_RS18870 however it seems that it is regulated on a post-transcriptional level by sRNA90.

A lot of work remains to characterise the role of sRNA90 in *A. baumannii* AB5075 particularly in how it controls the effect the translation and degradation of ABUW_RS18870 mRNA. The work done here indicates that it is involved in fine tuning ABUW_RS18870 protein levels on a post-transcriptional level at least in *E. coli*. Furthermore as the top three predicted targets of sRNA90 are all predicted to be lipoproteins. It remains to be established if sRNA90 might operate as a master regulator of lipoproteins on a post transcriptional level (Hamrock et al. 2024). It could be that the deleterious growth of the *A. baumannii* AB5075 Δ *sigAB* in certain conditions relating to stress on the cell membrane (osmotic stress, SDS). The mechanism for this also remains to be identified, it however suggests that the absence of sRNA90 to function in its role in regulating the translation of lipoproteins is causing a reduced capacity to respond to these stressors. It could also be an indirect effect of the absence of *sigAB*. It is also uncertain

which role that sRNA90 may play in the response to chloramphenicol. From transcriptional data, it is evident that sRNA90 is highly upregulated in response to a chloramphenicol shock (Bakheet 2024). However contrary to expectation, the *A. baumannii* AB5075 $\Delta sigAB$ mutant grew significantly better when exposed to high levels of chloramphenicol, this could be another indirect effect of SigAB, although it remains to be seen how sRNA90 is involved. The predicted binding interaction between sRNA90 and ABUW_RS18870 by IntaRNA could be correct due to the results seen in Figure 3.18, because disrupting the predicted duplex abrogated the interaction. However, more control experiments are required, e.g., compensatory mutations should be introduced into pXG10-ABUW_RS18870 to restore the interaction and *in vitro* experiments could strengthen the data, e.g., EMSA and in-line probing experiments. Attempts to identify a seed sequence for sRNA90 proved difficult. A seed sequence is a short run of bases that aid the interaction with the mRNA target it is also typically in a single stranded region, it is generally thought to play a disproportionate role in facilitating the sRNA-mRNA interaction and can be key to experimentally validate interactions (Bandyra et al. 2012). This is due to the varying predicted sRNA-mRNA interactions as seen in Figure 3.20. Here the sRNA90-ABUW_RS18870 interaction has no overlap with the other interaction sites. There does appear to be a possible seed sequence GCC located 36 nt into sRNA90, this sequence appears in four of the top ten predicted targets of sRNA90, however, it is very short. Due to the multiple different binding sites predicted in sRNA90 it is possible that these different sites are used to regulate different targets with the site predicted for the sRNA90-ABUW_RS18870 solely regulating this interaction due to its lack of overlap. The two-plasmid system was used in *E. coli* and it is unknown if the sRNA90-ABUW_RS18870 interaction can be translated to *A. baumannii*. Follow-on work should be done to validate the sRNA90-ABUW_RS18870 *in vivo* in *A. baumannii*.

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APPENDIX

log2FoldChange	p adjusted value	Annotation	Product
-17.55	1.39E-46	ABUW_RS04845	RNA polymerase sigma factor
-13.12	0	sRNA90	
-8.22	1.52E-227	ABUW_RS04840	hypothetical protein
-8.11	6.83E-144	ABUW_RS04835	DUF3106 domain-containing protein
-4.94	1.80E-32	ABUW_RS20020	TniB family NTP-binding protein
-4.03	5.90E-63	ABUW_RS18185	F0F1 ATP synthase subunit B
-3.86	6.92E-46	ABUW_RS19255	GNAT family N-acetyltransferase
-3.52	2.88E-29	ABUW_RS01870	DEAD/DEAH box helicase
-3.38	1.46E-07	ABUW_RS12675	hypothetical protein
-3.36	1.10E-44	ABUW_RS11930	isovaleryl-CoA dehydrogenase
-3.34	2.15E-47	ABUW_RS18190	F0F1 ATP synthase subunit C
-3.31	3.97E-28	ABUW_RS19260	sulfonamide-resistant dihydropteroate synthase Sul1
-3.16	3.79E-46	ABUW_RS00995	amino acid permease
-3.16	4.24E-43	ABUW_RS00380	urocanate hydratase
-3.15	1.84E-50	ABUW_RS11935	methylcrotonoyl-CoA carboxylase
-3.07	5.97E-06	ABUW_RS08150	chlorhexidine efflux PACE transporter AceI
-2.99	3.66E-25	ABUW_RS19270	trimethoprim-resistant dihydrofolate reductase DfrA7
-2.96	7.84E-33	ABUW_RS01495	pilin
-2.92	1.72E-47	ABUW_RS18565	L-lactate permease
-2.89	3.47E-55	ABUW_RS18195	F0F1 ATP synthase subunit A
-2.80	2.99E-07	ABUW_RS19275	aminoglycoside N-acetyltransferase AAC(6')-Ib3
-2.70	1.81E-19	ABUW_RS02620	tRNA guanosine(34) transglycosylase Tgt
-2.69	1.67E-45	ABUW_RS15580	FAD-dependent tricarballoylate dehydrogenase TcuA
-2.63	6.34E-20	ABUW_RS19265	quaternary ammonium compound efflux SMR transporter QacE delta 1
-2.59	8.18E-34	ABUW_RS01005	4-aminobutyrate--2-oxoglutarate transaminase
-2.55	7.81E-20	ABUW_RS00390	amino acid permease
-2.54	1.98E-23	ABUW_RS12665	divalent metal cation transporter
-2.53	0.000281		
-2.53	375	sRNA61	
-2.53	4.13E-17	ABUW_RS00395	imidazolonepropionase
-2.51	4.00E-10	ABUW_RS19295	APH(6)-I family aminoglycoside O-phosphotransferase
-2.49	8.27E-13	ABUW_RS10350	alpha-ketoacid dehydrogenase subunit beta
-2.46	8.79E-27	ABUW_RS11940	enoyl-CoA hydratase/isomerase family protein
-2.44	8.17E-09	ABUW_RS19355	hypothetical protein
-2.42	2.34E-35	ABUW_RS08740	cytochrome bd oxidase subunit I
-2.41	9.69E-26	ABUW_RS18170	F0F1 ATP synthase subunit gamma
-2.37	2.36E-28	ABUW_RS18180	F0F1 ATP synthase subunit delta
-2.36	1.38E-15	ABUW_RS17200	Na ⁺ /H ⁺ antiporter subunit C
-2.33	4.21E-27	ABUW_RS18165	F0F1 ATP synthase subunit beta
-2.32	5.53E-20	ABUW_RS10585	acetyltransferase
-2.32	4.94E-16	ABUW_RS17645	phosphomethylpyrimidine synthase ThiC

-2.32	4.64E-21	ABUW_RS04480	phosphoenolpyruvate carboxykinase (GTP)
-2.31	8.49E-24	ABUW_RS16495	phosphogluconate dehydratase
-2.30	2.71E-27	ABUW_RS01265	RNA-binding transcriptional accessory protein
-2.28	0.036630	375	iron-containing alcohol dehydrogenase
-2.24	3.80E-21	ABUW_RS18160	F0F1 ATP synthase subunit epsilon
-2.23	2.71E-27	ABUW_RS02105	30S ribosomal protein S13
-2.22	1.15E-21	ABUW_RS00385	histidine ammonia-lyase
-2.17	7.29E-09	ABUW_RS19010	membrane protein insertion efficiency factor YidD
-2.12	4.67E-21	ABUW_RS01250	acetyl-CoA hydrolase/transferase family protein
-2.11	2.31E-11	ABUW_RS12330	phenylacetic acid degradation bifunctional protein PaaZ
-2.10	4.99E-14	ABUW_RS12650	5-oxoprolinase/urea amidolyase family protein
-2.10	5.94E-18	ABUW_RS15950	50S ribosomal protein L20
-2.09	1.89E-24	ABUW_RS16475	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
-2.09	9.93E-05	sRNA60	
-2.08	3.83E-21	ABUW_RS05720	acinetobactin non-ribosomal peptide synthetase subunit BasB
-2.08	9.60E-11	ABUW_RS13735	ribonuclease T
-2.07	3.16E-21	ABUW_RS12825	type I secretion system permease/ATPase
-2.07	9.57E-13	ABUW_RS16425	23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN
-2.06	1.64E-22	ABUW_RS15585	tricarballoylate utilization 4Fe-4S protein TcuB
-2.06	4.15E-12	ABUW_RS10355	thiamine pyrophosphate-dependent dehydrogenase E1 component subunit alpha
-2.05	1.95E-21	ABUW_RS02110	30S ribosomal protein S11
-2.04	8.09E-17	ABUW_RS01400	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
-2.04	1.17E-12	ABUW_RS05770	histidine decarboxylase
-2.04	2.64E-06	ABUW_RS08745	hypothetical protein
-2.03	1.91E-22	ABUW_RS18175	F0F1 ATP synthase subunit alpha
-2.02	9.22E-22	ABUW_RS02115	30S ribosomal protein S4
-2.02	8.36E-12	ABUW_RS05765	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF
-2.01	1.32E-06	ABUW_RS17835	signal peptidase II
-2.01	4.57E-16	ABUW_RS16490	bifunctional 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxy-phosphogluconate aldolase
-2.00	6.80E-10	ABUW_RS19280	class A extended-spectrum beta-lactamase GES-11
-1.98	6.38E-07	ABUW_RS10525	hypothetical protein
-1.97	1.08E-13	ABUW_RS04970	7-carboxy-7-deazaguanine synthase QueE
-1.95	3.12E-12	ABUW_RS15525	DUF1852 domain-containing protein
-1.94	1.27E-13	ABUW_RS01730	succinylglutamate-semialdehyde dehydrogenase
-1.93	1.01E-18	ABUW_RS15410	NADH-quinone oxidoreductase subunit NuoF
-1.93	5.10E-16	ABUW_RS04385	glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit
-1.92	4.70E-08	sRNA6	
-1.90	6.37E-07	ABUW_RS03530	rod shape-determining protein MreD
-1.90	2.76E-17	ABUW_RS11945	acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha
-1.89	3.52E-12	ABUW_RS16555	homoserine O-acetyltransferase
-1.87	9.12E-07	ABUW_RS16105	DMT family transporter
-1.87	2.20E-15	ABUW_RS04135	multidrug efflux RND transporter periplasmic adaptor subunit Adel
-1.87	1.50E-10	ABUW_RS03125	patatin family protein

-1.87	2.09E-19	ABUW_RS00920	BCCT family transporter
-1.86	3.03E-17	ABUW_RS03525	rod shape-determining protein MreC
-1.85	1.32E-17	ABUW_RS14490	hypothetical protein
-1.85	8.86E-17	ABUW_RS11950	hydroxymethylglutaryl-CoA lyase
-1.84	8.94E-17	ABUW_RS13190	ATP-dependent RNA helicase HrpA
-1.84	1.05E-17	ABUW_RS04130	multidrug efflux RND transporter permease subunit AdeJ
-1.84	7.68E-17	ABUW_RS16485	permease
-1.84	2.02E-10	ABUW_RS05750	putative histamine N-monooxygenase
-1.84	1.84E-17	ABUW_RS16840	3-isopropylmalate dehydratase large subunit
-1.83	8.09E-16	ABUW_RS12820	HlyD family type I secretion periplasmic adaptor subunit
-1.83	7.88E-07	ABUW_RS14475	heme oxygenase
-1.83	6.11E-09	ABUW_RS13300	OsmC family protein
-1.82	6.68E-15	sRNA84	
-1.82	3.08E-12	ABUW_RS01735	N-succinylarginine dihydrolase
-1.82	1.99E-08	ABUW_RS17840	sodium:proton antiporter
-1.82	2.40E-14	ABUW_RS11170	methionine adenosyltransferase
-1.82	1.32E-11	ABUW_RS05760	(2%2C3-dihydroxybenzoyl)adenylate synthase
-1.81	2.69E-11	ABUW_RS08405	D-amino acid dehydrogenase
-1.80	1.38E-13	ABUW_RS01800	glycine--tRNA ligase subunit alpha
-1.77	7.68E-17	ABUW_RS16420	type IV pilus biogenesis/stability protein PilW
-1.77	1.84E-08	ABUW_RS01440	hypothetical protein
-1.77	2.38E-15	ABUW_RS01405	phospho-N-acetylmuramoyl-pentapeptide-transferase
-1.76	7.33E-09	ABUW_RS09965	type 1 fimbrial protein
-1.76	6.20E-07	ABUW_RS12655	putative hydro-lyase
-1.76	2.81E-10	ABUW_RS11680	triphosphoribosyl-dephospho-CoA synthase
-1.75	1.23E-08	ABUW_RS15900	acetyl-CoA carboxylase carboxyltransferase subunit alpha
-1.75	1.84E-18	ABUW_RS01220	imidazole glycerol phosphate synthase subunit HisH
-1.75	7.48E-17	ABUW_RS17475	DNA-directed RNA polymerase subunit beta
-1.75	8.55E-21	ABUW_RS15035	ribose-phosphate pyrophosphokinase
-1.74	6.24E-14	ABUW_RS02425	50S ribosomal protein L13
-1.74	7.72E-10	ABUW_RS19130	SAM-dependent DNA methyltransferase
-1.74	3.72E-13	ABUW_RS02940	aspartate--tRNA ligase
-1.74	1.80E-11	ABUW_RS04380	carbamoyl-phosphate synthase large subunit
-1.73	3.84E-16	ABUW_RS15400	NADH-quinone oxidoreductase subunit NuoH
-1.73	6.02E-10	ABUW_RS05890	MFS transporter
-1.72	2.10E-11	ABUW_RS00765	M23 family metallopeptidase
-1.71	6.74E-15	ABUW_RS18555	alpha-hydroxy-acid oxidizing protein
-1.71	3.09E-12	ABUW_RS19140	ParA family protein
-1.69	9.77E-13	ABUW_RS01140	hypothetical protein
-1.69	3.13E-10	ABUW_RS17205	monovalent cation/H+ antiporter subunit D
-1.69	4.09E-12	ABUW_RS00065	anhydro-N-acetylmuramic acid kinase
-1.68	1.74E-16	ABUW_RS15375	NADH-quinone oxidoreductase subunit M
-1.68	4.28E-09	ABUW_RS15570	ABC transporter substrate-binding protein
-1.67	8.82E-09	ABUW_RS00400	formimidoylglutamase

-1.66	1.22E-15	ABUW_RS15415	NADH-quinone oxidoreductase subunit NuoE
-1.66	1.05E-18	ABUW_RS15405	NADH-quinone oxidoreductase subunit NuoG
-1.66	4.95E-15	ABUW_RS02295	malate dehydrogenase
-1.65	3.48E-10	ABUW_RS12660	LamB/YcsF family protein
-1.65	1.05E-10	ABUW_RS15370	NADH-quinone oxidoreductase subunit NuoN
-1.65	2.93E-15	ABUW_RS17115	polyribonucleotide nucleotidyltransferase
-1.64	1.75E-11	ABUW_RS08735	cytochrome d ubiquinol oxidase subunit II
-1.63	2.61E-07	ABUW_RS19015	ribonuclease P protein component
-1.63	1.24E-06	ABUW_RS16910	hypothetical protein
-1.61	3.97E-10	ABUW_RS04095	valine--tRNA ligase
-1.61	7.88E-09	ABUW_RS13375	NCS2 family permease
-1.60	3.37E-18	ABUW_RS16915	Rne/Rng family ribonuclease
-1.60	3.73E-07	ABUW_RS17210	Na ⁺ /H ⁺ antiporter subunit E
-1.60	2.28E-13	ABUW_RS08465	phosphatidate cytidyltransferase
-1.60	1.38E-15	ABUW_RS15385	NADH-quinone oxidoreductase subunit NuoK
-1.59	2.08E-12	ABUW_RS01795	glycine--tRNA ligase subunit beta
-1.58	1.15E-12	ABUW_RS00925	carbapenem susceptibility porin CarO
-1.58	5.44E-13	ABUW_RS10620	lucA/lucC family siderophore biosynthesis protein
-1.57	0.119893		aldehyde dehydrogenase family protein
-1.57	254	ABUW_RS07910	
-1.57	0.000737		50S ribosomal protein L34
-1.57	011	ABUW_RS19020	
-1.57	2.56E-13	ABUW_RS18615	glycosyltransferase family 4 protein
-1.57	8.73E-15	ABUW_RS16405	histidine--tRNA ligase
-1.56	1.54E-07	ABUW_RS10060	polyphosphate kinase 1
-1.56	7.21E-16	ABUW_RS15390	NADH-quinone oxidoreductase subunit J
-1.56	9.25E-13	ABUW_RS02060	30S ribosomal protein S14
-1.56	8.49E-16	ABUW_RS03510	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit Gata
-1.55	1.34E-13	ABUW_RS15420	NADH-quinone oxidoreductase subunit C/D
-1.55	1.25E-15	ABUW_RS02280	tRNA (N6-isopentenyl adenosine(37)-C2)-methylthiotransferase MiaB
-1.54	2.00E-09	ABUW_RS00910	cation acetate symporter
-1.54	7.34E-07	ABUW_RS10345	diaminohydroxyphosphoribosylaminopyrimidine deaminase
-1.53	2.09E-13	ABUW_RS01580	ribosome maturation factor RimM
-1.53	3.60E-12	ABUW_RS01585	tRNA (guanosine(37)-N1)-methyltransferase TrmD
-1.53	8.29E-09	ABUW_RS01380	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH
-1.51	5.30E-13	ABUW_RS02080	30S ribosomal protein S5
-1.51	4.50E-13	ABUW_RS11855	catalase HP11
-1.51	5.17E-07	ABUW_RS09465	methylenetetrahydrofolate reductase
-1.50	9.45E-08	ABUW_RS18610	sugar transferase
-1.49	1.65E-06	ABUW_RS03465	alanine:cation symporter family protein
-1.49	5.91E-06	ABUW_RS05230	hypothetical protein
-1.49	1.52E-12	ABUW_RS15380	NADH-quinone oxidoreductase subunit L
-1.49	1.38E-13	ABUW_RS15520	methionine synthase
-1.48	1.51E-15	ABUW_RS16410	flavodoxin-dependent (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase
-1.48	1.63E-09	ABUW_RS12335	L-serine ammonia-lyase

-1.48	2.82E-11	ABUW_RS16835	3-isopropylmalate dehydratase small subunit
-1.47	1.81E-09	ABUW_RS03160	glucose/quininate/shikimate family membrane-bound PQQ-dependent dehydrogenase
-1.47	1.52E-11	ABUW_RS15395	NADH-quinone oxidoreductase subunit Nuol
-1.46	1.59E-10	ABUW_RS18100	TonB-dependent copper receptor
-1.46	7.72E-10	ABUW_RS15215	signal recognition particle protein
-1.46	6.22E-08	ABUW_RS13780	NADH:flavin oxidoreductase/NADH oxidase family protein
-1.45	1.06E-11	ABUW_RS17265	triose-phosphate isomerase
-1.44	2.13E-07	ABUW_RS14645	gamma-glutamyltransferase
-1.43	2.35E-08	ABUW_RS07685	butyryl-CoA dehydrogenase
-1.43	7.97E-12	ABUW_RS09185	alpha/beta hydrolase
-1.42	8.59E-05	ABUW_RS19465	hypothetical protein
-1.42	0.000217		hypothetical protein
-1.42	041	ABUW_RS19360	
-1.42	2.94E-12	ABUW_RS04275	succinate dehydrogenase iron-sulfur subunit
-1.42	1.84E-12	ABUW_RS16905	RluA family pseudouridine synthase
-1.41	1.51E-14	ABUW_RS02120	DNA-directed RNA polymerase subunit alpha
-1.41	1.20E-15	ABUW_RS01225	imidazoleglycerol-phosphate dehydratase HisB
-1.41	1.21E-08	ABUW_RS15955	50S ribosomal protein L35
-1.41	9.49E-11	ABUW_RS05050	elongation factor 4
-1.41	1.64E-08	ABUW_RS12295	2-(1%2C2-epoxy-1%2C2-dihydrophenyl)acetyl-CoA isomerase
-1.41	2.18E-08	ABUW_RS15565	MFS transporter
-1.40	0.003420		aromatic-ring-hydroxylating dioxygenase subunit beta
-1.40	94	ABUW_RS09065	
-1.40	1.70E-10	ABUW_RS17195	monovalent cation/H+ antiporter subunit A
-1.40	4.16E-05	ABUW_RS11660	malonate decarboxylase holo-ACP synthase
-1.40	0.048633		amino acid permease
-1.40	416	ABUW_RS18435	
-1.40	0.040381		hypothetical protein
-1.39	404	ABUW_RS19235	hypothetical protein
-1.39	7.64E-11	ABUW_RS04670	
-1.39	3.62E-12	ABUW_RS02055	50S ribosomal protein L5
-1.37	2.86E-07	ABUW_RS14360	poly-beta-1%2C6-N-acetyl-D-glucosamine biosynthesis protein PgaD
-1.37	4.47E-07	ABUW_RS12300	enoyl-CoA hydratase
-1.37	1.12E-06	ABUW_RS17220	Na+/H+ antiporter subunit G
-1.37	1.55E-09	ABUW_RS08425	ornithine carbamoyltransferase
-1.36	1.96E-05	ABUW_RS13235	tRNA (guanosine(46)-N7)-methyltransferase TrmB
-1.36	1.89E-10	ABUW_RS14435	malate dehydrogenase (quinone)
-1.36	7.29E-12	ABUW_RS18920	5-(carboxyamino)imidazole ribonucleotide mutase
-1.35	0.000151		hypothetical protein
-1.35	914	ABUW_RS16095	
-1.35	1.43E-05	ABUW_RS07155	PIG-L family deacetylase
-1.35	1.40E-09	ABUW_RS13325	adenylosuccinate synthase
-1.34	2.08E-08	ABUW_RS12310	phenylacetate-CoA oxygenase subunit PaaJ
-1.34	1.79E-09	ABUW_RS11015	nucleotidyltransferase family protein
-1.34	1.70E-10	ABUW_RS03000	YdiU family protein
-1.34	2.65E-07	ABUW_RS16100	Re/Si-specific NAD(P)(+) transhydrogenase subunit alpha
-1.34	4.53E-12	ABUW_RS04270	succinate dehydrogenase flavoprotein subunit

	0.000463		hypothetical protein
-1.33	904	ABUW_RS19135	
-1.33	1.46E-05	ABUW_RS01715	Glu/Leu/Phe/Val dehydrogenase
	0.000125		type 1 fimbrial protein
-1.33	828	ABUW_RS11235	
-1.32	6.38E-09	ABUW_RS11960	indolepyruvate ferredoxin oxidoreductase family protein
	0.000785		hypothetical protein
-1.32	228	ABUW_RS15465	
			hypothetical protein
-1.32	2.80E-05	ABUW_RS11910	
-1.32	3.91E-09	ABUW_RS02070	50S ribosomal protein L6
			tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit
-1.32	3.03E-05	ABUW_RS15710	type 1 TsaB
	0.000934		hypothetical protein
-1.31	483	ABUW_RS02960	
			acetyl-CoA carboxylase biotin carboxylase subunit
-1.31	3.15E-12	ABUW_RS08260	
			30S ribosomal protein S8
-1.31	1.14E-09	ABUW_RS02065	
			50S ribosomal protein L14
-1.31	5.43E-12	ABUW_RS02045	
			succinylglutamate desuccinylase
-1.31	2.51E-07	ABUW_RS01740	
			tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG
-1.31	2.23E-08	ABUW_RS07505	
			leucine--tRNA ligase
-1.30	2.17E-08	ABUW_RS16320	
			ribose-phosphate pyrophosphokinase
-1.30	2.56E-10	ABUW_RS09450	
	0.000198		arsenate reductase
-1.30	512	ABUW_RS00695	
			thiazole synthase
-1.30	3.24E-10	ABUW_RS06695	
			siderophore achromobactin biosynthesis protein AcsC
-1.30	2.02E-07	ABUW_RS10625	
			membrane protein insertase YidC
-1.30	1.28E-11	ABUW_RS19005	
			NAD-dependent succinate-semialdehyde dehydrogenase
-1.30	5.63E-12	ABUW_RS01010	
			threonine synthase
-1.29	1.61E-09	ABUW_RS17710	
			23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB
-1.29	3.54E-05	ABUW_RS17295	
			ATP-grasp domain-containing protein
-1.29	1.10E-06	ABUW_RS12645	
			membrane protein
-1.29	1.51E-12	ABUW_RS09195	
			50S ribosomal protein L17
-1.29	1.64E-10	ABUW_RS02125	
			choline transporter
-1.28	2.32E-09	ABUW_RS14410	
			23S rRNA pseudouridine(2605) synthase RluB
-1.27	3.62E-11	ABUW_RS15130	
			amino acid permease
-1.26	1.72E-05	ABUW_RS05450	
			argininosuccinate synthase
-1.26	2.08E-08	ABUW_RS13720	
	0.000823		N-acetyltransferase
-1.25	085	ABUW_RS11195	
			NADH-quinone oxidoreductase subunit A
-1.25	7.46E-09	ABUW_RS15430	
			(2Fe-2S)-binding protein
-1.25	9.61E-05	ABUW_RS10615	
			ribosome maturation factor RimP
-1.25	1.90E-05	ABUW_RS17240	
			nicotinate phosphoribosyltransferase
-1.25	1.10E-08	ABUW_RS09455	
			rod shape-determining protein
-1.25	3.50E-10	ABUW_RS03520	
			catalase/peroxidase HPI
-1.25	2.73E-06	ABUW_RS16870	
			tryptophan synthase subunit beta
-1.25	8.77E-12	ABUW_RS03035	
			radical SAM family heme chaperone HemW
-1.24	1.50E-09	ABUW_RS16945	
			dihydroorotase
-1.24	2.50E-08	ABUW_RS13730	
			Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB
-1.24	1.51E-08	ABUW_RS03505	
			phosphatidylserine decarboxylase
-1.24	2.54E-08	ABUW_RS00510	

	0.168910		aminoglycoside O-phosphotransferase APH(3'')-Ib
-1.23	139	ABUW_RS19300	
-1.23	2.82E-07	ABUW_RS15915	transcription termination factor Rho
	0.000115		transketolase
-1.23	635	ABUW_RS14215	
	0.000155		PACE efflux transporter
-1.22	529	ABUW_RS11280	
-1.22	9.42E-07	ABUW_RS02025	30S ribosomal protein S3
-1.21	1.54E-08	ABUW_RS16455	beta-N-acetylhexosaminidase
-1.21	3.06E-09	ABUW_RS10195	thiolase family protein
-1.21	2.99E-05	ABUW_RS17440	membrane protein
-1.21	3.20E-10	ABUW_RS02050	50S ribosomal protein L24
-1.21	3.62E-06	ABUW_RS04770	EamA family transporter
-1.20	1.20E-07	ABUW_RS04265	succinate dehydrogenase%2C hydrophobic membrane anchor protein
-1.19	7.59E-05	ABUW_RS16430	nucleoside-diphosphate kinase
-1.18	1.34E-07	ABUW_RS01995	50S ribosomal protein L3
-1.18	4.36E-06	ABUW_RS11390	redox-regulated ATPase YchF
	0.000750		amino acid synthesis family protein
-1.18	294	ABUW_RS12165	
-1.18	2.24E-06	ABUW_RS02000	50S ribosomal protein L4
-1.18	4.85E-07	ABUW_RS01855	GTP cyclohydrolase II
-1.18	3.02E-07	ABUW_RS00830	peptide chain release factor 2
-1.17	1.92E-05	ABUW_RS13160	2Fe-2S iron-sulfur cluster binding domain-containing protein
	0.000193		phosphate acetyltransferase
-1.17	039	ABUW_RS16505	
	0.000303		MBL fold metallo-hydrolase
-1.17	292	ABUW_RS00795	
-1.17	6.93E-10	ABUW_RS14430	choline dehydrogenase
-1.17	3.13E-07	ABUW_RS00175	hypothetical protein
-1.17	3.52E-08	ABUW_RS15885	YggT family protein
-1.17	4.21E-06	ABUW_RS02015	30S ribosomal protein S19
	0.000152		3-phosphoserine/phosphohydroxythreonine transaminase
-1.16	043	ABUW_RS04755	
	0.000428		ammonium transporter
-1.16	522	ABUW_RS04070	
-1.16	5.99E-07	ABUW_RS11115	sodium/proline symporter PutP
-1.16	2.10E-05	ABUW_RS12525	type VI secretion system tube protein Hcp
-1.16	5.55E-09	ABUW_RS14240	galactose mutarotase
	0.000118		cupin
-1.16	959	ABUW_RS11060	
-1.16	5.90E-10	ABUW_RS07560	protoheme IX farnesyltransferase
-1.16	1.39E-05	ABUW_RS06700	sulfur carrier protein ThiS
	0.000140		8-amino-7-oxononanoate synthase
-1.16	361	ABUW_RS15145	
	0.000527		acinetobactin non-ribosomal peptide synthetase subunit BasD
-1.15	756	ABUW_RS05755	
-1.15	1.83E-05	ABUW_RS19125	hypothetical protein
-1.15	6.91E-05	ABUW_RS08725	hypothetical protein
-1.15	6.91E-06	ABUW_RS14075	lysine--tRNA ligase
-1.15	1.03E-05	ABUW_RS05445	alpha-keto acid decarboxylase family protein
-1.15	6.15E-09	ABUW_RS18020	YgiQ family radical SAM protein
-1.14	1.51E-07	ABUW_RS02610	protein translocase subunit SecD

-1.14	0.000101	ABUW_RS09110	3-oxoadipate enol-lactonase
-1.14	131	ABUW_RS17260	preprotein translocase subunit SecG
-1.14	4.13E-07	ABUW_RS02420	30S ribosomal protein S9
-1.14	0.000935		
-1.14	096	sRNA13	
-1.13	6.62E-05	ABUW_RS17820	SulP family inorganic anion transporter
-1.13	1.81E-05	ABUW_RS07045	amidophosphoribosyltransferase
-1.13	3.75E-09	ABUW_RS00225	NAD(P)-dependent alcohol dehydrogenase
-1.13	8.41E-07	ABUW_RS04255	citrate (Si)-synthase
-1.13	8.60E-09	ABUW_RS02030	50S ribosomal protein L16
-1.13	8.00E-06	ABUW_RS15995	HPr family phosphocarrier protein
-1.13	4.41E-07	ABUW_RS13340	alanine--tRNA ligase
-1.12	1.14E-08	ABUW_RS09225	hydrolase
-1.12	5.71E-06	ABUW_RS11915	class I SAM-dependent methyltransferase
-1.12	5.36E-05	ABUW_RS10360	lipoyl synthase
-1.12	0.003660	ABUW_RS17470	DNA-directed RNA polymerase subunit beta'
-1.12	644	ABUW_RS03590	undecaprenyl-diphosphate phosphatase
-1.12	8.40E-06	ABUW_RS15770	histidinol dehydrogenase
-1.12	0.000189	ABUW_RS00730	UDP-N-acetylmuramate--L-alanine ligase
-1.11	483	ABUW_RS17750	LPS export ABC transporter permease LptF
-1.11	6.16E-08	ABUW_RS00345	fumarylacetoacetase
-1.11	8.36E-08	ABUW_RS02010	50S ribosomal protein L2
-1.10	2.40E-06	ABUW_RS09615	alpha/beta hydrolase
-1.10	5.12E-05	ABUW_RS04710	DNA gyrase subunit A
-1.10	1.92E-05	ABUW_RS16090	NAD(P)(+) transhydrogenase (Re/Si-specific) subunit beta
-1.10	2.24E-05	ABUW_RS13880	hypothetical protein
-1.10	9.16E-08	ABUW_RS17610	argininosuccinate lyase
-1.10	0.000149	ABUW_RS10515	lipid-A-disaccharide synthase
-1.10	035	ABUW_RS06575	ferredoxin--NADP reductase
-1.09	1.93E-06	ABUW_RS03185	thiolase family protein
-1.09	2.47E-07	ABUW_RS04660	DNA repair protein RadA
-1.09	6.65E-05	ABUW_RS04260	succinate dehydrogenase%2C cytochrome b556 subunit
-1.09	0.000117	ABUW_RS10105	anthranilate 1%2C2-dioxygenase large subunit
-1.09	61	ABUW_RS10810	ABC transporter permease
-1.09	2.65E-06	ABUW_RS01965	Rrf2 family transcriptional regulator
-1.09	2.21E-06	ABUW_RS06720	cold-shock protein
-1.08	1.98E-07	ABUW_RS14105	hydrogen peroxide-inducible genes activator
-1.08	0.000324	ABUW_RS17930	dihydrodipicolinate synthase family protein
-1.08	244	ABUW_RS15670	copper resistance system multicopper oxidase
-1.08	0.000339	ABUW_RS05225	glycosyltransferase family 2 protein
-1.08	782	ABUW_RS00700	exodeoxyribonuclease III
-1.08	0.000114	ABUW_RS08265	acetyl-CoA carboxylase biotin carboxyl carrier protein
-1.08	691		
-1.08	0.002897		
-1.08	404		
-1.08	4.19E-08		
-1.08	0.004105		
-1.07	368		
-1.07	5.33E-06		
-1.07	3.88E-05		
-1.07	2.71E-06		
-1.07	1.09E-07		

-1.07	3.69E-06	ABUW_RS15425	NADH-quinone oxidoreductase subunit B
-1.07	7.86E-08	ABUW_RS13305	cAMP-activated global transcriptional regulator CRP
-1.07	9.89E-06	ABUW_RS01970	flavohepotein
-1.07	2.83E-06	ABUW_RS07325	MCE family protein
-1.07	5.95E-05	ABUW_RS19350	hypothetical protein
-1.07	1.36E-05	ABUW_RS11580	taurine ABC transporter permease TauC
-1.06	6.43E-07	ABUW_RS13330	ATP phosphoribosyltransferase regulatory subunit
-1.06	0.000422	ABUW_RS16250	tRNA threonylcarbamoyladenosine dehydratase
-1.06	432	ABUW_RS16250	methionine ABC transporter ATP-binding protein
-1.06	2.94E-05	ABUW_RS07465	ribonuclease HII
-1.06	0.001674	ABUW_RS13355	AMP-binding protein
-1.06	588	ABUW_RS13355	glutamine-hydrolyzing GMP synthase
-1.06	6.40E-07	ABUW_RS11920	diaminopimelate decarboxylase
-1.06	3.63E-08	ABUW_RS18280	amino acid permease
-1.06	6.66E-07	ABUW_RS04675	Fe-S protein assembly chaperone HscA
-1.06	0.000105	ABUW_RS18430	ion channel protein Tsx
-1.06	334	ABUW_RS18430	50S ribosomal protein L18
-1.05	1.93E-06	ABUW_RS10725	pyrroline-5-carboxylate reductase
-1.05	0.006457	ABUW_RS10725	CDP-diacylglycerol--serine O-phosphatidyltransferase
-1.05	954	ABUW_RS00635	hypothetical protein
-1.05	1.13E-07	ABUW_RS02075	MFS transporter
-1.04	1.20E-08	ABUW_RS15890	peptide deformylase
-1.04	3.16E-08	ABUW_RS02320	aldehyde dehydrogenase (NADP(+))
-1.04	1.50E-07	ABUW_RS07065	5-(carboxyamino)imidazole ribonucleotide synthase
-1.04	9.38E-05	ABUW_RS03105	hypothetical protein
-1.04	1.20E-07	ABUW_RS18110	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE
-1.04	0.000490	ABUW_RS18110	DUF2799 domain-containing protein
-1.04	415	sRNA89	Zn-dependent oligopeptidase
-1.04	6.91E-05	ABUW_RS12355	glycosyltransferase
-1.04	1.64E-06	ABUW_RS18915	DNA polymerase III subunit delta
-1.04	0.046210	ABUW_RS18915	multidrug efflux transcriptional repressor AdeL
-1.04	538	ABUW_RS06835	sulfurtransferase complex subunit TusD
-1.04	1.31E-05	ABUW_RS19000	hypothetical protein
-1.04	0.004058	ABUW_RS19000	ribosome small subunit-dependent GTPase A
-1.03	218	ABUW_RS07750	DUF490 domain-containing protein
-1.03	4.02E-05	ABUW_RS10815	hypothetical protein
-1.03	0.000765	ABUW_RS07165	preprotein translocase subunit SecY
-1.03	783	ABUW_RS07165	pilus assembly protein PilM
-1.03	0.000264	ABUW_RS16330	Holliday junction branch migration DNA helicase RuvB
-1.03	394	ABUW_RS16330	LysR family transcriptional regulator
-1.03	5.20E-07	ABUW_RS06525	
-1.02	6.95E-07	ABUW_RS08375	
-1.02	0.068365	ABUW_RS13070	
-1.02	61	ABUW_RS13070	
-1.02	1.62E-05	ABUW_RS16365	
-1.02	6.88E-08	ABUW_RS07770	
-1.02	0.000552	ABUW_RS00490	
-1.02	218	ABUW_RS00490	
-1.02	1.02E-06	ABUW_RS02095	
-1.02	0.000522	ABUW_RS01425	
-1.02	193	ABUW_RS01425	
-1.01	4.62E-06	ABUW_RS04900	
-1.01	0.003655	ABUW_RS11900	
-1.01	019	ABUW_RS11900	

-1.01	7.54E-05	ABUW_RS11665	biotin-independent malonate decarboxylase subunit gamma
-1.01	6.59E-06	ABUW_RS15935	phenylalanine--tRNA ligase subunit alpha
-1.01	1.60E-05	ABUW_RS18550	D-lactate dehydrogenase
-1.01	2.92E-05	ABUW_RS00485	hypothetical protein
-1.01	2.98E-05	ABUW_RS09220	Rrf2 family transcriptional regulator
-1.01	1.51E-07	ABUW_RS06665	bifunctional prephenate dehydrogenase/3-phosphoshikimate 1-carboxyvinyltransferase
-1.00	0.000330		GTP cyclohydrolase I FoIE
-1.00	987	ABUW_RS05835	30S ribosomal protein S16
-1.00	6.06E-07	ABUW_RS01575	acyltransferase
-1.00	0.003872		
-1.00	981	ABUW_RS11310	ATP-dependent Clp protease ATP-binding subunit ClpX
-1.00	1.14E-05	ABUW_RS16525	ribosome-associated protein
-1.00	4.40E-05	ABUW_RS15990	membrane protein
-1.00	0.002397		
-1.00	196	ABUW_RS01610	hypothetical protein
-1.00	3.69E-06	ABUW_RS11875	EAL domain-containing protein
-1.00	0.000178		
-1.00	199	ABUW_RS05570	
-1.00	0.117708		
-0.99	987	sRNA104	hypothetical protein
-0.99	1.98E-05	ABUW_RS08165	outer membrane protein assembly factor BamB
-0.99	4.21E-08	ABUW_RS16395	FadR family transcriptional regulator
-0.99	2.54E-05	ABUW_RS13620	RluA family pseudouridine synthase
-0.99	2.31E-05	ABUW_RS05380	monovalent cation/H+ antiporter subunit F
-0.99	0.010079		
-0.99	145	ABUW_RS17215	restriction endonuclease subunit M
-0.99	6.12E-07	ABUW_RS17780	hypothetical protein
-0.99	0.000490		
-0.99	917	ABUW_RS03640	NfeD family protein
-0.99	2.77E-07	ABUW_RS04025	sulfate adenyltransferase subunit CysN
-0.98	1.90E-06	ABUW_RS14060	biotin--[acetyl-CoA-carboxylase] ligase
-0.98	2.31E-05	ABUW_RS15205	type VI secretion system contractile sheath large subunit
-0.98	0.000685		
-0.98	47	ABUW_RS12530	prolipoprotein diacylglycerol transferase
-0.98	3.54E-06	ABUW_RS16610	DHA2 family efflux MFS transporter permease subunit
-0.98	6.59E-06	ABUW_RS10630	efflux RND transporter permease subunit
-0.98	4.21E-05	ABUW_RS03320	acinetobactin non-ribosomal peptide synthetase subunit BasA
-0.98	0.000630		
-0.98	525	ABUW_RS05715	adenosylmethionine--8-amino-7-oxononanoate transaminase
-0.98	0.000190		
-0.98	048	ABUW_RS15150	aspartate ammonia-lyase
-0.98	0.004062		
-0.98	703	ABUW_RS10220	TetR/AcrR family transcriptional regulator
-0.98	0.000589		
-0.97	188	ABUW_RS11925	sigma-54-dependent Fis family transcriptional regulator
-0.97	0.000350		
-0.97	719	ABUW_RS17730	META domain-containing protein
-0.97	0.000523		
-0.97	76	ABUW_RS13935	DsbC family protein
-0.97	3.68E-05	ABUW_RS17700	DUF1294 domain-containing protein
-0.97	0.006124		
-0.97	875	ABUW_RS01185	gluconokinase
-0.97	6.99E-05	ABUW_RS16480	DUF333 domain-containing protein
-0.97	0.013671		
-0.97	601	ABUW_RS12405	MFS transporter
-0.97	1.64E-06	ABUW_RS08180	

-0.96	3.10E-05	ABUW_RS14800	cell division topological specificity factor MinE
-0.96	2.34E-07	ABUW_RS18600	DegT/DnrJ/EryC1/StrS aminotransferase family protein
-0.96	1.61E-06	ABUW_RS08760	adenosine kinase
-0.96	2.68E-05	ABUW_RS18675	murein biosynthesis integral membrane protein MurJ
-0.96	0.058165	571 sRNA58	
-0.96	4.06E-06	ABUW_RS09400	HlyD family secretion protein
-0.96	3.79E-07	ABUW_RS16955	multidrug efflux MATE transporter AbeM
-0.96	0.008392	526 ABUW_RS02445	DUF2147 domain-containing protein
-0.95	0.002530	099 ABUW_RS00350	amino acid permease
-0.95	5.70E-05	ABUW_RS11730	glutathione-dependent disulfide-bond oxidoreductase
-0.95	6.21E-06	ABUW_RS17675	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase
-0.95	0.011115	886 ABUW_RS14460	DUF1275 domain-containing protein
-0.95	0.012123	145 ABUW_RS19345	molecular chaperone DnaJ
-0.95	0.024119	315 ABUW_RS19705	hypothetical protein
-0.94	0.000207	628 ABUW_RS06495	DNA exonuclease
-0.94	0.000478	115 ABUW_RS12315	phenylacetate-CoA oxygenase subunit Paal
-0.94	0.019514	139 ABUW_RS08945	protocatechuate 3%2C4-dioxygenase subunit beta
-0.94	1.29E-05	ABUW_RS05565	50S ribosomal protein L31
-0.94	0.001043	315 ABUW_RS19425	IS30-like element ISAb125 family transposase
-0.93	1.92E-05	ABUW_RS00475	hypothetical protein
-0.93	1.57E-06	ABUW_RS12290	3-hydroxyacyl-CoA dehydrogenase
-0.93	0.001738	766 ABUW_RS03345	purine-binding chemotaxis protein CheW
-0.93	2.13E-05	ABUW_RS01710	amino acid permease
-0.93	1.20E-05	ABUW_RS01395	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2%2C6-diaminopimelate ligase
-0.92	0.003113	829 ABUW_RS13790	ABC transporter permease
-0.92	3.12E-06	ABUW_RS18275	aminoglycoside nucleotidyltransferase ANT(3'')-IIa
-0.92	3.50E-05	ABUW_RS16535	trigger factor
-0.92	1.48E-06	ABUW_RS07470	hypothetical protein
-0.91	6.61E-05	ABUW_RS16765	glycosyltransferase family 4 protein
-0.91	4.07E-05	ABUW_RS18935	low temperature requirement protein A
-0.91	0.001002	38 ABUW_RS01755	peptidase S8
-0.91	9.86E-07	ABUW_RS14065	sulfate adenyltransferase subunit CysD
-0.91	0.000374	989 ABUW_RS12180	cytochrome b
-0.91	4.07E-05	ABUW_RS06705	DUF423 domain-containing protein
-0.91	0.102877	29 ABUW_RS13085	transposase
-0.91	0.000551	991 ABUW_RS11625	cytochrome d ubiquinol oxidase subunit II
-0.91	7.64E-05	ABUW_RS03350	methyl-accepting chemotaxis protein
-0.90	0.000134	847 ABUW_RS06625	penicillin-binding protein 1B
-0.90	0.000105	234 ABUW_RS01590	50S ribosomal protein L19

-0.90	2.87E-05	ABUW_RS18140	MFS transporter
-0.90	2.30E-07	ABUW_RS00020	DNA topoisomerase (ATP-hydrolyzing) subunit B
-0.90	1.88E-06	ABUW_RS08880	CTP synthase
-0.90	0.673658	078	acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha
-0.90	5.79E-05	ABUW_RS02400	phosphatase PAP2 family protein
-0.90	4.85E-06	ABUW_RS16415	helix-turn-helix domain-containing protein
-0.89	0.000208	757	phenylacetate-CoA oxygenase/reductase subunit PaaK
-0.89	0.000232	443	sorbose dehydrogenase family protein
-0.89	0.000111	9	nitrite/sulfite reductase
-0.88	1.15E-06	ABUW_RS13955	adenylate kinase
-0.88	7.64E-05	ABUW_RS05270	rRNA large subunit pseudouridine synthase E
-0.88	4.52E-05	ABUW_RS17555	type II secretion system protein GspD
-0.88	1.29E-05	ABUW_RS17680	hypothetical protein
-0.88	0.001206	519	PAS domain-containing sensor histidine kinase
-0.88	4.93E-06	ABUW_RS08435	nitrogen regulation protein NR(I)
-0.88	0.000449	22	SPFH/Band 7/PHB domain protein
-0.88	2.59E-05	ABUW_RS18560	transcriptional regulator LldR
-0.88	6.20E-05	ABUW_RS02490	YfiR family protein
-0.88	0.000105	537	citrate transporter
-0.88	0.001756	606	PLP-dependent aminotransferase family protein
-0.88	0.000144	538	hemolysin III
-0.87	1.58E-05	ABUW_RS01990	30S ribosomal protein S10
-0.87	0.001181	763	cation transporter
-0.87	0.000269	551	sulfite exporter TauE/SafE family protein
-0.87	0.040427	229	hypothetical protein
-0.87	1.37E-05	ABUW_RS01390	penicillin-binding protein PBP3
-0.87	0.001298	13	LysR family transcriptional regulator
-0.87	0.000420	578	transcription elongation factor GreA
-0.87	0.000188	42	peptide chain release factor 1
-0.87	1.24E-06	ABUW_RS00440	glutamine--fructose-6-phosphate transaminase (isomerizing)
-0.87	0.001722	167	arginine N-succinyltransferase
-0.87	0.012207	154	threonine transporter RhtB
-0.86	0.000278	356	septum formation protein Maf
-0.86	0.011791	973	class I SAM-dependent methyltransferase
-0.86	4.28E-06	ABUW_RS18805	isoleucine--tRNA ligase
-0.86	0.000679	72	esterase
-0.86	0.000207	628	FAD-dependent oxidoreductase
-0.86	0.000370	386	LPS export ABC transporter permease LptG
-0.86			

	0.008241		hypothetical protein
-0.86	828	ABUW_RS06845	
	0.000343		BCCT family transporter
-0.85	813	ABUW_RS14415	
	0.001229		bile acid:sodium symporter family protein
-0.85	537	ABUW_RS00310	
			elongation factor G
-0.85	2.45E-05	ABUW_RS14855	
	0.000473		histidinol-phosphate transaminase
-0.85	527	ABUW_RS15765	
			poly-beta-1%2C6 N-acetyl-D-glucosamine synthase
-0.85	6.86E-05	ABUW_RS14365	
	0.002457		disulfide bond formation protein B
-0.85	284	ABUW_RS00570	
	0.000275		chorismate synthase
-0.85	854	ABUW_RS10380	
	0.000268		orotate phosphoribosyltransferase
-0.85	701	ABUW_RS00705	
	0.000101		30S ribosomal protein S12 methylthiotransferase RimO
-0.85	131	ABUW_RS08445	
			hypothetical protein
-0.85	2.60E-05	ABUW_RS00295	
	0.005444		cupin domain-containing protein
-0.85	325	ABUW_RS14300	
	0.003717		NAD(P)-dependent oxidoreductase
-0.85	982	ABUW_RS16070	
	0.000533		SDR family oxidoreductase
-0.85	567	ABUW_RS11740	
			tRNA lysidine(34) synthetase TilS
-0.85	1.26E-05	ABUW_RS15895	
	0.000382		ASCH domain-containing protein
-0.84	136	ABUW_RS16700	
			RNA methyltransferase
-0.84	6.99E-05	ABUW_RS11485	
	0.009848		hypothetical protein
-0.84	29	ABUW_RS13360	
			30S ribosomal protein S17
-0.84	6.57E-05	ABUW_RS02040	
	0.004194		maleylacetoacetate isomerase
-0.84	541	ABUW_RS00340	
			MATE family efflux transporter
-0.84	3.73E-05	ABUW_RS00540	
	0.086820		
-0.84	601	sRNA93	
	0.001214		PKHD-type hydroxylase
-0.84	432	ABUW_RS16545	
	0.001934		RNA pyrophosphohydrolase
-0.84	431	ABUW_RS16860	
			bifunctional phosphopantothenoylecysteine decarboxylase/phosphopantothenate--
-0.83	4.19E-05	ABUW_RS02600	
	0.023261		cysteine ligase CoaBC
-0.83	298	ABUW_RS10125	
			hypothetical protein
-0.83	2.45E-05	ABUW_RS08885	
			3-deoxy-8-phosphooctulonate synthase
-0.83	8.85E-05	ABUW_RS16020	
			polynucleotide adenyllyltransferase PcnB
-0.83	9.66E-06	ABUW_RS10985	
			lipid A export permease/ATP-binding protein MsbA
-0.83	9.75E-05	ABUW_RS17670	
	0.061482		putative lipid II flippase FtsW
-0.83	954	ABUW_RS12990	
	0.000435		hypothetical protein
-0.82	972	ABUW_RS05845	
	0.003655		xanthine dehydrogenase molybdopterin binding subunit
-0.82	019	ABUW_RS01720	
	0.023669		aspartate aminotransferase family protein
-0.82	882	sRNA19	
	0.006683		
-0.82	006	ABUW_RS07160	
	0.033284		class I SAM-dependent methyltransferase
-0.82	299	ABUW_RS14050	
	0.013506		hypothetical protein
-0.82	931	ABUW_RS15840	
			carbon-nitrogen hydrolase family protein
-0.82	9.32E-06	ABUW_RS17505	
			preprotein translocase subunit SecE

-0.81	8.08E-05	ABUW_RS04180	serine--tRNA ligase
-0.81	3.88E-05	ABUW_RS07575	cytochrome o ubiquinol oxidase subunit I
-0.81	0.008815		
-0.81	674	sRNA88	
-0.81	0.002199		aldehyde dehydrogenase (NADP(+))
-0.81	018	ABUW_RS13535	
-0.81	0.002332		cell envelope integrity protein TolA
-0.81	765	ABUW_RS04875	
-0.81	0.018488		poly-beta-1%2C6 N-acetyl-D-glucosamine synthase
-0.81	549	ABUW_RS07610	
-0.81	0.000204		AzIC family ABC transporter permease
-0.81	155	ABUW_RS11415	
-0.81	0.005396		L-valine transporter subunit YgaH
-0.81	365	ABUW_RS11420	
-0.81	0.000615		hypothetical protein
-0.81	905	ABUW_RS12460	
-0.81	0.004944		SDR family oxidoreductase
-0.81	983	ABUW_RS14225	
-0.81	0.000834		apolipoprotein N-acyltransferase
-0.81	208	ABUW_RS17055	
-0.81	0.020801		hypothetical protein
-0.81	972	ABUW_RS09515	
-0.81	0.000577		bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate
-0.80	055	ABUW_RS04450	cyclohydrolase FoLD
-0.80	0.149104		hypothetical protein
-0.80	638	ABUW_RS13075	
-0.80	0.024792		tRNA pseudouridine(55) synthase TruB
-0.80	324	ABUW_RS01605	
-0.80	0.001142		tRNA 2-thiouridine(34) synthase MnmA
-0.80	888	ABUW_RS05500	
-0.80	0.003952		16S rRNA (guanine(966)-N(2))-methyltransferase RsmD
-0.80	719	ABUW_RS13975	
-0.80	0.003918		1%2C2-phenylacetyl-CoA epoxidase subunit A
-0.80	798	ABUW_RS12325	
-0.80	0.000382		SDR family NAD(P)-dependent oxidoreductase
-0.80	524	ABUW_RS16085	
-0.80	0.000202		FAD-binding oxidoreductase
-0.80	395	ABUW_RS13635	
-0.80	0.001248		DMT family transporter
-0.80	605	ABUW_RS17290	
-0.80	0.001118		HAD-IIIa family hydrolase
-0.80	428	ABUW_RS12850	
-0.80	0.001934		1%2C2-phenylacetyl-CoA epoxidase subunit B
-0.79	431	ABUW_RS12320	
-0.79	0.000684		ATP-binding cassette domain-containing protein
-0.79	338	ABUW_RS11585	
-0.79	0.003892		CoA-acylating methylmalonate-semialdehyde dehydrogenase
-0.79	005	ABUW_RS07135	
-0.79	0.000230		M3 family metalloproteinase
-0.79	142	ABUW_RS02175	
-0.79	0.001063		pyridoxal phosphate-dependent aminotransferase
-0.79	552	ABUW_RS05120	
-0.79	0.001407		LysR family transcriptional regulator
-0.78	4	ABUW_RS07210	
-0.78	0.006872		transketolase
-0.78	841	ABUW_RS14210	
-0.78	0.004463		
-0.78	913	sRNA100	
-0.78	0.002829		type VI secretion system tip protein VgrG
-0.78	848	ABUW_RS00575	
-0.78	0.000201		amino acid permease
-0.78	631	ABUW_RS04665	
-0.78	0.000330		iron-containing redox enzyme family protein
-0.78	741	ABUW_RS11860	
-0.78	0.000141		riboflavin synthase
-0.78	461	ABUW_RS17775	
-0.78	0.039642		chromate transporter
-0.77	89	ABUW_RS11515	
-0.77	0.001859		signal peptidase I
-0.77	53	ABUW_RS05055	

	0.000420		ISC system 2Fe-2S type ferredoxin
-0.77	744	ABUW_RS10730	
	0.000110		uroporphyrinogen-III C-methyltransferase
-0.77	494	ABUW_RS04185	
	0.000443		YnfA family protein
-0.77	354	ABUW_RS08830	
	8.86E-06	ABUW_RS07040	CvpA family protein
	0.002241		oligoribonuclease
-0.77	167	ABUW_RS16360	
	0.001121		symmetrical bis(5'-nucleosyl)-tetraphosphatase
-0.77	823	ABUW_RS02440	
	0.000816		HAD-IB family hydrolase
-0.77	706	ABUW_RS16855	
	0.002033		alpha/beta hydrolase
-0.77	6	ABUW_RS00685	
	0.000220		sodium:proton antiporter
-0.77	183	ABUW_RS04330	
	0.011365		RNA-binding protein
-0.77	152	ABUW_RS16705	
	0.010454		2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase
-0.77	763	ABUW_RS16015	
	0.008795		hypothetical protein
-0.77	181	ABUW_RS18345	
	0.000296		50S ribosomal protein L36
-0.76	746	ABUW_RS02100	
	0.000240		lipoprotein signal peptidase
-0.76	149	ABUW_RS18810	
	0.019217		hypoxanthine phosphoribosyltransferase
-0.76	061	ABUW_RS18975	
	0.006187		VOC family protein
-0.76	552	ABUW_RS14685	
	0.006441		purine permease
-0.76	956	ABUW_RS00640	
	0.009704		microcin C ABC transporter permease YejB
-0.76	085	ABUW_RS13795	
	0.002149		fibronectin type III domain-containing protein
-0.75	115	ABUW_RS12915	
	0.067753		protocatechuate 3%2C4-dioxygenase subunit alpha
-0.75	136	ABUW_RS08950	
	0.001161		NAD(P)/FAD-dependent oxidoreductase
-0.75	507	ABUW_RS05250	
	0.004590		hypothetical protein
-0.75	355	ABUW_RS13705	
	0.000347		50S ribosomal protein L1
-0.75	129	ABUW_RS17490	
	8.48E-05	ABUW_RS15905	exopolyphosphatase
-0.75	0.003601		ABC transporter substrate-binding protein
-0.75	349	ABUW_RS06530	
	0.001721		phosphoenolpyruvate--protein phosphotransferase
-0.75	805	ABUW_RS08630	
	0.019689		ABC transporter permease
-0.75	651	ABUW_RS07460	
	0.000113		leucyl aminopeptidase
-0.75	87	ABUW_RS17755	
	9.20E-05	ABUW_RS17140	exonuclease V subunit gamma
-0.75	0.000882		aspartate/tyrosine/aromatic aminotransferase
-0.75	807	ABUW_RS18545	
	0.002742		peptide chain release factor 3
-0.75	885	ABUW_RS16275	
	0.000752		1-deoxy-D-xylulose-5-phosphate synthase
-0.75	009	ABUW_RS01860	
	0.033453		membrane protein
-0.74	371	ABUW_RS01430	
	0.000890		HlyD family secretion protein
-0.74	531	ABUW_RS15310	
	0.000340		hypothetical protein
-0.74	013	ABUW_RS12545	
	0.019539		SDR family oxidoreductase
-0.74	041	ABUW_RS09070	

	0.073615		4-carboxymuconolactone decarboxylase
-0.74	588	ABUW_RS05990	
	0.019861		3-oxoadipyl-CoA thiolase
-0.74	735	ABUW_RS12025	
	0.000234		acyl-CoA dehydrogenase
-0.74	275	ABUW_RS10665	
	0.054802		copper resistance protein B
-0.74	036	ABUW_RS15665	
	0.000612		DNA mismatch repair protein MutS
-0.74	753	ABUW_RS12780	
	0.004493		tannase/feruloyl esterase family alpha/beta hydrolase
-0.74	86	ABUW_RS13525	
	0.001573		phosphoribosylaminoimidazolesuccinocarboxamide synthase
-0.74	478	ABUW_RS00290	
	0.010245		pyridoxal phosphate-dependent aminotransferase
-0.74	068	ABUW_RS11465	
	6.04E-05		energy-dependent translational throttle protein ETTA
-0.73	0.000340	ABUW_RS01285	
	385	ABUW_RS05370	glutamate-1-semialdehyde 2C1-aminomutase
	0.000273		DUF2946 domain-containing protein
-0.73	507	ABUW_RS18105	
	0.000664		lipid asymmetry maintenance ABC transporter permease subunit MlaE
-0.73	67	ABUW_RS01885	
	0.017294		50S ribosomal protein L3 N(5)-glutamine methyltransferase
-0.73	302	ABUW_RS10385	
	0.001672		YheV family putative metal-binding protein
-0.73	947	ABUW_RS02170	
	0.244029		RidA family protein
-0.72	643	ABUW_RS18440	
	0.000963		dihydrolipoyl dehydrogenase
-0.72	975	ABUW_RS10340	
	0.001121		methionine--tRNA ligase
-0.72	251	ABUW_RS15285	
	0.000518		porphobilinogen synthase
-0.72	386	ABUW_RS14665	
	0.011481		UDP-N-acetylmuramate dehydrogenase
-0.72	316	ABUW_RS08215	
	0.001273		50S ribosomal protein L30
-0.72	206	ABUW_RS02085	
	0.001312		tetratricopeptide repeat protein
-0.72	25	ABUW_RS15000	
	0.004177		phosphate ABC transporter permease subunit PstC
-0.71	518	ABUW_RS05460	
	0.001910		homoserine kinase
-0.71	584	ABUW_RS01180	
	0.002989		hypothetical protein
-0.71	795	ABUW_RS09665	
	0.001558		TerC family protein
-0.71	472	ABUW_RS17985	
	0.035412		ribosome assembly RNA-binding protein YhbY
-0.71	199	ABUW_RS04400	
	0.081317		DUF4951 domain-containing protein
-0.71	29	ABUW_RS15845	
	0.001059		FAD-dependent monooxygenase
-0.71	833	ABUW_RS13875	
	0.006930		DUF4105 domain-containing protein
-0.71	308	ABUW_RS05825	
	0.001041		LysR family transcriptional regulator
-0.71	959	ABUW_RS05295	
	0.009356		xanthine dehydrogenase accessory protein XdhC
-0.71	61	ABUW_RS05850	
	0.002618		lipoprotein-releasing ABC transporter ATP-binding protein LolD
-0.71	317	ABUW_RS04780	
	0.001893		septal ring lytic transglycosylase RlpA family protein
-0.71	693	ABUW_RS06070	
	0.000852		GFA family protein
-0.70	008	ABUW_RS16990	
	0.024119		DUF4184 family protein
-0.70	315	ABUW_RS02945	

	0.001106		DNA polymerase III subunit beta
-0.70	647	ABUW_RS00010	
	0.000298		glutamyl-tRNA reductase
-0.70	302	ABUW_RS14995	
	0.064368		type III pantothenate kinase
-0.70	581	ABUW_RS15210	
	0.010670		anthranilate 1%2C2-dioxygenase small subunit
-0.70	335	ABUW_RS10110	
	0.011998		amino acid ABC transporter permease
-0.70	622	ABUW_RS11335	
	0.313967		helix-turn-helix transcriptional regulator
-0.70	707	ABUW_RS11200	
	0.000446		50S ribosomal protein L15
-0.70	907	ABUW_RS02090	
	0.005890		urease accessory protein
-0.69	046	ABUW_RS13980	
	0.005687		glucose/quininate/shikimate family membrane-bound PQQ-dependent dehydrogenase
-0.69	605	ABUW_RS08970	
	0.043966		
-0.69	987	sRNA42	
	0.098578		hypothetical protein
-0.69	456	ABUW_RS19075	
	0.000602		response regulator
-0.69	809	ABUW_RS00900	
	0.002516		DUF2171 domain-containing protein
-0.69	508	ABUW_RS07145	
	0.001252		hybrid sensor histidine kinase/response regulator
-0.69	682	ABUW_RS03355	
	0.050556		spore coat protein U domain-containing protein
-0.69	853	ABUW_RS07250	
	0.035317		cytochrome bd-I oxidase subunit CydX
-0.69	933	ABUW_RS08730	
	0.098531		
-0.69	747	sRNA21	
	0.014878		amino acid permease
-0.68	468	ABUW_RS04000	
	0.009525		50S ribosomal protein L22
-0.68	595	ABUW_RS02020	
	0.001017		sulfurtransferase
-0.68	587	ABUW_RS00505	
	0.000167		ABC transporter ATP-binding protein
-0.68	692	ABUW_RS11090	
	0.006646		efflux RND transporter periplasmic adaptor subunit
-0.68	223	ABUW_RS00165	
	0.078131		lytic transglycosylase domain-containing protein
-0.68	375	ABUW_RS04540	
	0.006482		spore coat protein U domain-containing protein
-0.68	556	ABUW_RS07975	
	0.001106		NAD-dependent DNA ligase LigA
-0.68	647	ABUW_RS15180	
	0.005816		TonB-dependent siderophore receptor
-0.68	688	ABUW_RS18465	
	0.004027		thymidylate synthase
-0.68	055	ABUW_RS16625	
	0.009404		multidrug efflux RND transporter outer membrane subunit AdeH
-0.68	821	ABUW_RS06510	
	0.000608		chromosomal replication initiator protein DnaA
-0.68	596	ABUW_RS00005	
	0.018962		malonyl-ACP O-methyltransferase BioC
-0.68	645	ABUW_RS15140	
	0.003997		dicarboxylate/amino acid:cation symporter
-0.68	935	ABUW_RS11470	
	0.109801		type IV conjugative transfer system protein TraL
-0.67	132	ABUW_RS19470	
	0.001233		phage tail tape measure protein
-0.67	272	ABUW_RS02750	
	0.055057		glutathione transferase
-0.67	656	ABUW_RS11725	
	0.014264		taurine ABC transporter substrate-binding protein
-0.67	461	ABUW_RS11590	

	0.002242		biopolymer transporter ExbD
-0.67	163	ABUW_RS10990	
	0.002248		hypothetical protein
-0.67	432	ABUW_RS05220	
	0.000872		LysR family transcriptional regulator
-0.67	351	ABUW_RS14035	
	0.005994		D-alanyl-D-alanine carboxypeptidase PBP6B
-0.67	038	ABUW_RS05255	
	0.002229		type I DNA topoisomerase
-0.67	209	ABUW_RS16725	
	0.000682		ATP-binding protein
-0.67	414	ABUW_RS17190	
	0.003373		adenylosuccinate lyase
-0.66	774	ABUW_RS05490	
	0.001231		peroxiredoxin
-0.66	691	ABUW_RS13195	
	0.002562		ribonuclease G
-0.66	371	ABUW_RS03540	
	0.020247		hypothetical protein
-0.66	438	ABUW_RS14495	
	0.007817		ATP-binding cassette domain-containing protein
-0.66	479	ABUW_RS00035	
	0.004536		aldehyde dehydrogenase family protein
-0.66	805	ABUW_RS05435	
	0.005152		aspartate aminotransferase family protein
-0.66	249	ABUW_RS08680	
	0.080035		hypothetical protein
-0.66	464	ABUW_RS03615	
	0.000986		D-alanine--D-alanine ligase
-0.66	047	ABUW_RS00735	
	0.015117		DNA-directed RNA polymerase subunit omega
-0.66	886	ABUW_RS01525	
	0.047450		hypothetical protein
-0.66	426	ABUW_RS03635	
	0.001656		2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase
-0.66	146	ABUW_RS04285	
	0.016371		LysR family transcriptional regulator
-0.66	547	ABUW_RS11720	
	0.011380		peptide antibiotic transporter SbmA
-0.66	244	ABUW_RS03480	
	0.029675		4-phosphoerythronate dehydrogenase
-0.66	818	ABUW_RS04645	
	0.002229		ABC transporter permease
-0.66	209	ABUW_RS06095	
	0.001975		phosphate ABC transporter permease PstA
-0.66	73	ABUW_RS05465	
	0.072024		DOMON-like domain-containing protein
-0.65	065	ABUW_RS04395	
	0.008254		MFS transporter
-0.65	514	ABUW_RS10150	
	0.037702		peptide chain release factor N(5)-glutamine methyltransferase
-0.65	741	ABUW_RS07660	
	0.041946		MFS transporter
-0.65	649	ABUW_RS10230	
	0.006347		intracellular septation protein (IspZ)
-0.65	453	ABUW_RS02580	
	0.008988		nicotinate-nicotinamide nucleotide adenylyltransferase
-0.64	694	ABUW_RS04940	
	0.002842		50S ribosomal protein L33
-0.64	952	ABUW_RS16680	
	0.007253		protein TolQ
-0.64	452	ABUW_RS04885	
	0.006954		cytochrome b562
-0.64	268	ABUW_RS00025	
	0.016631		APC family permease
-0.64	05	ABUW_RS12350	
	0.002505		ATP-dependent dsDNA exonuclease
-0.64	262	ABUW_RS14700	
	0.001135		NAD-dependent epimerase/dehydratase family protein
-0.64	012	ABUW_RS01930	

	0.002170		50S ribosomal protein L27
-0.64	249	ABUW_RS04165	
	0.003601		BapA prefix-like domain-containing protein
-0.64	349	ABUW_RS04495	
	0.000962		4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase
-0.64	029	ABUW_RS15010	
	0.035409		3-hydroxyacyl-CoA dehydrogenase
-0.64	201	ABUW_RS07680	
	0.003188		3-deoxy-D-manno-octulosonic acid transferase
-0.64	223	ABUW_RS00845	
	0.013764		Cd(II)/Pb(II)-responsive transcriptional regulator
-0.64	191	ABUW_RS17845	
	0.005768		lauroyl acyltransferase
-0.64	401	ABUW_RS12760	
	0.019333		hypothetical protein
-0.63	751	ABUW_RS06165	
	0.161528		pyridine nucleotide-disulfide oxidoreductase
-0.63	814	ABUW_RS09215	
	0.021416		protein translocase subunit SecF
-0.63	818	ABUW_RS02605	
	0.018076		GNAT family N-acetyltransferase
-0.63	266	ABUW_RS07430	
	0.060478		ABC transporter permease
-0.63	481	ABUW_RS11385	
	0.236022		DNA-binding protein
-0.63	501	ABUW_RS14625	
	0.016309		urea carboxylase
-0.63	836	ABUW_RS12590	
	0.036672		16S rRNA (cytidine(1402)-2'-O)-methyltransferase
-0.63	025	ABUW_RS13840	
	0.004312		hypothetical protein
-0.62	042	ABUW_RS10325	
	0.000763		hypothetical protein
-0.62	757	ABUW_RS15700	
	0.014879		hypothetical protein
-0.62	47	ABUW_RS16325	
	0.007135		glutamate--tRNA ligase
-0.62	464	ABUW_RS01365	
	0.549070		
-0.62	457	sRNA65	
	0.000942		dihydrolipoyl dehydrogenase
-0.62	389	ABUW_RS04290	
	0.003877		bifunctional (p)ppGpp synthetase/guanosine-3'-bis(diphosphate) 3'-pyrophosphohydrolase
-0.62	193	ABUW_RS16040	
	0.018135		tol-pal system-associated acyl-CoA thioesterase
-0.62	814	ABUW_RS04890	
	0.029455		nitrite reductase small subunit NirD
-0.62	954	ABUW_RS08300	
	0.066856		hypothetical protein
-0.61	635	ABUW_RS03730	
	0.016296		cytochrome ubiquinol oxidase subunit I
-0.61	942	ABUW_RS11620	
	0.065484		CoA transferase subunit B
-0.61	668	ABUW_RS10185	
	0.046135		muconate cycloisomerase
-0.61	728	ABUW_RS09140	
	0.006226		Holliday junction branch migration protein RuvA
-0.61	388	ABUW_RS04905	
	0.002993		UDP-N-acetyl-D-mannosamine dehydrogenase
-0.61	626	ABUW_RS18635	
	0.019989		glutamate/aspartate:proton symporter GltP
-0.61	074	ABUW_RS16770	
	0.007700		hypothetical protein
-0.61	201	ABUW_RS08815	
	0.005456		molybdenum cofactor biosynthesis protein MoaE
-0.61	948	ABUW_RS08330	
	0.011736		APH(3')-VI family aminoglycoside O-phosphotransferase
-0.61	558	ABUW_RS19420	
	0.004777		glucose 1-dehydrogenase
-0.60	591	ABUW_RS11850	

	0.002641		ATP-dependent DNA helicase PcrA
-0.60	076	ABUW_RS16710	
	0.022240		hypothetical protein
-0.60	513	ABUW_RS15110	
	0.001936		DNA helicase
-0.60	827	ABUW_RS17185	
	0.038417		
-0.60	504	sRNA91	
	0.004426		TIGR00730 family Rossman fold protein
-0.60	634	ABUW_RS01910	
	0.008344		Xaa-Pro aminopeptidase
-0.60	304	ABUW_RS13885	
	0.051343		hypothetical protein
-0.60	883	ABUW_RS17955	
	0.001659		hypothetical protein
-0.60	217	ABUW_RS16730	
	0.161466		hypothetical protein
-0.60	279	ABUW_RS03460	
	0.001699		HAMP domain-containing protein
-0.59	681	ABUW_RS01255	
	0.018888		H-NS histone family protein
-0.59	753	ABUW_RS19085	
	0.013427		HIT family protein
-0.59	864	ABUW_RS00250	
	0.001166		50S ribosomal protein L28
-0.59	859	ABUW_RS16675	
	0.002089		1-deoxy-D-xylulose-5-phosphate reductoisomerase
-0.59	978	ABUW_RS08470	
	0.002872		ribonucleotide-diphosphate reductase subunit beta
-0.59	171	ABUW_RS15470	
	0.029807		ABC transporter permease
-0.59	566	ABUW_RS10805	
	0.002981		hypothetical protein
-0.59	354	ABUW_RS03100	
	0.015691		glutaminase
-0.59	548	ABUW_RS14255	
	0.021591		PilT/PilU family type 4a pilus ATPase
-0.59	298	ABUW_RS14715	
	0.003918		glutamate synthase large subunit
-0.59	798	ABUW_RS01465	
	0.003771		efflux RND transporter permease subunit
-0.59	57	ABUW_RS00170	
	0.021676		ferrous iron transporter B
-0.59	029	ABUW_RS17685	
	0.021961		MFS transporter
-0.58	094	ABUW_RS14245	
	0.003223		ParB/RepB/Spo0J family partition protein
-0.58	719	ABUW_RS19145	
	0.004227		sensor histidine kinase KdpD
-0.58	121	ABUW_RS07735	
	0.004163		acetyltransferase
-0.58	087	ABUW_RS18605	
	0.001859		membrane protein
-0.58	53	ABUW_RS05145	
	0.003832		adenosylhomocysteinase
-0.58	318	ABUW_RS05980	
	0.006681		3-methyl-2-oxobutanoate hydroxymethyltransferase
-0.58	124	ABUW_RS16010	
	0.058003		MFS transporter
-0.58	936	ABUW_RS01660	
	0.004426		oxygen-dependent coproporphyrinogen oxidase
-0.58	634	ABUW_RS01850	
	0.041339		ABC transporter permease
-0.58	579	ABUW_RS04735	
	0.035805		peptidoglycan editing factor PgeF
-0.58	108	ABUW_RS14975	
	0.009318		penicillin-binding protein 2
-0.58	031	ABUW_RS13970	
	0.120050		cache protein
-0.57	874	ABUW_RS13625	

	0.050739		low molecular weight phosphotyrosine protein phosphatase
-0.57	866	ABUW_RS08210	
	0.017378		hypothetical protein
-0.57	884	ABUW_RS08315	
	0.037879		ImmA/IrrE family metallo-endopeptidase
-0.57	468	ABUW_RS16125	
	0.005095		Holliday junction resolvase RuvX
-0.57	637	ABUW_RS17320	
	0.016138		MacB family efflux pump subunit
-0.57	861	ABUW_RS16340	
	0.026949		hypothetical protein
-0.57	836	ABUW_RS17580	
	0.002773		2-octaprenylphenol hydroxylase
-0.57	498	ABUW_RS17170	
	0.010863		ABC transporter ATP-binding protein
-0.57	794	ABUW_RS06100	
	0.080632		glutamine amidotransferase
-0.57	072	ABUW_RS07890	
	0.550178		
-0.57	986	sRNA8	
	0.021157		DUF445 domain-containing protein
-0.57	485	ABUW_RS00550	
	0.010383		MotA/TolQ/ExbB proton channel family protein
-0.57	15	ABUW_RS16650	
	0.005850		AI-2E family transporter
-0.57	808	ABUW_RS01675	
	0.044427		hypothetical protein
-0.57	897	ABUW_RS09700	
	0.006263		transcriptional repressor NrdR
-0.57	133	ABUW_RS17790	
	0.069853		FAD-binding oxidoreductase
-0.57	011	ABUW_RS05640	
	0.091386		rhodanese-related sulfurtransferase
-0.57	776	ABUW_RS04245	
	0.005287		serine hydroxymethyltransferase
-0.57	968	ABUW_RS06505	
	0.024133		amino acid permease
-0.57	643	ABUW_RS13590	
	0.139365		formate dehydrogenase accessory sulfurtransferase FdhD
-0.57	239	ABUW_RS04635	
	0.428398		
-0.57	76	sRNA77	
	0.024377		RdgB/HAM1 family non-canonical purine NTP pyrophosphatase
-0.57	535	ABUW_RS16570	
	0.021416		DUF441 domain-containing protein
-0.56	818	ABUW_RS07815	
	0.073304		trimeric intracellular cation channel family protein
-0.56	718	ABUW_RS17975	
	0.009613		protease HtpX
-0.56	992	ABUW_RS04535	
	0.082837		phage recombination protein Bet
-0.56	031	ABUW_RS06790	
	0.025937		ferrous iron transport protein A
-0.56	637	ABUW_RS17690	
	0.006872		23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD
-0.56	841	ABUW_RS16045	
	0.063731		YbaB/EbFC family nucleoid-associated protein
-0.55	772	ABUW_RS10440	
	0.056894		hypothetical protein
-0.55	208	ABUW_RS05215	
	0.026712		MFS transporter
-0.55	005	ABUW_RS17970	
	0.168910		cell division protein FtsL
-0.55	139	ABUW_RS01385	
	0.015033		hypothetical protein
-0.55	437	ABUW_RS08370	
	0.048158		amino acid permease
-0.55	038	ABUW_RS13640	
	0.035216		Yail/YqxD family protein
-0.55	695	ABUW_RS04765	

	0.004934		bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP
-0.55	377	ABUW_RS07480	cyclohydrolase
	0.207068		ankyrin repeat domain-containing protein
-0.55	846	ABUW_RS18825	
	0.016335		YdcF family protein
-0.55	708	ABUW_RS08220	
	0.007479		molybdopterin molybdotransferase MoeA
-0.55	178	ABUW_RS08340	
	0.004793		ferrochelatase
-0.55	804	ABUW_RS17015	
	0.038463		phosphate regulon sensor histidine kinase PhoR
-0.54	484	ABUW_RS00520	
	0.026735		ribonuclease III
-0.54	133	ABUW_RS05065	
	0.033284		bile acid:sodium symporter
-0.54	299	ABUW_RS05560	
	0.006261		inositol monophosphatase
-0.54	713	ABUW_RS01865	
	0.037121		hypothetical protein
-0.54	757	ABUW_RS07150	
	0.111264		hypothetical protein
-0.54	864	ABUW_RS06985	
	0.005410		pyridoxal phosphate-dependent aminotransferase
-0.54	761	ABUW_RS00545	
	0.006822		tetratricopeptide repeat protein
-0.54	844	ABUW_RS16400	
	0.004827		penicillin-binding protein PBP1a
-0.54	941	ABUW_RS01420	
	0.016371		methyltransferase domain-containing protein
-0.54	547	ABUW_RS01415	
	0.021591		catechol 1%2C2-dioxygenase
-0.54	298	ABUW_RS09130	
	0.027315		energy transducer TonB
-0.54	197	ABUW_RS16655	
	0.034559		glycerol kinase GlpK
-0.54	252	ABUW_RS04470	
	0.005602		protein-disulfide reductase DsbD
-0.53	574	ABUW_RS00675	
	0.023354		GTP-binding protein
-0.53	03	ABUW_RS14390	
	0.013643		murein L%2CD-transpeptidase
-0.53	637	ABUW_RS05805	
	0.007978		acyl-CoA dehydrogenase
-0.53	042	ABUW_RS05995	
	0.008330		acyl-CoA thioesterase
-0.53	842	ABUW_RS02545	
	0.012915		cysteine--tRNA ligase
-0.53	103	ABUW_RS12860	
	0.033791		glutamate synthase subunit beta
-0.53	361	ABUW_RS01470	
	0.068914		sulfite exporter TauE/SafE family protein
-0.53	12	ABUW_RS10305	
	0.085652		MarC family protein
-0.53	989	ABUW_RS14405	
	0.049718		pyrroloquinoline-quinone synthase PqqC
-0.53	118	ABUW_RS10050	
	0.016677		lipoprotein-releasing ABC transporter permease subunit
-0.53	102	ABUW_RS04775	
	0.047249		TerC family protein
-0.52	012	ABUW_RS18945	
	0.591109		ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2
-0.52	053	ABUW_RS19305	
	0.026943		glyceraldehyde-3-phosphate dehydrogenase
-0.52	565	ABUW_RS05155	
	0.119272		CoA transferase
-0.52	307	ABUW_RS15590	
	0.023260		aquaporin Z
-0.52	385	ABUW_RS01160	
	0.019405		trehalose-6-phosphate synthase
-0.52	136	ABUW_RS15165	

	0.018271		RHS repeat-associated core domain-containing protein
-0.52	308	ABUW_RS13755	
	0.012582		4-hydroxy-tetrahydrodipicolinate reductase
-0.52	83	ABUW_RS00190	
	0.118306		alanine racemase
-0.52	095	ABUW_RS18445	
	0.014679		anthranilate phosphoribosyltransferase
-0.52	374	ABUW_RS05865	
	0.045570		tRNA pseudouridine(38-40) synthase TruA
-0.52	985	ABUW_RS16800	
	0.036630		amidohydrolase
-0.52	375	ABUW_RS11545	
	0.008418		proline--tRNA ligase
-0.52	245	ABUW_RS03315	
	0.057713		LysR family transcriptional regulator
-0.52	249	ABUW_RS11520	
	0.117716		tRNA (uridine(54)-C5)-methyltransferase TrmA
-0.52	106	ABUW_RS11135	
	0.021347		phosphopyruvate hydratase
-0.51	476	ABUW_RS08890	
	0.245416		hypothetical protein
-0.51	74	ABUW_RS06130	
	0.373501		hypothetical protein
-0.51	984	ABUW_RS16200	
	0.083051		dihydrofolate reductase
-0.51	568	ABUW_RS16630	
	0.032979		YcgN family cysteine cluster protein
-0.51	029	ABUW_RS00265	
	0.364583		cold-shock protein
-0.51	702	ABUW_RS12225	
	0.010530		imidazole glycerol phosphate synthase subunit HisF
-0.51	949	ABUW_RS01175	
	0.042603		branched-chain amino acid transaminase
-0.51	191	ABUW_RS02885	
	0.095991		4-carboxymuconolactone decarboxylase
-0.50	966	ABUW_RS12125	
	0.485283		CmlA family chloramphenicol efflux MFS transporter
-0.50	901	ABUW_RS19310	
	0.124698		membrane protein
-0.50	376	ABUW_RS01190	
	0.239612		ribbon-helix-helix protein%2C CopG family
-0.50	23	ABUW_RS06840	
	0.062636		allantoicase
-0.50	049	ABUW_RS00625	
	0.031971		amino acid permease
-0.50	364	ABUW_RS03210	
	0.010449		response regulator
-0.50	307	ABUW_RS17720	
	0.042768		GntP family permease
-0.50	943	ABUW_RS10165	
	0.071596		hypothetical protein
-0.49	385	ABUW_RS06335	
	0.021172		septum site-determining protein MinC
-0.49	559	ABUW_RS14790	
	0.046334		elongation factor Tu
-0.49	063	ABUW_RS14850	
	0.033453		D-Ala-D-Ala carboxypeptidase
-0.49	371	ABUW_RS12455	
	0.053896		GntR family transcriptional regulator
-0.49	534	ABUW_RS09370	
	0.165828		Maf-like protein
-0.49	876	ABUW_RS03535	
	0.018135		50S ribosomal protein L21
-0.49	814	ABUW_RS04160	
	0.026917		NAD-dependent succinate-semialdehyde dehydrogenase
-0.49	868	ABUW_RS12130	
	0.241045		hypothetical protein
-0.49	107	ABUW_RS08400	
	0.025440		hypothetical protein
-0.49	784	ABUW_RS06260	

	0.086773		protein deglycase HchA
-0.49	718	ABUW_RS03605	
	0.047946		aldehyde dehydrogenase
-0.49	267	ABUW_RS12145	
	0.045430		alpha/beta fold hydrolase
-0.49	527	ABUW_RS18340	
	0.023593		elongation factor Ts
-0.49	757	ABUW_RS06040	
	0.386223		hypothetical protein
-0.49	125	ABUW_RS06240	
	0.024056		dienelactone hydrolase family protein
-0.48	677	ABUW_RS00255	
	0.051115		S-formylglutathione hydrolase
-0.48	822	ABUW_RS15695	
	0.023155		serine/threonine transporter SstT
-0.48	366	ABUW_RS11075	
	0.133051		excalibur calcium-binding domain-containing protein
-0.48	92	ABUW_RS15355	
	0.151072		chromate transporter
-0.48	083	ABUW_RS11510	
	0.061572		LLM class flavin-dependent oxidoreductase
-0.48	564	ABUW_RS12150	
	0.047946		LysM peptidoglycan-binding domain-containing protein
-0.48	267	ABUW_RS18115	
	0.031895		aspartate carbamoyltransferase
-0.48	57	ABUW_RS13255	
	0.071839		drug/metabolite DMT transporter permease
-0.48	547	ABUW_RS07420	
	0.036545		NUDIX domain-containing protein
-0.48	261	ABUW_RS01915	
	0.016631		DUF1289 domain-containing protein
-0.47	05	ABUW_RS04250	
	0.085381		DNA-3-methyladenine glycosylase I
-0.47	152	ABUW_RS00230	
	0.034178		50S ribosomal protein L29
-0.47	028	ABUW_RS02035	
	0.225391		translation initiation factor IF-1
-0.47	968	ABUW_RS16810	
	0.049061		TRAP transporter large permease subunit
-0.47	767	ABUW_RS02160	
	0.137046		hypothetical protein
-0.47	988	ABUW_RS01555	
	0.103159		hypothetical protein
-0.47	426	ABUW_RS08325	
	0.195426		50S ribosomal protein L9
-0.47	161	ABUW_RS07545	
	0.130353		16S rRNA (uracil(1498)-N(3))-methyltransferase
-0.47	772	ABUW_RS00850	
	0.063138		NAD-dependent succinate-semialdehyde dehydrogenase
-0.47	947	ABUW_RS14915	
	0.015943		glutamate-5-semialdehyde dehydrogenase
-0.47	884	ABUW_RS16470	
	0.104777		SPOR domain-containing protein
-0.47	87	ABUW_RS03075	
	0.019785		aspartate-semialdehyde dehydrogenase
-0.47	1	ABUW_RS16780	
	0.051658		phosphoribosylglycinamide formyltransferase
-0.47	172	ABUW_RS04805	
	0.024895		acyl-CoA thioesterase II
-0.47	868	ABUW_RS01945	
	0.031052		GTPase Era
-0.47	655	ABUW_RS05070	
	0.027769		hypothetical protein
-0.46	974	ABUW_RS17165	
	0.030591		2-oxoglutarate dehydrogenase E1 component
-0.46	401	ABUW_RS04280	
	0.033730		SDR family oxidoreductase
-0.46	555	ABUW_RS07220	
	0.137297		LysR family transcriptional regulator
-0.46	065	ABUW_RS00145	

	0.050076		alpha/beta hydrolase
-0.46	91	ABUW_RS08225	
	0.062675		phosphotransferase family protein
-0.46	534	ABUW_RS09010	
	0.061448		signal peptide peptidase SppA
-0.46	282	ABUW_RS04795	
	0.209319		hypothetical protein
-0.46	554	ABUW_RS06190	
	0.019985		alpha/beta fold hydrolase
-0.46	723	ABUW_RS00515	
	0.275596		exonuclease
-0.46	439	ABUW_RS06785	
	0.046020		TetR/AcrR family transcriptional regulator
-0.46	651	ABUW_RS00530	
	0.015571		beta-ketoacyl-ACP synthase III
-0.46	941	ABUW_RS13185	
	0.313567		poly-beta-1%2C6-N-acetyl-D-glucosamine biosynthesis protein PgaD
-0.45	512	ABUW_RS07615	
	0.149809		acetoin reductase
-0.45	039	ABUW_RS10335	
	0.022665		RHS repeat protein
-0.45	668	ABUW_RS13680	
	0.087534		PAS domain-containing protein
-0.45	435	ABUW_RS08440	
	0.043964		metal ABC transporter permease
-0.45	716	ABUW_RS18220	
	0.078732		lytic transglycosylase domain-containing protein
-0.45	804	ABUW_RS06965	
	0.226348		succinate dehydrogenase assembly factor 2
-0.45	795	ABUW_RS02140	
	0.200824		phage major capsid protein%2C P2 family
-0.45	306	ABUW_RS02855	
	0.050556		peptidylprolyl isomerase
-0.45	853	ABUW_RS18815	
	0.033228		electron transfer flavoprotein-ubiquinone oxidoreductase
-0.45	526	ABUW_RS17035	
	0.073414		kinase/pyrophosphorylase
-0.45	519	ABUW_RS07595	
	0.258149		MotA/TolQ/ExbB proton channel family protein
-0.44	232	ABUW_RS10995	
	0.105850		SDR family NAD(P)-dependent oxidoreductase
-0.44	979	ABUW_RS01275	
	0.047249		hypothetical protein
-0.44	012	ABUW_RS03130	
	0.033405		Fe/S-dependent 2-methylisocitrate dehydratase AcnD
-0.44	714	ABUW_RS18525	
	0.025926		2%2C3%2C4%2C5-tetrahydropyridine-2%2C6-dicarboxylate N-succinyltransferase
-0.44	54	ABUW_RS04975	
	0.044997		TetR/AcrR family transcriptional regulator
-0.44	265	ABUW_RS16665	
	0.045334		SRPBCC family protein
-0.44	161	ABUW_RS07225	
	0.057202		phosphoribosylanthranilate isomerase
-0.44	864	ABUW_RS03030	
	0.087364		NADP-specific glutamate dehydrogenase
-0.44	026	ABUW_RS13940	
	0.055988		PLP-dependent aminotransferase family protein
-0.43	698	ABUW_RS06565	
	0.075557		hypothetical protein
-0.43	627	ABUW_RS15240	
	0.059336		single-stranded-DNA-specific exonuclease RecJ
-0.43	36	ABUW_RS00820	
	0.185967		preprotein translocase subunit YajC
-0.43	413	ABUW_RS02615	
	0.115681		type II secretion system F family protein
-0.43	404	ABUW_RS17275	
	0.174150		DMT family transporter
-0.43	316	ABUW_RS16950	
	0.073606		hypothetical protein
-0.43	982	ABUW_RS06170	

	0.215723		DUF1330 domain-containing protein
-0.43	097	ABUW_RS12175	
	0.180113		DUF4236 domain-containing protein
-0.43	735	ABUW_RS03900	
	0.128769		adenosine deaminase
-0.43	417	ABUW_RS13370	
	0.132438		sulfite exporter TauE/SafE family protein
-0.43	338	ABUW_RS00140	
	0.069776		OmpH family outer membrane protein
-0.43	855	ABUW_RS08485	
	0.051115		23S rRNA pseudouridine(1911/1915/1917) synthase RluD
-0.43	404	ABUW_RS14980	
	0.059265		trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase
-0.42	16	ABUW_RS11125	
	0.126649		di-trans%2Cpoly-cis-decaprenylcistransferase
-0.42	196	ABUW_RS08460	
	0.311222		DUF485 domain-containing protein
-0.42	765	ABUW_RS00905	
	0.039655		hypothetical protein
-0.42	568	ABUW_RS04310	
	0.110447		urease accessory protein UreE
-0.42	863	ABUW_RS13995	
	0.047249		poly-beta-1%2C6-N-acetyl-D-glucosamine N-deacetylase PgaB
-0.42	012	ABUW_RS14370	
	0.063981		NAD+ synthase
-0.42	122	ABUW_RS14895	
	0.352828		hypothetical protein
-0.42	788	ABUW_RS06765	
	0.065626		type I methionyl aminopeptidase
-0.42	095	ABUW_RS06030	
	0.167067		outer membrane lipoprotein LolB
-0.42	595	ABUW_RS15005	
	0.156620		hypothetical protein
-0.42	78	ABUW_RS08245	
	0.036731		methionine synthase
-0.42	404	ABUW_RS14205	
	0.028071		polysaccharide biosynthesis protein
-0.42	315	ABUW_RS18595	
	0.030900		septum site-determining protein MinD
-0.42	894	ABUW_RS14795	
	0.021497		ubiquinol oxidase subunit II
-0.41	473	ABUW_RS07580	
	0.081927		PHP domain-containing protein
-0.41	044	ABUW_RS02585	
	0.038503		DUF3861 domain-containing protein
-0.41	183	ABUW_RS18265	
	0.085652		hypothetical protein
-0.41	989	ABUW_RS16280	
	0.075557		crotonase/enoyl-CoA hydratase family protein
-0.41	627	ABUW_RS16065	
	0.247311		DNA-binding protein
-0.41	27	ABUW_RS05705	
	0.222731		30S ribosomal protein S18
-0.41	003	ABUW_RS07550	
	0.145340		MFS transporter
-0.41	984	ABUW_RS12435	
	0.060730		NADP-dependent isocitrate dehydrogenase
-0.40	062	ABUW_RS05265	
	0.088668		ATP synthase subunit I
-0.40	002	ABUW_RS18200	
	0.129147		response regulator transcription factor
-0.40	545	ABUW_RS17600	
	0.117491		paraquat-inducible protein A
-0.40	529	ABUW_RS07320	
	0.402778		carboxymuconolactone decarboxylase family protein
-0.40	275	ABUW_RS01090	
	0.204625		VOC family protein
-0.40	585	ABUW_RS00335	
	0.031746		preprotein translocase subunit SecA
-0.40	654	ABUW_RS03095	

	0.221428		sulfate ABC transporter permease subunit CysW
-0.40	699	ABUW_RS04995	
	0.142320		DUF4845 domain-containing protein
-0.40	379	ABUW_RS05060	
	0.056398		glycosyl transferase family protein
-0.40	497	ABUW_RS06640	
	0.080035		M1 family peptidase
-0.40	464	ABUW_RS05875	
	0.138081		hypothetical protein
-0.40	476	ABUW_RS15280	
	0.338921		acyltransferase
-0.40	865	ABUW_RS07005	
	0.066635		ACR3 family arsenite efflux transporter
-0.40	091	ABUW_RS17870	
	0.261800		hypothetical protein
-0.40	265	ABUW_RS12235	
	0.074245		RIP metalloprotease RseP
-0.40	722	ABUW_RS08475	
	0.146793		NUDIX hydrolase
-0.39	112	ABUW_RS15725	
	0.080068		hypothetical protein
-0.39	35	ABUW_RS04980	
	0.134662		EstA family serine hydrolase
-0.39	294	ABUW_RS17125	
	0.090269		ATP phosphoribosyltransferase
-0.39	36	ABUW_RS15775	
	0.340902		LrgB family protein
-0.39	02	ABUW_RS11710	
	0.099502		PTS fructose transporter subunit IIBC
-0.39	157	ABUW_RS08620	
	0.161592		50S ribosomal protein L23
-0.39	748	ABUW_RS02005	
	0.056074		Bcr/CflA family efflux MFS transporter
-0.39	693	ABUW_RS03450	
	0.063177		bifunctional molybdenum cofactor biosynthesis protein MoaC/MoaB
-0.39	749	ABUW_RS08335	
	0.123030		formyltetrahydrofolate deformylase
-0.39	077	ABUW_RS16660	
	0.105511		histidine phosphatase family protein
-0.39	348	ABUW_RS09015	
	0.037587		succinate--CoA ligase subunit alpha
-0.39	357	ABUW_RS04300	
	0.127077		hypothetical protein
-0.39	655	ABUW_RS01500	
	0.052804		YecA family protein
-0.39	655	ABUW_RS04240	
	0.056053		bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD
-0.38	889	ABUW_RS17785	
	0.087534		DNA polymerase I
-0.38	435	ABUW_RS15880	
	0.092003		LysR family transcriptional regulator
-0.38	707	ABUW_RS11955	
	0.045430		ribulose-phosphate 3-epimerase
-0.38	527	ABUW_RS15685	
	0.104873		DNA repair protein HhH-GPD
-0.38	272	ABUW_RS18205	
	0.062636		50S ribosomal protein L10
-0.38	049	ABUW_RS17485	
	0.243084		histidine ABC transporter permease HisM
-0.38	327	ABUW_RS06540	
	0.081172		copper-translocating P-type ATPase
-0.38	597	ABUW_RS13135	
	0.065611		tetraacyldisaccharide 4'-kinase
-0.38	656	ABUW_RS10980	
	0.104300		MoxR family ATPase
-0.38	133	ABUW_RS10400	
	0.176957		hypothetical protein
-0.38	941	ABUW_RS17465	
	0.152464		methyltransferase domain-containing protein
-0.38	099	ABUW_RS03215	

	0.074245		crossover junction endodeoxyribonuclease RuvC
-0.38	722	ABUW_RS11205	
	0.123887		type IV pilus secretin PilQ
-0.37	375	ABUW_RS01445	
	0.095111		amino acid permease
-0.37	298	ABUW_RS01350	
	0.442099		hypothetical protein
-0.37	261	ABUW_RS00585	
	0.329194		cell division protein
-0.37	98	ABUW_RS14110	
	0.058938		23S rRNA (adenine(2030)-N(6))-methyltransferase RlmJ
-0.37	728	ABUW_RS02315	
	0.204038		primase
-0.37	436	ABUW_RS02740	
	0.161855		TetR/AcrR family transcriptional regulator
-0.37	324	ABUW_RS00160	
	0.065626		UDP-N-acetylglucosamine 1-carboxyvinyltransferase
-0.37	095	ABUW_RS15780	
	0.134955		class 1 fructose-bisphosphatase
-0.37	853	ABUW_RS04855	
	0.108211		coniferyl aldehyde dehydrogenase
-0.37	216	ABUW_RS13570	
	0.047697		dihydroxy-acid dehydratase
-0.37	406	ABUW_RS00130	
	0.293265		hypothetical protein
-0.37	575	ABUW_RS06935	
	0.087287		methylated-DNA--[protein]-cysteine S-methyltransferase
-0.37	642	ABUW_RS17350	
	0.087582		TIGR00730 family Rossmann fold protein
-0.37	896	ABUW_RS17990	
	0.164247		prepilin peptidase
-0.37	831	ABUW_RS17280	
	0.161592		sulfate permease
-0.37	748	ABUW_RS01270	
	0.204625		helix-turn-helix transcriptional regulator
-0.36	585	ABUW_RS02230	
	0.072702		threonine--tRNA ligase
-0.36	754	ABUW_RS15980	
	0.054695		ATP-dependent Clp endopeptidase proteolytic subunit ClpP
-0.36	415	ABUW_RS16530	
	0.129002		multidrug efflux RND transporter permease subunit AdeB
-0.36	426	ABUW_RS09605	
	0.087039		hypothetical protein
-0.36	302	ABUW_RS15245	
	0.164247		formate/nitrite transporter family protein
-0.36	831	ABUW_RS00280	
	0.075715		RNase adapter RapZ
-0.36	531	ABUW_RS16000	
	0.100945		type I-F CRISPR-associated endoribonuclease Cas6/Csy4
-0.36	959	ABUW_RS05360	
	0.183648		aldo/keto reductase
-0.36	222	ABUW_RS07215	
	0.199442		3'-5' exonuclease
-0.36	587	ABUW_RS16050	
	0.147101		ABC transporter ATP-binding protein
-0.36	317	ABUW_RS10800	
	0.093168		transcription termination/antitermination protein NusG
-0.36	336	ABUW_RS17500	
	0.105850		DUF2237 domain-containing protein
-0.36	979	ABUW_RS11050	
	0.191683		helix-turn-helix transcriptional regulator
-0.36	118	ABUW_RS01110	
	0.149490		carbon starvation protein A
-0.36	468	ABUW_RS05590	
	0.085906		fructose-bisphosphate aldolase class II
-0.36	181	ABUW_RS11035	
	0.095504		cell division protein FtsZ
-0.35	162	ABUW_RS00750	
	0.150834		inorganic phosphate transporter
-0.35	237	ABUW_RS14200	

	0.094932		30S ribosomal protein S12
-0.35	991	ABUW_RS14865	
	0.162116		transcriptional regulator
-0.35	487	ABUW_RS00835	
	0.118681		multidrug efflux RND transporter permease subunit
-0.35	044	ABUW_RS04525	
	0.215835		SDR family oxidoreductase
-0.35	938	ABUW_RS04615	
	0.178483		tRNA (cytidine(34)-2'-O)-methyltransferase
-0.35	342	ABUW_RS04190	
	0.130926		UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase
-0.35	738	ABUW_RS00445	
	0.104484		alpha/beta hydrolase
-0.35	816	ABUW_RS14100	
	0.116623		phosphoribosylformylglycinamide cyclo-ligase
-0.35	634	ABUW_RS04810	
	0.117491		DotU family type IV/VI secretion system protein
-0.35	529	ABUW_RS12465	
	0.133814		DUF805 domain-containing protein
-0.35	582	ABUW_RS01215	
	0.178311		50S ribosomal protein L7/L12
-0.35	069	ABUW_RS17480	
	0.094963		rhomboid family intramembrane serine protease
-0.35	109	ABUW_RS14125	
	0.233237		ATP-dependent metalloproteinase FtsH/Yme1/Tma family protein
-0.35	935	ABUW_RS04410	
	0.425048		Lrp/AsnC family transcriptional regulator
-0.35	85	ABUW_RS13605	
	0.137106		Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC
-0.34	17	ABUW_RS03515	
	0.228113		NAD(P)H:quinone oxidoreductase
-0.34	213	ABUW_RS02245	
	0.077408		16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase RsmA
-0.34	746	ABUW_RS02435	
	0.303322		hypothetical protein
-0.34	255	ABUW_RS16575	
	0.296974		glutathione S-transferase
-0.34	663	ABUW_RS18250	
	0.161855		phosphotransferase
-0.34	324	ABUW_RS11020	
	0.145340		iron-containing alcohol dehydrogenase
-0.34	984	ABUW_RS04210	
	0.142530		Bax inhibitor-1/YccA family protein
-0.34	038	ABUW_RS16355	
	0.201678		cystathionine beta-lyase
-0.34	296	ABUW_RS01980	
	0.185634		recombinase
-0.34	866	ABUW_RS04145	
	0.147068		NAD(P)/FAD-dependent oxidoreductase
-0.34	578	ABUW_RS02130	
	0.177912		RNA chaperone Hfq
-0.34	897	ABUW_RS07860	
	0.258828		DUF3015 domain-containing protein
-0.34	798	ABUW_RS05820	
	0.322868		HU family DNA-binding protein
-0.34	832	ABUW_RS10685	
	0.262695		hypothetical protein
-0.34	803	ABUW_RS01830	
	0.098282		type VI secretion system baseplate subunit TssK
-0.33	564	ABUW_RS12470	
	0.158659		MBL fold metallo-hydrolase
-0.33	376	ABUW_RS17010	
	0.498106		fluoride efflux transporter CrcB
-0.33	312	ABUW_RS16985	
	0.101192		Hsp33 family molecular chaperone HsLO
-0.33	412	ABUW_RS17090	
	0.298732		hypothetical protein
-0.33	338	ABUW_RS02700	
	0.181379		solanesyl diphosphate synthase
-0.33	283	ABUW_RS04150	

	0.366751		hypothetical protein
-0.33	456	ABUW_RS18095	
	0.204625		MFS transporter
-0.33	585	ABUW_RS15305	
	0.214496		VWA domain-containing protein
-0.33	348	ABUW_RS10395	
	0.180524		peptidoglycan-associated lipoprotein Pal
-0.33	419	ABUW_RS04865	
	0.289392		enoyl-CoA hydratase
-0.33	287	ABUW_RS18400	
	0.125925		NADH:flavin oxidoreductase/NADH oxidase family protein
-0.33	105	ABUW_RS09190	
	0.692736		
-0.33	341	sRNA55	
	0.238738		bifunctional metallophosphatase/5'-nucleotidase
-0.33	417	ABUW_RS10065	
	0.176591		TonB-dependent siderophore receptor
-0.33	9	ABUW_RS14160	
	0.123424		hypothetical protein
-0.33	665	ABUW_RS06620	
	0.202344		ATP-dependent dethiobiotin synthetase BioD
-0.32	384	ABUW_RS15135	
	0.568047		hypothetical protein
-0.32	261	ABUW_RS12680	
	0.388457		MFS transporter
-0.32	12	ABUW_RS18390	
	0.316598		RND transporter
-0.32	92	ABUW_RS12830	
	0.129712		hydroxymethylbilane synthase
-0.32	341	ABUW_RS17595	
	0.593372		hypothetical protein
-0.32	056	ABUW_RS03745	
	0.155392		catalase family peroxidase
-0.32	507	ABUW_RS12185	
	0.383376		threonine transporter RhtB
-0.32	852	ABUW_RS18225	
	0.087138		insulinase family protein
-0.32	893	ABUW_RS05310	
	0.189514		fimbrial biogenesis outer membrane usher protein
-0.31	607	ABUW_RS07970	
	0.317688		amino acid ABC transporter permease
-0.31	078	ABUW_RS11340	
	0.153327		hypothetical protein
-0.31	55	ABUW_RS01670	
	0.214496		cytochrome o ubiquinol oxidase subunit IV
-0.31	348	ABUW_RS07565	
	0.144786		excinuclease ABC subunit UvrA
-0.31	828	ABUW_RS00935	
	0.216581		hypothetical protein
-0.31	036	ABUW_RS18625	
	0.087379		outer membrane protein assembly factor
-0.31	494	ABUW_RS07765	
	0.320575		esterase
-0.31	44	ABUW_RS04030	
	0.246757		LysR family transcriptional regulator
-0.31	573	ABUW_RS18880	
	0.166680		acetolactate synthase 3 large subunit
-0.31	548	ABUW_RS16310	
	0.452204		
-0.31	901	sRNA46	
	0.287299		threo-3-hydroxy-L-aspartate ammonia-lyase
-0.31	15	ABUW_RS05700	
	0.133399		VWA domain-containing protein
-0.31	134	ABUW_RS01560	
	0.291869		carboxylating nicotinate-nucleotide diphosphorylase
-0.31	205	ABUW_RS18685	
	0.397661		MFS transporter
-0.31	515	ABUW_RS09355	
	0.391357		LysR family transcriptional regulator
-0.31	524	ABUW_RS12120	

	0.438451		DMT family transporter
-0.31	234	ABUW_RS02235	
	0.641509		
-0.31	053	sRNA59	
	0.161053		GTPase HflX
-0.31	648	ABUW_RS02460	
	0.241034		ATP-binding cassette domain-containing protein
-0.31	746	ABUW_RS16750	
	0.263261		aspartate carbamoyltransferase
-0.30	948	ABUW_RS13260	
	0.229202		thioesterase family protein
-0.30	376	ABUW_RS14660	
	0.319206		general secretion pathway protein
-0.30	849	ABUW_RS17560	
	0.179521		PadR family transcriptional regulator
-0.29	948	ABUW_RS18270	
	0.287391		neutral zinc metalloproteinase
-0.29	188	ABUW_RS04325	
	0.506197		transglycosylase
-0.29	568	ABUW_RS18045	
	0.236779		integrase
-0.29	304	ABUW_RS16230	
	0.286173		carbonic anhydrase
-0.29	773	ABUW_RS12270	
	0.240832		16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB
-0.29	404	ABUW_RS00120	
	0.180760		DNA translocase FtsK
-0.29	674	ABUW_RS14815	
	0.144503		HAMP domain-containing protein
-0.29	736	ABUW_RS15445	
	0.147850		transcription-repair coupling factor
-0.28	844	ABUW_RS10745	
	0.353952		ABC transporter substrate-binding protein
-0.28	341	ABUW_RS12560	
	0.292218		tRNA dihydrouridine synthase DusB
-0.28	214	ABUW_RS05190	
	0.388435		SfnB family sulfur acquisition oxidoreductase
-0.28	764	ABUW_RS11360	
	0.254042		LysR family transcriptional regulator
-0.28	125	ABUW_RS07810	
	0.172299		alpha/beta hydrolase
-0.28	614	ABUW_RS08865	
	0.216520		class I SAM-dependent methyltransferase
-0.28	687	ABUW_RS07385	
	0.567782		
-0.28	699	sRNA109	
	0.283480		hypothetical protein
-0.28	959	ABUW_RS08985	
	0.542663		DUF2523 domain-containing protein
-0.28	881	ABUW_RS09685	
	0.161592		class II fumarate hydratase
-0.28	748	ABUW_RS08385	
	0.177027		potassium transporter
-0.28	556	ABUW_RS17085	
	0.357669		histidine phosphatase family protein
-0.27	363	ABUW_RS10560	
	0.229214		YqgE/AlgH family protein
-0.27	614	ABUW_RS17315	
	0.369228		response regulator transcription factor
-0.27	37	ABUW_RS07740	
	0.315010		undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase
-0.27	176	ABUW_RS00725	
	0.233634		oxidoreductase
-0.27	661	ABUW_RS03600	
	0.352622		dihydroxy-acid dehydratase
-0.27	867	ABUW_RS09160	
	0.274061		UDP-3-O-acetyl-N-acetylglucosamine deacetylase
-0.27	295	ABUW_RS00755	
	0.289756		arsenical resistance protein ArsH
-0.27	573	ABUW_RS17875	

	0.292664		nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
-0.27	04	ABUW_RS10565	
	0.280758		transporter
-0.27	583	ABUW_RS03265	
	0.266325		succinyl-diaminopimelate desuccinylase
-0.27	269	ABUW_RS03375	
	0.328644		ammonium transporter
-0.27	148	ABUW_RS17795	
	0.308529		urease subunit alpha
-0.27	308	ABUW_RS14000	
	0.521023		GNAT family N-acetyltransferase
-0.27	623	ABUW_RS12785	
	0.215974		3-deoxy-manno-octulosonate cytidyltransferase
-0.26	994	ABUW_RS10975	
	0.286183		MaoC family dehydratase
-0.26	461	ABUW_RS11095	
	0.346027		potassium transporter
-0.26	536	ABUW_RS09290	
	0.413919		hypothetical protein
-0.26	445	ABUW_RS06405	
	0.327640		urease accessory protein
-0.26	203	ABUW_RS13990	
	0.433219		hypothetical protein
-0.26	868	ABUW_RS19725	
	0.216581		bifunctional 3%2C4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II
-0.26	036	ABUW_RS00470	
	0.416748		hypothetical protein
-0.26	106	ABUW_RS06140	
	0.268110		phosphoglycerate mutase family protein
-0.26	967	ABUW_RS10780	
	0.409937		GGDEF domain-containing protein
-0.25	171	ABUW_RS15435	
	0.320575		helicase
-0.25	44	ABUW_RS14565	
	0.245635		diaminobutyrate--2-oxoglutarate transaminase
-0.25	411	ABUW_RS05425	
	0.278597		phosphoserine phosphatase SerB
-0.25	34	ABUW_RS00480	
	0.590970		DUF1304 domain-containing protein
-0.25	013	ABUW_RS00950	
	0.311128		DoxX family protein
-0.25	333	ABUW_RS18290	
	0.374152		glutamate 5-kinase
-0.25	296	ABUW_RS05175	
	0.246489		CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
-0.25	407	ABUW_RS17355	
	0.504276		phosphonoacetaldehyde hydrolase
-0.25	277	ABUW_RS12070	
	0.214096		ACP S-malonyltransferase
-0.25	633	ABUW_RS15095	
	0.360822		TIGR01777 family protein
-0.25	877	ABUW_RS14675	
	0.634727		Arc family DNA-binding protein
-0.25	071	ABUW_RS03920	
	0.410989		U32 family peptidase
-0.25	703	ABUW_RS06560	
	0.673387		hypothetical protein
-0.24	44	ABUW_RS06155	
	0.384283		DUF1543 domain-containing protein
-0.24	994	ABUW_RS03040	
	0.440922		hypothetical protein
-0.24	669	ABUW_RS08365	
	0.266325		FAD-dependent oxidoreductase
-0.24	269	ABUW_RS14095	
	0.709878		
-0.24	222	sRNA101	
	0.316867		nitroreductase family protein
-0.24	833	ABUW_RS04610	
	0.602737		RraA family protein
-0.24	646	ABUW_RS10610	

	0.518205		1%2C6-dihydroxycyclohexa-2%2C4-diene-1-carboxylate dehydrogenase
-0.24	81	ABUW_RS13165	
	0.516664		DMT family transporter
-0.24	955	ABUW_RS09395	
	0.294165		taurine dioxygenase
-0.24	297	ABUW_RS11575	
	0.255588		DNA polymerase III subunit alpha
-0.24	29	ABUW_RS11480	
	0.543975		M23 family metalloproteinase
-0.24	001	ABUW_RS00240	
	0.434414		methylenetetrahydrofolate reductase [NAD(P)H]
-0.24	572	ABUW_RS05975	
	0.458499		TMEM165/GDT1 family protein
-0.24	305	ABUW_RS00785	
	0.294797		Ig-like domain-containing protein
-0.24	998	ABUW_RS19720	
	0.307999		Bcr/CflA family efflux MFS transporter
-0.24	822	ABUW_RS04920	
	0.483092		DUF475 domain-containing protein
-0.24	252	ABUW_RS00965	
	0.303451		hypothetical protein
-0.24	552	ABUW_RS10405	
	0.335644		SCPU domain-containing protein
-0.24	012	ABUW_RS07960	
	0.430379		NAD-dependent phenylacetaldehyde dehydrogenase
-0.24	585	ABUW_RS09100	
	0.211052		recombinase RecA
-0.23	138	ABUW_RS08515	
	0.250350		phenylalanine--tRNA ligase subunit beta
-0.23	322	ABUW_RS15930	
	0.406801		EF-P lysine aminoacylase GenX
-0.23	196	ABUW_RS04650	
	0.480358		EamA family transporter
-0.23	008	ABUW_RS01625	
	0.458888		two-component sensor histidine kinase AdeS
-0.23	101	ABUW_RS09590	
	0.404919		acyl-CoA synthetase
-0.23	055	ABUW_RS15985	
	0.428558		magnesium-translocating P-type ATPase
-0.23	555	ABUW_RS08115	
	0.434414		carbohydrate porin
-0.23	572	ABUW_RS08965	
	0.317306		short-chain fatty acid transporter
-0.23	975	ABUW_RS10190	
	0.540194		thioesterase
-0.23	807	ABUW_RS05790	
	0.454942		nitroreductase
-0.23	097	ABUW_RS03455	
	0.280799		two-component system response regulator OmpR
-0.23	275	ABUW_RS01260	
	0.481415		recombination protein RecR
-0.23	144	ABUW_RS10435	
	0.604037		SRPBCC family protein
-0.23	775	ABUW_RS10910	
	0.421411		YeeE/YedE family protein
-0.23	139	ABUW_RS08980	
	0.375636		deoxyguanosinetriphosphate triphosphohydrolase
-0.22	822	ABUW_RS04910	
	0.309387		iron-sulfur cluster carrier protein ApbC
-0.22	597	ABUW_RS15275	
	0.477408		LysR family transcriptional regulator
-0.22	165	ABUW_RS13145	
	0.380995		2-C-methyl-D-erythritol 4-phosphate cytidyltransferase
-0.22	721	ABUW_RS08905	
	0.261958		phosphoribosylformylglycinamide synthase
-0.22	235	ABUW_RS04915	
	0.318294		sodium/glutamate symporter
-0.22	897	ABUW_RS07200	
	0.781566		DUF2158 domain-containing protein
-0.22	51	ABUW_RS12940	

	0.338833		FKBP-type peptidyl-prolyl cis-trans isomerase
-0.22	439	ABUW_RS18670	
	0.287391		DEAD/DEAH box helicase
-0.22	188	ABUW_RS14550	
	0.472671		30S ribosomal protein S20
-0.22	288	ABUW_RS10775	
	0.498302		chloramphenicol acetyltransferase CAT
-0.22	329	ABUW_RS12810	
	0.440922		3'-5'-cyclic-AMP phosphodiesterase
-0.22	669	ABUW_RS17655	
	0.328156		fimbrial biogenesis outer membrane usher protein
-0.22	155	ABUW_RS09975	
	0.476683		NUDIX hydrolase
-0.22	346	ABUW_RS05505	
	0.408342		amidohydrolase
-0.21	381	ABUW_RS15550	
	0.504874		hypothetical protein
-0.21	449	ABUW_RS13675	
	0.321090		AdeC/AdeK/OprM family multidrug efflux complex outer membrane factor
-0.21	146	ABUW_RS16345	
	0.441088		glutamate racemase
-0.21	751	ABUW_RS00415	
	0.436254		bifunctional phosphoserine phosphatase/homoserine phosphotransferase ThrH
-0.21	744	ABUW_RS03560	
	0.460043		UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)
-0.21	036	ABUW_RS02925	
	0.320575		ADP-forming succinate--CoA ligase subunit beta
-0.21	44	ABUW_RS04295	
	0.542641		GntR family transcriptional regulator
-0.21	522	ABUW_RS03690	
	0.449653		isochorismatase family protein
-0.21	865	ABUW_RS10075	
	0.345689		S-(hydroxymethyl)glutathione dehydrogenase/class III alcohol dehydrogenase
-0.21	711	ABUW_RS09990	
	0.341220		chromosome segregation protein SMC
-0.21	03	ABUW_RS15190	
	0.458539		dicarboxylate/amino acid:cation symporter
-0.21	183	ABUW_RS07445	
	0.641229		Fur family transcriptional regulator
-0.21	744	ABUW_RS10070	
	0.414609		LysM peptidoglycan-binding domain-containing protein
-0.21	369	ABUW_RS19650	
	0.406004		peptidyl-prolyl cis-trans isomerase
-0.21	494	ABUW_RS03240	
	0.406318		30S ribosomal protein S1
-0.21	546	ABUW_RS10900	
	0.500925		cold-shock protein
-0.20	48	ABUW_RS13055	
	0.361250		aspartate kinase
-0.20	086	ABUW_RS13345	
	0.386711		FdhF/YdeP family oxidoreductase
-0.20	255	ABUW_RS04630	
	0.574588		hypothetical protein
-0.20	039	ABUW_RS05235	
	0.924776		acyl-CoA dehydrogenase
-0.20	259	ABUW_RS02365	
	0.360219		LPS-assembly protein LptD
-0.20	839	ABUW_RS11025	
	0.324513		4-hydroxy-3-methylbut-2-enyl diphosphate reductase
-0.20	386	ABUW_RS01535	
	0.470238		membrane integrity-associated transporter subunit PqiC
-0.20	38	ABUW_RS07330	
	0.388435		SDR family oxidoreductase
-0.20	764	ABUW_RS09020	
	0.338261		ribonucleoside-diphosphate reductase subunit alpha
-0.20	664	ABUW_RS15460	
	0.564437		thermonuclease family protein
-0.20	653	ABUW_RS19080	
	0.497172		rubredoxin/rubredoxin reductase
-0.20	42	ABUW_RS05635	

	0.434199		pyrimidine permease
-0.20	265	ABUW_RS00150	
	0.411447		methionyl-tRNA formyltransferase
-0.20	851	ABUW_RS00125	
	0.538576		universal stress protein
-0.19	558	ABUW_RS17825	
	0.327040		50S ribosomal protein L11
-0.19	963	ABUW_RS17495	
	0.366539		aminopeptidase P family protein
-0.19	531	ABUW_RS05885	
	0.341220		pirin family protein
-0.19	03	ABUW_RS13400	
	0.420827		MFS transporter
-0.19	351	ABUW_RS16115	
	0.618558		
-0.19	312	sRNA1	
	0.527276		2-aminoethylphosphonate--pyruvate transaminase
-0.19	167	ABUW_RS12075	
	0.427460		transcription antitermination factor NusB
-0.19	92	ABUW_RS00460	
	0.798638		hypothetical protein
-0.19	563	ABUW_RS19675	
	0.402778		GNAT family N-acetyltransferase
-0.19	275	ABUW_RS01230	
	0.473417		OmpA family protein
-0.19	487	ABUW_RS02480	
	0.543148		monooxygenase
-0.19	903	ABUW_RS11610	
	0.386686		acetylglutamate kinase
-0.18	674	ABUW_RS14755	
	0.437502		cytochrome o ubiquinol oxidase subunit III
-0.18	764	ABUW_RS07570	
	0.562781		tRNA 2-thiocytydine(32) synthetase TtcA
-0.18	949	ABUW_RS04545	
	0.418679		UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase
-0.18	982	ABUW_RS18930	
	0.449130		outer membrane lipid asymmetry maintenance protein MlaD
-0.18	004	ABUW_RS01890	
	0.534200		LLM class flavin-dependent oxidoreductase
-0.18	005	ABUW_RS11605	
	0.657801		ATP-binding cassette domain-containing protein
-0.18	342	ABUW_RS18780	
	0.457784		YihA family ribosome biogenesis GTP-binding protein
-0.18	265	ABUW_RS01960	
	0.708981		flavin reductase family protein
-0.18	391	ABUW_RS10130	
	0.619329		malonate transporter subunit MadM
-0.17	07	ABUW_RS11645	
	0.415020		outer membrane protein assembly factor BameE
-0.17	85	ABUW_RS14725	
	0.583277		PLP-dependent aminotransferase family protein
-0.17	425	ABUW_RS11705	
	0.495765		DNA topoisomerase IV subunit B
-0.17	763	ABUW_RS00615	
	0.503805		aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme
-0.17	809	ABUW_RS01280	
	0.526696		AMP-binding protein
-0.17	478	ABUW_RS07690	
	0.552662		FAD-dependent monooxygenase
-0.17	273	ABUW_RS17175	
	0.615931		ABC transporter ATP-binding protein
-0.17	466	ABUW_RS14135	
	0.545711		universal stress protein
-0.17	54	ABUW_RS17850	
	0.513305		arsenate reductase ArsC
-0.17	764	ABUW_RS17865	
	0.677579		nicotinamide mononucleotide transporter
-0.17	609	ABUW_RS14350	
	0.649879		DUF2213 domain-containing protein
-0.17	106	ABUW_RS12930	

	0.610447		LysR family transcriptional regulator
-0.17	121	ABUW_RS11260	
	0.711772		hypothetical protein
-0.17	894	ABUW_RS06125	
	0.452204		coniferyl aldehyde dehydrogenase
-0.17	901	ABUW_RS16670	
	0.582461		HlyD family secretion protein
-0.17	905	ABUW_RS17325	
	0.718563		hypothetical protein
-0.17	408	ABUW_RS18155	
	0.607299		hypothetical protein
-0.16	794	ABUW_RS10470	
	0.409937		rhodanese-like domain-containing protein
-0.16	171	ABUW_RS16370	
	0.483952		bifunctional riboflavin kinase/FAD synthetase
-0.16	259	ABUW_RS18800	
	0.592447		GTP 3'-cyclic nucleotide phosphatase MoaA
-0.16	671	ABUW_RS08320	
	0.768907		hypothetical protein
-0.16	801	ABUW_RS04580	
	0.411537		lytic murein transglycosylase
-0.16	714	ABUW_RS18910	
	0.564514		lysine exporter LysO family protein
-0.16	702	ABUW_RS10880	
	0.498529		excinuclease ABC subunit UvrC
-0.16	1	ABUW_RS17365	
	0.584313		chromate efflux transporter
-0.16	108	ABUW_RS10275	
	0.590751		GntR family transcriptional regulator
-0.16	04	ABUW_RS12390	
	0.781566		single-stranded DNA-binding protein
-0.16	51	ABUW_RS14595	
	0.517942		bifunctional DNA-formamidopyrimidine glycosylase/DNA-(apurinic or apyrimidinic site) lyase
-0.16	748	ABUW_RS03245	
	0.587441		LysR family transcriptional regulator
-0.16	609	ABUW_RS11735	
	0.581006		hypothetical protein
-0.16	168	ABUW_RS19385	
	0.543582		6-methyl-8-ribityllumazine synthase
-0.16	295	ABUW_RS00465	
	0.498405		guanine deaminase
-0.15	513	ABUW_RS18965	
	0.453331		bifunctional tetrahydrofolate synthase/dihydrofolate synthase
-0.15	006	ABUW_RS03070	
	0.568961		hypothetical protein
-0.15	097	ABUW_RS00555	
	0.684905		protein TolR
-0.15	658	ABUW_RS04880	
	0.678111		SDR family NAD(P)-dependent oxidoreductase
-0.15	172	ABUW_RS07985	
	0.552687		hypothetical protein
-0.15	446	ABUW_RS01840	
	0.543762		putative porin
-0.15	575	ABUW_RS00825	
	0.453335		outer membrane protein assembly factor Bama
-0.15	162	ABUW_RS08480	
	0.442897		bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase
-0.15	512	ABUW_RS07780	
	0.543235		acyl-CoA dehydrogenase
-0.15	387	ABUW_RS09005	
	0.681136		type VI secretion system contractile sheath small subunit
-0.15	635	ABUW_RS12535	
	0.464955		transcription termination/antitermination protein NusA
-0.15	574	ABUW_RS17235	
	0.574938		diguanylate cyclase
-0.15	534	ABUW_RS02485	
	0.597503		amino acid ABC transporter ATP-binding protein
-0.15	048	ABUW_RS11330	
	0.643568		FMN-dependent NADH-azoreductase
-0.15	671	ABUW_RS10280	

	0.727347		ethanolamine ammonia-lyase subunit EutB
-0.15	498	ABUW_RS07900	
	0.659675		hypothetical protein
-0.15	193	ABUW_RS02165	
	0.521022		phospholipase
-0.15	507	ABUW_RS08775	
	0.722806		hypothetical protein
-0.15	157	ABUW_RS03675	
	0.618081		RNA methyltransferase
-0.14	023	ABUW_RS04850	
	0.695587		hypothetical protein
-0.14	071	ABUW_RS06905	
	0.521472		FtsX-like permease family protein
-0.14	458	ABUW_RS14130	
	0.811928		hypothetical protein
-0.14	109	ABUW_RS06195	
	0.576210		AI-2E family transporter
-0.14	089	ABUW_RS04815	
	0.724575		hypothetical protein
-0.14	155	ABUW_RS16195	
	0.543582		isochorismatase
-0.14	295	ABUW_RS05375	
	0.576210		tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1
-0.14	089	ABUW_RS07845	TsaE
	0.799934		hypothetical protein
-0.14	051	ABUW_RS12995	
	0.741081		LysE family translocator
-0.14	67	ABUW_RS11825	
	0.670326		membrane protein
-0.14	176	ABUW_RS17950	
	0.568413		potassium transporter Kup
-0.14	346	ABUW_RS01135	
	0.740026		DsbC family protein
-0.14	45	ABUW_RS03275	
	0.627815		
-0.14	868	sRNA97	
	0.637614		tRNA dihydrouridine(20/20a) synthase DusA
-0.14	802	ABUW_RS16235	
	0.557271		TonB-dependent receptor
-0.14	528	ABUW_RS03255	
	0.734452		SDR family oxidoreductase
-0.14	699	ABUW_RS16940	
	0.543235		YggS family pyridoxal phosphate-dependent enzyme
-0.14	387	ABUW_RS14705	
	0.521918		DUF4468 domain-containing protein
-0.13	562	ABUW_RS06410	
	0.569397		PhzF family phenazine biosynthesis protein
-0.13	151	ABUW_RS06570	
	0.671616		transcriptional regulator
-0.13	264	ABUW_RS10365	
	0.664359		cation transporter
-0.13	704	ABUW_RS13860	
	0.539039		acyl-ACP--UDP-N-acetylglucosamine O-acyltransferase
-0.13	91	ABUW_RS08500	
	0.581324		sigma-54-dependent Fis family transcriptional regulator
-0.13	235	ABUW_RS10320	
	0.635649		Lrp/AsnC family transcriptional regulator
-0.13	23	ABUW_RS11320	
	0.728080		BCCT family carnitine transporter
-0.13	657	ABUW_RS14930	
	0.720583		MFS transporter
-0.13	693	ABUW_RS11600	
	0.760527		SDR family oxidoreductase
-0.13	029	ABUW_RS10080	
	0.647850		NAD(P)/FAD-dependent oxidoreductase
-0.13	769	ABUW_RS17885	
	0.584758		LpxL/LpxP family Kdo(2)-lipid IV(A) lauroyl/palmitoleoyl acyltransferase
-0.13	159	ABUW_RS16760	
	0.722806		hydroxymethylglutaryl-CoA lyase
-0.13	157	ABUW_RS12195	

	0.554210		3-oxoacyl-ACP reductase
-0.13	942	ABUW_RS08160	
	0.572436		NUDIX hydrolase
-0.13	019	ABUW_RS09460	
	0.599344		biotin/lipoyl-binding protein
-0.13	197	ABUW_RS00775	
	0.603488		(d)CMP kinase
-0.13	105	ABUW_RS10905	
	0.614377		hypothetical protein
-0.12	215	ABUW_RS17895	
	0.591109		bifunctional 23S rRNA (guanine(2069)-N(7))-methyltransferase RlmK/23S rRNA
-0.12	053	ABUW_RS13270	(guanine(2445)-N(2))-methyltransferase RlmL
	0.663891		lysine/ornithine N-monooxygenase
-0.12	142	ABUW_RS10635	
	0.650640		hypothetical protein
-0.12	269	ABUW_RS17585	
	0.585858		glutaredoxin 3
-0.12	926	ABUW_RS16375	
	0.900607		
-0.12	267	sRNA81	
	0.734452		acyl-CoA thioesterase
-0.12	699	ABUW_RS05045	
	0.600473		50S ribosomal protein L25
-0.12	063	ABUW_RS15040	
	0.601090		dTMP kinase
-0.12	656	ABUW_RS05025	
	0.709878		TonB-dependent siderophore receptor
-0.12	222	ABUW_RS08070	
	0.601234		rhomboid family intramembrane serine protease
-0.12	27	ABUW_RS14170	
	0.617305		sulfate ABC transporter ATP-binding protein
-0.12	764	ABUW_RS04990	
	0.599344		electron transfer flavoprotein subunit alpha
-0.12	197	ABUW_RS04705	
	0.783938		histidine utilization repressor
-0.12	723	ABUW_RS00370	
	0.675641		TetR family transcriptional regulator
-0.12	375	ABUW_RS18715	
	0.678375		NAD(P)/FAD-dependent oxidoreductase
-0.12	592	ABUW_RS15320	
	0.744319		alpha/beta hydrolase
-0.11	612	ABUW_RS14925	
	0.772791		hypothetical protein
-0.11	618	ABUW_RS01070	
	0.664359		tRNA-(ms[2]io[6]A)-hydroxylase
-0.11	704	ABUW_RS05090	
	0.615097		long-chain-fatty-acid--CoA ligase
-0.11	553	ABUW_RS17960	
	0.625877		4-hydroxy-tetrahydrodipicolinate synthase
-0.11	924	ABUW_RS00300	
	0.632966		RNA-binding protein
-0.11	497	ABUW_RS08520	
	0.715219		hypothetical protein
-0.11	857	ABUW_RS02575	
	0.763509		hypothetical protein
-0.11	988	ABUW_RS19390	
	0.641275		bifunctional glutamate N-acetyltransferase/amino-acid acetyltransferase ArgJ
-0.11	554	ABUW_RS15645	
	0.684077		NADP-dependent isocitrate dehydrogenase
-0.11	272	ABUW_RS05275	
	0.715309		4-hydroxybenzoate octaprenyltransferase
-0.11	598	ABUW_RS05905	
	0.735016		bifunctional adenosylcobinamide kinase/adenosylcobinamide-phosphate
-0.11	883	ABUW_RS10570	guanylyltransferase
	0.781566		replication protein
-0.11	51	ABUW_RS06200	
	0.804715		methionine transporter
-0.11	39	ABUW_RS11375	
	0.703504		acyl-CoA dehydrogenase
-0.11	692	ABUW_RS01835	

-0.11	0.734452		LysR family transcriptional regulator
	699	ABUW_RS12205	
	0.666076		translation initiation factor IF-2
-0.10	261	ABUW_RS17230	
	0.734452		4-hydroxybenzoate 3-monooxygenase
-0.10	699	ABUW_RS12105	
	0.735557		type II 3-dehydroquinate dehydratase
-0.10	491	ABUW_RS08270	
	0.735016		zinc-binding dehydrogenase
-0.10	883	ABUW_RS15610	
	0.787457		hypothetical protein
-0.10	707	ABUW_RS06760	
	0.671616		RHS repeat protein
-0.10	264	ABUW_RS13760	
	0.719025		M48 family metalloproteinase
-0.10	001	ABUW_RS08800	
	0.627815		methionine biosynthesis protein MetW
-0.10	868	ABUW_RS16560	
	0.769933		hypothetical protein
-0.10	023	ABUW_RS01705	
	0.808042		hypothetical protein
-0.10	664	ABUW_RS16790	
	0.693377		transcriptional regulator
-0.10	764	ABUW_RS19805	
	0.678375		Fe-S protein assembly co-chaperone HscB
-0.10	592	ABUW_RS10720	
	0.808826		LysR family transcriptional regulator
-0.10	439	ABUW_RS15605	
	0.647850		ketol-acid reductoisomerase
-0.10	769	ABUW_RS16300	
	0.678375		outer membrane protein assembly factor BamD
-0.10	592	ABUW_RS14985	
	0.758783		FxsA family protein
-0.10	098	ABUW_RS11185	
	0.787494		glutathione S-transferase family protein
-0.10	919	ABUW_RS07980	
	0.780491		hypothetical protein
-0.10	214	ABUW_RS11145	
	0.798329		hypothetical protein
-0.09	25	ABUW_RS14785	
	0.810738		hypothetical protein
-0.09	524	ABUW_RS03970	
	0.731392		pyridoxine 5'-phosphate synthase
-0.09	672	ABUW_RS05085	
	0.829347		CatB-related O-acetyltransferase
-0.09	994	ABUW_RS04370	
	0.783928		hypothetical protein
-0.09	681	ABUW_RS02655	
	0.781566		amidohydrolase
-0.09	51	ABUW_RS09300	
	0.869348		
-0.09	757	sRNA3	
	0.730481		ferredoxin reductase
-0.09	447	ABUW_RS05400	
	0.740902		TusE/DsrC/DsvC family sulfur relay protein
-0.09	143	ABUW_RS08360	
	0.675564		type IV secretion protein Rhs
-0.09	677	ABUW_RS12705	
	0.731110		threonine ammonia-lyase%2C biosynthetic
-0.09	372	ABUW_RS08790	
	0.787457		DUF445 family protein
-0.09	707	ABUW_RS18285	
	0.873322		acyl-CoA thioesterase
-0.09	071	ABUW_RS17575	
	0.787150		membrane protein
-0.09	385	ABUW_RS00030	
	0.828726		flavodoxin family protein
-0.08	258	ABUW_RS18040	
	0.737828		primosomal protein N'
-0.08	392	ABUW_RS17080	

	0.798329		LysR family transcriptional regulator
-0.08	25	ABUW_RS09430	
	0.757452		hypothetical protein
-0.08	775	ABUW_RS15865	
	0.770410		metal ABC transporter ATP-binding protein
-0.08	098	ABUW_RS18215	
	0.867210		hypothetical protein
-0.08	683	ABUW_RS02670	
	0.763509		guanylate kinase
-0.08	988	ABUW_RS01530	
	0.824934		fumarylacetoacetate hydrolase
-0.08	28	ABUW_RS02225	
	0.770410		ATP-dependent Clp protease ATP-binding subunit ClpA
-0.08	098	ABUW_RS08825	
	0.734452		LysR family transcriptional regulator
-0.08	699	ABUW_RS05540	
	0.781566		mechanosensitive ion channel family protein
-0.07	51	ABUW_RS15870	
	0.772157		peptidoglycan-binding protein LysM
-0.07	446	ABUW_RS15080	
	0.788654		3-hydroxybutyrate dehydrogenase
-0.07	461	ABUW_RS10160	
	0.771267		gamma carbonic anhydrase family protein
-0.07	983	ABUW_RS15715	
	0.858661		acinetobactin biosynthesis isochorismate synthase BasJ
-0.07	625	ABUW_RS05800	
	0.921038		
-0.07	017	sRNA94	
	0.811802		DNA repair protein RecO
-0.07	76	ABUW_RS05080	
	0.763214		Zn-dependent hydrolase
-0.07	503	ABUW_RS16875	
	0.832341		hypothetical protein
-0.07	417	ABUW_RS01410	
	0.797328		phosphomannomutase/phosphoglucomutase
-0.07	183	ABUW_RS14760	
	0.798329		hypothetical protein
-0.07	25	ABUW_RS18315	
	0.849050		DMT transporter permease
-0.07	216	ABUW_RS10295	
	0.787370		membrane protein
-0.07	262	ABUW_RS13960	
	0.822135		hypothetical protein
-0.07	616	ABUW_RS06980	
	0.794385		putative multidrug efflux protein AdeT2
-0.07	016	ABUW_RS01935	
	0.774320		phosphoadenylyl-sulfate reductase
-0.06	493	ABUW_RS03555	
	0.822059		sulfurtransferase Tusa family protein
-0.06	749	ABUW_RS06715	
	0.797591		3-oxoadipyl-CoA thiolase
-0.06	135	ABUW_RS12285	
	0.798329		BolA family transcriptional regulator
-0.06	25	ABUW_RS18320	
	0.833272		DNA polymerase III subunit epsilon
-0.06	829	ABUW_RS13810	
	0.871186		regulatory protein RecX
-0.06	028	ABUW_RS08510	
	0.810738		pantoate--beta-alanine ligase
-0.06	524	ABUW_RS16005	
	0.804993		TonB-dependent siderophore receptor
-0.06	682	ABUW_RS05745	
	0.843928		acetate--CoA ligase
-0.06	09	ABUW_RS00865	
	0.813326		BapA prefix-like domain-containing protein
-0.06	93	ABUW_RS05480	
	0.886578		potassium-transporting ATPase subunit KdpC
-0.06	453	ABUW_RS07730	
	0.800293		UTP--glucose-1-phosphate uridylyltransferase GalU
-0.06	298	ABUW_RS18590	

	0.813326		two-component system sensor histidine kinase PmrB
-0.06	93	ABUW_RS04060	
	0.835710		elongation factor P
-0.06	622	ABUW_RS05585	
	0.843928		aspartate aminotransferase family protein
-0.06	09	ABUW_RS05430	
	0.834970		DUF2059 domain-containing protein
-0.06	131	ABUW_RS16515	
	0.875611		MFS transporter
-0.06	865	ABUW_RS15170	
	0.815870		tyrosine--tRNA ligase
-0.05	022	ABUW_RS00070	
	0.858100		5'-nucleosidase
-0.05	18	ABUW_RS15270	
	0.833272		hypothetical protein
-0.05	829	ABUW_RS16605	
	0.833915		DUF493 domain-containing protein
-0.05	167	ABUW_RS04225	
	0.837585		bifunctional demethylmenaquinone methyltransferase/2-methoxy-6-polyprenyl-1%2C4-
-0.05	179	ABUW_RS17160	benzoquinol methylase UbiE
	0.862352		alpha/beta hydrolase
-0.05	172	ABUW_RS13825	
	0.835805		type II secretion system protein GspF
-0.05	668	ABUW_RS17075	
	0.827319		nitronate monooxygenase
-0.05	93	ABUW_RS05195	
	0.833303		3-hydroxyacyl-CoA dehydrogenase
-0.05	481	ABUW_RS03135	
	0.842649		nitroreductase
-0.05	058	ABUW_RS06735	
	0.829347		NADPH-dependent 7-cyano-7-deazaguanine reductase QueF
-0.05	994	ABUW_RS06090	
	0.921038		type 4 fimbrial biogenesis protein
-0.05	017	ABUW_RS10965	
	0.903391		pyrroloquinoline quinone biosynthesis peptide chaperone PqqD
-0.05	919	ABUW_RS10045	
	0.907482		hypothetical protein
-0.05	654	ABUW_RS02680	
	0.833915		circularly permuted type 2 ATP-grasp protein
-0.05	167	ABUW_RS07515	
	0.905570		5'-nucleotidase SurE
-0.05	681	ABUW_RS05530	
	0.898402		hypothetical protein
-0.04	998	ABUW_RS02570	
	0.868347		flavodoxin family protein
-0.04	731	ABUW_RS04200	
	0.847601		VacJ family lipoprotein
-0.04	976	ABUW_RS15825	
	0.905974		CoA transferase subunit A
-0.04	004	ABUW_RS10180	
	0.866102		xanthine dehydrogenase small subunit
-0.04	147	ABUW_RS05840	
	0.879504		glutathione S-transferase family protein
-0.04	218	ABUW_RS16890	
	0.950035		hypothetical protein
-0.04	275	ABUW_RS03620	
	0.899747		phosphoglycerate kinase
-0.04	204	ABUW_RS11045	
	0.892150		pyrroloquinoline quinone biosynthesis protein PqqE
-0.04	653	ABUW_RS10040	
	0.862954		2-methylcitrate synthase
-0.04	378	ABUW_RS18530	
	0.900607		sulfurtransferase
-0.04	267	ABUW_RS02560	
	0.869948		thioredoxin-disulfide reductase
-0.04	425	ABUW_RS17880	
	0.885420		low molecular weight phosphotyrosine protein phosphatase
-0.04	908	ABUW_RS18655	
	0.923909		DNA-binding transcriptional regulator Fis
-0.04	399	ABUW_RS07485	

	0.900570		GlsB/YeaQ/YmgE family stress response membrane protein
-0.04	079	ABUW_RS18980	
	0.866102		electron transfer flavoprotein subunit beta/FixA family protein
-0.04	147	ABUW_RS04700	
	0.897761		LysR family transcriptional regulator ArgP
-0.04	647	ABUW_RS13850	
	0.945872		NUDIX domain-containing protein
-0.04	03	ABUW_RS06615	
	0.909447		hypothetical protein
-0.04	929	ABUW_RS19220	
	0.903391		MFS transporter
-0.04	919	ABUW_RS12035	
	0.898332		3-dehydroshikimate dehydratase
-0.03	596	ABUW_RS08960	
	0.899747		MFS transporter
-0.03	204	ABUW_RS00970	
	0.898504		inorganic diphosphatase
-0.03	411	ABUW_RS17945	
	0.945872		VRR-NUC domain-containing protein
-0.03	03	ABUW_RS03735	
	0.894788		winged helix-turn-helix domain-containing protein
-0.03	088	ABUW_RS12430	
	0.902315		hypothetical protein
-0.03	945	ABUW_RS14735	
	0.900993		endolytic transglycosylase MltG
-0.03	526	ABUW_RS05020	
	0.920620		uroporphyrinogen-III synthase
-0.03	516	ABUW_RS17590	
	0.909833		YbdD/YjiX family protein
-0.03	574	ABUW_RS05595	
	0.907389		signal recognition particle-docking protein FtsY
-0.03	18	ABUW_RS08710	
	0.973402		hypothetical protein
-0.03	86	ABUW_RS14575	
	0.929077		phosphate signaling complex protein PhoU
-0.03	937	ABUW_RS17620	
	0.907389		IcIR family transcriptional regulator
-0.03	18	ABUW_RS00330	
	0.945872		EamA family transporter
-0.03	03	ABUW_RS17630	
	0.972011		Sec-independent protein translocase subunit Tata
-0.02	869	ABUW_RS16580	
	0.912873		tail-specific protease
-0.02	404	ABUW_RS16450	
	0.918526		3%2C4-dihydroxy-2-butanone-4-phosphate synthase
-0.02	438	ABUW_RS15065	
	0.934135		tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit
-0.02	568	ABUW_RS07080	TsaD
	0.936677		LysR family transcriptional regulator
-0.02	627	ABUW_RS09280	
	0.936611		phenylacetic acid degradation operon negative regulatory protein PaaX
-0.02	118	ABUW_RS12275	
	0.967767		single-stranded DNA-binding protein
-0.02	409	ABUW_RS02665	
	0.953164		lactoylglutathione lyase
-0.02	544	ABUW_RS05555	
	0.962507		tRNA (N6-threonylcarbamoyladenine(37)-N6)-methyltransferase TrmO
-0.02	454	ABUW_RS06580	
	0.962507		elongation factor Tu
-0.02	454	ABUW_RS17515	
	0.944796		30S ribosomal protein S7
-0.02	513	ABUW_RS14860	
	0.961661		glycosyltransferase
-0.01	018	ABUW_RS02910	
	0.961849		hypothetical protein
-0.01	942	ABUW_RS05855	
	0.961661		L-cystine transporter
-0.01	018	ABUW_RS05300	
	0.974928		4-hydroxyphenylpyruvate dioxygenase
-0.01	464	ABUW_RS00325	

	0.980721		23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH
-0.01	355	ABUW_RS13925	
	0.962507		DNA mismatch repair endonuclease MutL
-0.01	454	ABUW_RS07850	
	0.982855		DUF1073 domain-containing protein
-0.01	496	ABUW_RS12950	
	0.979661		hypothetical protein
-0.01	357	ABUW_RS00050	
	0.985192		hypothetical protein
-0.01	43	ABUW_RS01300	
	0.974928		DUF2339 domain-containing protein
-0.01	464	ABUW_RS15875	
	0.977192		GMC family oxidoreductase
-0.01	783	ABUW_RS13450	
	0.982892		MFS transporter
-0.01	405	ABUW_RS12065	
	0.982060		DNA-binding protein
-0.01	305	ABUW_RS17100	
	0.986193		fatty acid oxidation complex subunit alpha FadB
-0.01	704	ABUW_RS17385	
	0.983917		NADP(H)-dependent aldo-keto reductase
-0.01	852	ABUW_RS13310	
	0.991406		
0.00	843	sRNA76	
	0.987881		LysM peptidoglycan-binding domain-containing protein
0.00	014	ABUW_RS05535	
	0.990065		DNA polymerase III subunit chi
0.00	197	ABUW_RS17760	
	0.990222		alpha/beta hydrolase
0.00	413	ABUW_RS00060	
	0.988338		bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP diphosphatase
0.00	646	ABUW_RS17180	HisIE
	0.990975		leucyl/phenylalanyl-tRNA--protein transferase
0.00	051	ABUW_RS14825	
	0.994499		pyrroline-5-carboxylate reductase
0.00	468	ABUW_RS13045	
	0.995622		exodeoxyribonuclease V subunit alpha
0.00	728	ABUW_RS17130	
	0.996782		NADPH-dependent 2%2C4-dienoyl-CoA reductase
0.00	193	ABUW_RS13715	
	0.999412		hypothetical protein
0.00	087	ABUW_RS19070	
	0.999412		hypothetical protein
0.00	087	ABUW_RS19735	
	0.998211		type IV conjugative transfer system lipoprotein TraV
0.00	245	ABUW_RS19500	
	0.996499		5-carboxymethyl-2-hydroxymuconate Delta-isomerase
0.00	912	ABUW_RS07935	
	0.996499		alpha/beta hydrolase
0.00	912	ABUW_RS07920	
	0.991837		heavy metal-associated domain protein
0.00	376	ABUW_RS13140	
	0.989583		flavin reductase family protein
0.00	269	ABUW_RS09080	
	0.989583		translation initiation factor IF-3
0.00	269	ABUW_RS15975	
	0.985011		hypothetical protein
0.01	015	ABUW_RS15235	
	0.983917		thiamine-phosphate kinase
0.01	852	ABUW_RS00455	
	0.982442		30S ribosomal protein S2
0.01	121	ABUW_RS06035	
	0.983429		MBL fold metallo-hydrolase
0.01	276	ABUW_RS08990	
	0.989328		twin-arginine translocase subunit TatB
0.01	725	ABUW_RS16585	
	0.982313		dihydroxy-acid dehydratase
0.01	408	ABUW_RS09420	
	0.966449		3-oxoacyl-ACP reductase FabG
0.01	584	ABUW_RS15090	

	0.977192		molybdenum cofactor guanylyltransferase
0.01	783	ABUW_RS08310	
	0.970024		acetyl-CoA C-acyltransferase FadA
0.01	845	ABUW_RS17390	
	0.961823		AarF/ABC1/UbiB kinase family protein
0.01	051	ABUW_RS10655	
	0.968389		homoserine dehydrogenase
0.01	653	ABUW_RS17705	
	0.950464		membrane protein
0.02	841	ABUW_RS18650	
	0.960474		hypothetical protein
0.02	343	ABUW_RS00895	
	0.943198		sel1 repeat family protein
0.02	935	ABUW_RS16565	
	0.959003		hypothetical protein
0.02	995	ABUW_RS14580	
	0.939922		hypothetical protein
0.02	095	ABUW_RS15330	
	0.930293		nitrate reductase
0.02	313	ABUW_RS08305	
	0.970087		hypothetical protein
0.02	308	ABUW_RS16620	
	0.936916		type II secretion system protein
0.02	147	ABUW_RS10950	
	0.948169		exonuclease SbcCD subunit D
0.02	7	ABUW_RS14695	
	0.922796		UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)
0.02	534	ABUW_RS18640	
	0.936017		dephospho-CoA kinase
0.02	194	ABUW_RS17285	
	0.937606		bifunctional nicotinamidase/pyrazinamidase
0.02	856	ABUW_RS00305	
	0.970087		hypothetical protein
0.02	308	ABUW_RS06110	
	0.961823		sigma-70 family RNA polymerase sigma factor
0.02	051	ABUW_RS14505	
	0.939922		enoyl-CoA hydratase/isomerase family protein
0.02	095	ABUW_RS18395	
	0.922747		replication-associated recombination protein A
0.02	659	ABUW_RS00275	
	0.923909		multidrug efflux transcriptional repressor AdeN
0.02	399	ABUW_RS08430	
	0.913071		50S ribosomal protein L32
0.03	773	ABUW_RS15100	
	0.921038		HAMP domain-containing histidine kinase
0.03	017	ABUW_RS07390	
	0.967767		hypothetical protein
0.03	409	ABUW_RS19395	
	0.924776		hypothetical protein
0.03	259	ABUW_RS02150	
	0.903621		TonB-dependent receptor
0.03	815	ABUW_RS10605	
	0.922358		uracil phosphoribosyltransferase
0.03	581	ABUW_RS15365	
	0.901756		DUF177 domain-containing protein
0.03	21	ABUW_RS15105	
	0.924776		DUF4112 domain-containing protein
0.03	259	ABUW_RS04530	
	0.934832		ATP-binding protein
0.03	448	ABUW_RS07230	
	0.895830		TonB-dependent receptor
0.03	706	ABUW_RS03025	
	0.906271		BolA/IbaG family iron-sulfur metabolism protein
0.03	891	ABUW_RS15785	
	0.892150		TonB-dependent receptor
0.04	653	ABUW_RS10830	
	0.886017		ParB/RepB/Spo0J family partition protein
0.04	722	ABUW_RS11000	
	0.885572		N-acetyl-gamma-glutamyl-phosphate reductase
0.04	705	ABUW_RS08810	

	0.874397		glutamine--tRNA ligase/YqeY domain fusion protein
0.04	67	ABUW_RS07885	
	0.892589		transcriptional regulator BetI
0.04	061	ABUW_RS14420	
	0.873579		thioredoxin TrxC
0.04	975	ABUW_RS02540	
	0.923244		hypothetical protein
0.04	027	ABUW_RS06960	
	0.861355		3-dehydroquinate synthase
0.04	572	ABUW_RS01455	
	0.886017		multidrug efflux SMR transporter
0.04	722	ABUW_RS06550	
	0.892229		5'-nucleosidase
0.04	722	ABUW_RS18790	
	0.934832		SDR family NAD(P)-dependent oxidoreductase
0.04	448	ABUW_RS09565	
	0.886017		toxin
0.04	722	ABUW_RS03285	
	0.873322		hypothetical protein
0.04	071	ABUW_RS14635	
	0.892150		AraC family transcriptional regulator
0.04	653	ABUW_RS03575	
	0.867950		LysR family transcriptional regulator
0.04	513	ABUW_RS15575	
	0.886017		DMT family transporter
0.05	722	ABUW_RS08355	
	0.871096		aminopeptidase P family protein
0.05	521	ABUW_RS05610	
	0.842735		hypothetical protein
0.05	951	ABUW_RS16120	
	0.893191		acetyl-CoA C-acetyltransferase
0.05	388	ABUW_RS03140	
	0.892589		C4-dicarboxylate ABC transporter
0.05	061	ABUW_RS18795	
	0.861257		esterase
0.05	171	ABUW_RS00610	
	0.852083		ribosome biogenesis GTPase Der
0.05	94	ABUW_RS16390	
	0.909513		type I glyceraldehyde-3-phosphate dehydrogenase
0.05	33	ABUW_RS13335	
	0.890769		SDR family NAD(P)-dependent oxidoreductase
0.05	269	ABUW_RS07990	
	0.837654		hypothetical protein
0.05	54	ABUW_RS06415	
	0.868347		2%2C3-butanediol dehydrogenase
0.05	731	ABUW_RS10330	
	0.842649		KpsF/GutQ family sugar-phosphate isomerase
0.05	058	ABUW_RS12855	
	0.882413		DUF2062 domain-containing protein
0.05	625	ABUW_RS15265	
	0.833131		MFS transporter
0.05	067	ABUW_RS05550	
	0.898332		
0.05	596	sRNA96	
	0.884719		NADPH-dependent 2%2C4-dienoyl-CoA reductase
0.05	126	ABUW_RS08850	
	0.835849		HAD family hydrolase
0.05	161	ABUW_RS16900	
	0.844953		class C extended-spectrum beta-lactamase ADC-11
0.05	763	ABUW_RS05830	
	0.843348		acyl-CoA dehydrogenase
0.05	934	ABUW_RS10660	
	0.866102		conjugal transfer protein TraH
0.05	147	ABUW_RS19550	
	0.848571		LrgB family protein
0.05	623	ABUW_RS02450	
	0.820849		NADP-dependent malic enzyme
0.05	966	ABUW_RS05960	
	0.825840		peroxide stress protein YaaA
0.05	941	ABUW_RS06690	

	0.878324		hypothetical protein
0.05	7	ABUW_RS00235	
	0.844001		DMT family transporter
0.06	23	ABUW_RS18130	
	0.890699		lysozyme
0.06	651	ABUW_RS06470	
	0.827194		ABC transporter ATP-binding protein
0.06	583	ABUW_RS01880	
	0.893191		hypothetical protein
0.06	388	ABUW_RS04420	
	0.898504		
0.06	411	sRNA18	
	0.813326		type VI secretion system protein TssA
0.06	93	ABUW_RS12475	
	0.842735		PLP-dependent aminotransferase family protein
0.06	951	ABUW_RS00220	
	0.845997		anti-anti-sigma factor GigB
0.06	989	ABUW_RS15835	
	0.770410		CBS domain-containing protein
0.06	098	ABUW_RS17050	
	0.812670		threonylcarbamoyl-AMP synthase
0.06	643	ABUW_RS18125	
	0.782542		flavodoxin family protein
0.06	544	ABUW_RS14970	
	0.799934		integration host factor subunit alpha
0.06	051	ABUW_RS15925	
	0.876756		hypothetical protein
0.06	92	ABUW_RS06770	
	0.822059		PDZ domain-containing protein
0.06	749	ABUW_RS05950	
	0.873513		DUF962 domain-containing protein
0.06	838	ABUW_RS11395	
	0.771355		ring-hydroxylating oxygenase subunit alpha
0.07	765	ABUW_RS14920	
	0.816317		lactonase family protein
0.07	359	ABUW_RS08205	
	0.780491		2%2C3-bisphosphoglycerate-independent phosphoglycerate mutase
0.07	214	ABUW_RS17740	
	0.873579		type IV pilus twitching motility protein PilT
0.07	975	ABUW_RS14710	
	0.867134		hypothetical protein
0.07	199	ABUW_RS06900	
	0.799336		type VI secretion system membrane subunit TssM
0.07	211	ABUW_RS12500	
	0.846031		1-phosphofructokinase
0.07	131	ABUW_RS08625	
	0.799113		PLP-dependent aminotransferase family protein
0.07	252	ABUW_RS17920	
	0.787939		lytic murein transglycosylase B
0.07	513	ABUW_RS06075	
	0.787715		cytochrome b
0.07	9	ABUW_RS13365	
	0.846031		oxidative damage protection protein
0.07	131	ABUW_RS17615	
	0.802111		DUF1615 domain-containing protein
0.07	048	ABUW_RS05185	
	0.840060		
0.07	311	sRNA63	
	0.757452		nucleotide exchange factor GrpE
0.07	775	ABUW_RS18885	
	0.759570		EF-P beta-lysylation protein EpmB
0.07	647	ABUW_RS05580	
	0.840387		DUF2804 domain-containing protein
0.07	194	ABUW_RS03045	
	0.737828		pirin family protein
0.07	392	ABUW_RS18260	
	0.799842		SMC-Scp complex subunit ScpB
0.08	115	ABUW_RS15125	
	0.823279		porin
0.08	266	ABUW_RS04045	

	0.798753		betaine-aldehyde dehydrogenase
0.08	696	ABUW_RS14425	
	0.775669		type IV secretion system DNA-binding domain-containing protein
0.08	303	ABUW_RS19375	
	0.835259		hypothetical protein
0.08	975	ABUW_RS03750	
	0.798329		DHA2 family efflux MFS transporter permease subunit
0.08	25	ABUW_RS17995	
	0.754317		iron-sulfur cluster insertion protein ErpA
0.08	788	ABUW_RS00055	
	0.747340		DUF4102 domain-containing protein
0.08	153	ABUW_RS14640	
	0.813326		benzoate 1%2C2-dioxygenase large subunit
0.08	93	ABUW_RS13150	
	0.703504		hypothetical protein
0.08	692	ABUW_RS16830	
	0.735936		50S ribosomal protein L11 methyltransferase
0.08	588	ABUW_RS07495	
	0.825813		hypothetical protein
0.08	202	ABUW_RS13065	
	0.820849		urease accessory protein UreG
0.08	966	ABUW_RS13985	
	0.774364		oxidoreductase
0.08	546	ABUW_RS14910	
	0.842221		endonuclease
0.08	311	ABUW_RS01685	
	0.766772		exodeoxyribonuclease VII large subunit
0.09	008	ABUW_RS13095	
	0.731392		RidA family protein
0.09	672	ABUW_RS01515	
	0.780755		hypothetical protein
0.09	605	ABUW_RS10695	
	0.696262		phosphohydrolase
0.09	541	ABUW_RS02475	
	0.734853		hypothetical protein
0.09	839	ABUW_RS03360	
	0.730948		wax ester/triacylglycerol synthase family O-acyltransferase
0.09	95	ABUW_RS03550	
	0.781566		ribosome-binding factor A
0.09	51	ABUW_RS17225	
	0.730407		AraC family transcriptional regulator
0.09	198	ABUW_RS03595	
	0.720644		FKBP-type peptidyl-prolyl cis-trans isomerase
0.09	114	ABUW_RS14375	
	0.754021		DUF927 domain-containing protein
0.09	878	ABUW_RS14600	
	0.965513		TetR/AcrR family transcriptional regulator
0.09	214	ABUW_RS02370	
	0.662160		ATP-dependent chaperone ClpB
0.09	045	ABUW_RS13285	
	0.862870		hypothetical protein
0.09	488	ABUW_RS06355	
	0.785787		LysR family transcriptional regulator
0.09	978	ABUW_RS15560	
	0.898504		AlpA family phage regulatory protein
0.09	411	ABUW_RS03610	
	0.693377		lysozyme
0.09	764	ABUW_RS18000	
	0.693451		hydroxyethylthiazole kinase
0.09	447	ABUW_RS07940	
	0.654588		acyl-CoA dehydrogenase
0.09	111	ABUW_RS02975	
	0.704308		peroxiredoxin
0.09	529	ABUW_RS03090	
	0.734952		hypothetical protein
0.10	158	ABUW_RS00435	
	0.796984		cold shock domain-containing protein
0.10	473	ABUW_RS15360	
	0.825266		YchJ family protein
0.10	156	ABUW_RS17980	

	0.667271		DUF1345 domain-containing protein
0.10	313	ABUW_RS16885	
	0.727848		potassium uptake protein (TrkH)
0.10	939	ABUW_RS08780	
	0.788654		thioesterase family protein
0.10	461	ABUW_RS17360	
	0.825957		DUF559 domain-containing protein
0.10	465	ABUW_RS06245	
	0.811928		hypothetical protein
0.10	109	ABUW_RS03740	
	0.721371		exodeoxyribonuclease VII
0.10	816	ABUW_RS13100	
	0.796984		rod shape-determining protein RodA
0.10	473	ABUW_RS06080	
	0.718437		pirin family protein
0.10	424	ABUW_RS01025	
	0.654465		dicarboxylate/amino acid:cation symporter
0.10	983	ABUW_RS01950	
	0.722578		thiol:disulfide oxidoreductase
0.11	212	ABUW_RS15970	
	0.842649		GNAT family N-acetyltransferase
0.11	058	ABUW_RS03120	
	0.681528		DUF3144 domain-containing protein
0.11	97	ABUW_RS05315	
	0.653772		TIGR01666 family membrane protein
0.11	981	ABUW_RS03445	
	0.832404		hypothetical protein
0.11	612	ABUW_RS06135	
	0.770920		AraC family transcriptional regulator
0.11	103	ABUW_RS14250	
	0.665990		GTPase ObgE
0.11	636	ABUW_RS05170	
	0.673658		phosphate regulon transcriptional regulatory protein PhoB
0.11	078	ABUW_RS00525	
	0.698833		SRPBCC family protein
0.11	38	ABUW_RS12610	
	0.734452		cysteine synthase CysM
0.11	699	ABUW_RS16055	
	0.645788		peptidylprolyl isomerase
0.11	386	ABUW_RS11030	
	0.615744		dihydrodipicolinate synthase family protein
0.11	073	ABUW_RS12400	
	0.684077		SMI1/KNR4 family protein
0.11	272	ABUW_RS09335	
	0.645376		guanylate cyclase
0.11	283	ABUW_RS10735	
	0.649311		lipid A hydroxylase LpxO
0.11	205	ABUW_RS17375	
	0.678375		HlyD family secretion protein
0.11	592	ABUW_RS04745	
	0.734211		tRNA adenosine(34) deaminase TadA
0.11	032	ABUW_RS10915	
	0.649849		phosphoenolpyruvate synthase
0.11	101	ABUW_RS07590	
	0.619998		2-methylnaconitate cis-trans isomerase PrpF
0.11	944	ABUW_RS04005	
	0.678375		DNA/RNA non-specific endonuclease
0.12	592	ABUW_RS01145	
	0.787370		3-(3-hydroxy-phenyl)propionate transporter MhpT
0.12	262	ABUW_RS13485	
	0.622394		malate synthase G
0.12	74	ABUW_RS10860	
	0.748363		hypothetical protein
0.12	534	ABUW_RS19190	
	0.611486		hypothetical protein
0.12	215	ABUW_RS15730	
	0.659833		DUF1275 domain-containing protein
0.12	967	ABUW_RS11080	
	0.641229		hypothetical protein
0.12	744	ABUW_RS08805	

	0.594978		NAD(+) kinase
0.12	12	ABUW_RS06630	
	0.657270		tail protein
0.12	096	ABUW_RS03935	
	0.563700		response regulator transcription factor
0.12	045	ABUW_RS00890	
	0.628464		L-aspartate oxidase
0.12	114	ABUW_RS05035	
	0.710950		hypothetical protein
0.12	953	ABUW_RS15340	
	0.614052		sodium:proton antiporter
0.12	538	ABUW_RS16685	
	0.651139		hypothetical protein
0.12	549	ABUW_RS01290	
	0.770920		PhzF family isomerase
0.12	103	ABUW_RS15480	
	0.673658		hypothetical protein
0.12	078	ABUW_RS05075	
	0.799934		DedA family protein
0.12	051	ABUW_RS15965	
	0.744319		tRNA-binding protein
0.12	612	ABUW_RS17060	
	0.718186		TraU family protein
0.12	674	ABUW_RS19525	
	0.627284		trehalose-phosphatase
0.12	093	ABUW_RS15160	
	0.619329		hypothetical protein
0.12	07	ABUW_RS00605	
	0.646034		general secretion pathway protein
0.13	518	ABUW_RS17565	
	0.771355		hypothetical protein
0.13	765	ABUW_RS06775	
	0.584278		LysR family transcriptional regulator
0.13	225	ABUW_RS01015	
	0.862055		hypothetical protein
0.13	964	ABUW_RS08050	
	0.568047		transporter
0.13	261	ABUW_RS00670	
	0.681136		hypothetical protein
0.13	635	ABUW_RS16980	
	0.671616		type I-F CRISPR-associated protein Csy3
0.13	264	ABUW_RS05355	
	0.541387		alpha/beta hydrolase
0.13	168	ABUW_RS03470	
	0.787457		hypothetical protein
0.13	707	ABUW_RS03725	
	0.735016		Paal family thioesterase
0.13	883	ABUW_RS05110	
	0.698489		site-specific tyrosine recombinase XerD
0.13	026	ABUW_RS17695	
	0.618371		phosphohistidine phosphatase
0.13	908	ABUW_RS06745	
	0.618896		type VI secretion system tip protein VgrG
0.13	107	ABUW_RS13685	
	0.576598		UMP kinase
0.13	336	ABUW_RS08450	
	0.580333		hypothetical protein
0.13	021	ABUW_RS01065	
	0.668991		hypothetical protein
0.13	967	ABUW_RS08255	
	0.596550		winged helix-turn-helix transcriptional regulator
0.13	59	ABUW_RS16735	
	0.532500		diaminopimelate epimerase
0.14	083	ABUW_RS04680	
	0.738229		LysR family transcriptional regulator
0.14	906	ABUW_RS01770	
	0.542524		ferredoxin--NADP reductase
0.14	823	ABUW_RS15345	
	0.582545		ParA family protein
0.14	26	ABUW_RS01680	

	0.546919		peptidase
0.14	407	ABUW_RS07530	
	0.498529		alpha/beta hydrolase
0.14	1	ABUW_RS02535	
	0.799336		hypothetical protein
0.14	211	ABUW_RS10025	
	0.559103		S8 family peptidase
0.14	433	ABUW_RS08570	
	0.766277		aspartate/glutamate racemase family protein
0.14	568	ABUW_RS07415	
	0.527276		FAD-binding oxidoreductase
0.14	167	ABUW_RS01635	
	0.812670		nuclear transport factor 2 family protein
0.15	643	ABUW_RS08855	
	0.611447		PEGA domain-containing protein
0.15	434	ABUW_RS08615	
	0.474089		glycerol-3-phosphate 1-O-acyltransferase PlsB
0.15	586	ABUW_RS01940	
	0.527078		hypothetical protein
0.15	841	ABUW_RS05320	
	0.593454		methylisocitrate lyase
0.15	763	ABUW_RS18535	
	0.763222		hypothetical protein
0.15	277	ABUW_RS10600	
	0.691326		oxidoreductase
0.15	255	ABUW_RS13470	
	0.702043		glycosyltransferase family 2 protein
0.15	788	ABUW_RS04725	
	0.597750		glutathione-dependent formaldehyde dehydrogenase
0.15	212	ABUW_RS12605	
	0.549194		hypothetical protein
0.15	213	ABUW_RS09670	
	0.738500		
0.15	96	sRNA49	
	0.613154		DNA internalization-related competence protein ComEC/Rec2
0.16	73	ABUW_RS04785	
	0.496588		acyl-CoA desaturase
0.16	304	ABUW_RS05405	
	0.527078		DUF808 domain-containing protein
0.16	841	ABUW_RS04320	
	0.535229		ribosome silencing factor
0.16	336	ABUW_RS16080	
	0.480244		HdeD family acid-resistance protein
0.16	633	ABUW_RS16715	
	0.734452		helix-turn-helix domain-containing protein
0.16	699	ABUW_RS01200	
	0.564437		YcgL domain-containing protein
0.16	653	ABUW_RS10410	
	0.718186		hypothetical protein
0.16	674	ABUW_RS16180	
	0.518205		HesA/MoeB/ThiF family protein
0.16	81	ABUW_RS07700	
	0.604803		alkaline phosphatase
0.16	149	ABUW_RS04435	
	0.557271		AraC family transcriptional regulator
0.16	528	ABUW_RS01080	
	0.523992		ATP-binding protein
0.16	807	ABUW_RS05545	
	0.498106		type II secretion system protein GspG
0.16	312	ABUW_RS17070	
	0.585614		CoA transferase
0.16	562	ABUW_RS12055	
	0.589450		hypothetical protein
0.16	663	ABUW_RS15745	
	0.481512		DNA repair protein RecN
0.17	603	ABUW_RS17310	
	0.537564		DNA polymerase III subunit delta'
0.17	045	ABUW_RS10970	
	0.471940		copper resistance system multicopper oxidase
0.17	648	ABUW_RS16135	

	0.413300		NAD(P)/FAD-dependent oxidoreductase
0.17	009	ABUW_RS09620	
	0.730948		hypothetical protein
0.17	95	ABUW_RS00590	
	0.530495		ureidoglycolate lyase
0.17	221	ABUW_RS00620	
	0.549070		tRNA epoxyqueuosine(34) reductase QueG
0.17	457	ABUW_RS11215	
	0.442574		LPS export ABC transporter ATP-binding protein
0.17	261	ABUW_RS12835	
	0.544163		hypothetical protein
0.17	69	ABUW_RS19060	
	0.514819		SulP family inorganic anion transporter
0.17	692	ABUW_RS08575	
	0.486479		polyphosphate--AMP phosphotransferase
0.17	507	ABUW_RS17150	
	0.563553		anthranilate 1%2C2-dioxygenase electron transfer component AntC
0.17	14	ABUW_RS10115	
	0.495765		HIT domain-containing protein
0.18	763	ABUW_RS10740	
	0.472671		DUF2157 domain-containing protein
0.18	288	ABUW_RS15060	
	0.430132		AarF/ABC1/UbiB kinase family protein
0.18	075	ABUW_RS07705	
	0.500858		hypothetical protein
0.18	15	ABUW_RS17155	
	0.502776		pirin family protein
0.18	814	ABUW_RS14885	
	0.418988		hypothetical protein
0.18	311	ABUW_RS13115	
	0.535229		TatD family deoxyribonuclease
0.18	336	ABUW_RS16260	
	0.669512		hypothetical protein
0.18	486	ABUW_RS00355	
	0.462904		DUF262 domain-containing protein
0.18	879	ABUW_RS14540	
	0.386711		transglutaminase family protein
0.18	255	ABUW_RS07525	
	0.450940		hypothetical protein
0.18	131	ABUW_RS03440	
	0.517591		AraC family transcriptional regulator
0.18	325	ABUW_RS13565	
	0.382081		YihY family inner membrane protein
0.18	95	ABUW_RS02240	
	0.352828		RNA polymerase sigma factor RpoH
0.18	788	ABUW_RS06710	
	0.408504		porin
0.19	985	ABUW_RS03155	
	0.562980		molybdate ABC transporter permease subunit
0.19	401	ABUW_RS10090	
	0.796984		hypothetical protein
0.19	473	ABUW_RS19775	
	0.705743		transporter substrate-binding domain-containing protein
0.19	106	ABUW_RS11775	
	0.557271		poly(hydroxyalcanoate) granule associated protein
0.19	528	ABUW_RS10690	
	0.533978		type I-F CRISPR-associated protein Csy2
0.19	115	ABUW_RS05350	
	0.463906		protein-export chaperone SecB
0.19	416	ABUW_RS16380	
	0.513305		carbon storage regulator CsrA
0.19	764	ABUW_RS13350	
	0.568047		sulfurtransferase Tusa
0.19	261	ABUW_RS17045	
	0.410354		3'%2C5'-cyclic-nucleotide phosphodiesterase
0.19	28	ABUW_RS04490	
	0.647850		hypothetical protein
0.19	769	ABUW_RS08670	
	0.446179		aldehyde-activating protein
0.19	57	ABUW_RS01040	

	0.387648		general secretion pathway protein GspL
0.19	909	ABUW_RS07025	
	0.400029		Dyp-type peroxidase
0.19	805	ABUW_RS10755	
	0.591109		ATP-binding cassette domain-containing protein
0.20	053	ABUW_RS11380	
	0.647850		malonate transporter subunit MadL
0.20	769	ABUW_RS11650	
	0.359835		phosphoglycerate dehydrogenase
0.20	308	ABUW_RS01630	
	0.549070		prepilin-type N-terminal cleavage/methylation domain-containing protein
0.20	457	ABUW_RS01565	
	0.350995		hypothetical protein
0.20	746	ABUW_RS18305	
	0.401814		molecular chaperone HtpG
0.20	343	ABUW_RS17430	
	0.640086		alpha/beta hydrolase
0.20	379	ABUW_RS08565	
	0.569386		aminoglycoside nucleotidyltransferase ANT(2'')-Ia
0.20	292	ABUW_RS19315	
	0.413198		hydrolase
0.20	714	ABUW_RS01020	
	0.670326		
0.20	176	sRNA37	
	0.439472		ferric iron uptake transcriptional regulator
0.20	755	ABUW_RS14720	
	0.572572		acyl-CoA dehydrogenase
0.20	523	ABUW_RS18405	
	0.372689		heavy metal translocating P-type ATPase
0.20	555	ABUW_RS16155	
	0.340698		fumarate hydratase
0.20	619	ABUW_RS16510	
	0.438451		hypothetical protein
0.20	234	ABUW_RS13965	
	0.570373		30S ribosomal protein S6
0.20	256	ABUW_RS07555	
	0.704308		hypothetical protein
0.21	529	ABUW_RS13770	
	0.344200		glycerol-3-phosphate dehydrogenase
0.21	292	ABUW_RS04475	
	0.461455		metalloregulator ArsR/SmtB family transcription factor
0.21	087	ABUW_RS17860	
	0.358483		phosphoenolpyruvate--protein phosphotransferase
0.21	988	ABUW_RS16865	
	0.405133		Cu(I)-responsive transcriptional regulator
0.21	307	ABUW_RS13130	
	0.424862		HAD family hydrolase
0.21	669	ABUW_RS18735	
	0.408792		SDR family NAD(P)-dependent oxidoreductase
0.21	951	ABUW_RS04105	
	0.307970		bifunctional [glutamate--ammonia ligase]-adenylyl-L-tyrosine phosphorylase/[glutamate-
0.21	148	ABUW_RS02880	-ammonia-ligase] adenylyltransferase
	0.552868		hypothetical protein
0.21	547	ABUW_RS06250	
	0.422184		glutamate--cysteine ligase
0.21	631	ABUW_RS00565	
	0.376433		LysR family transcriptional regulator
0.21	601	ABUW_RS12450	
	0.307818		TonB-dependent receptor
0.21	901	ABUW_RS19615	
	0.293339		protoporphyrinogen oxidase HemJ
0.21	222	ABUW_RS14880	
	0.432487		VOC family protein
0.21	786	ABUW_RS03180	
	0.457784		MBL fold metallo-hydrolase
0.22	265	ABUW_RS03085	
	0.438364		LysE family translocator
0.22	117	ABUW_RS16755	
	0.755369		membrane protein
0.22	828	ABUW_RS02835	

	0.401181		LysR family transcriptional regulator
0.22	553	ABUW_RS07645	
	0.403985		translational GTPase TypA
0.22	559	ABUW_RS03225	
	0.487724		hypothetical protein
0.22	052	ABUW_RS16615	
	0.397259		TetR/AcrR family transcriptional regulator
0.22	717	ABUW_RS04620	
	0.480856		nucleoside deaminase
0.22	702	ABUW_RS12440	
	0.270779		phosphoribosylamine--glycine ligase
0.22	736	ABUW_RS07475	
	0.527524		hypothetical protein
0.22	988	ABUW_RS17935	
	0.345432		DUF937 domain-containing protein
0.22	755	ABUW_RS10500	
	0.541269		Lrp/AsnC family transcriptional regulator
0.23	721	ABUW_RS11820	
	0.422184		enoyl-CoA hydratase/isomerase family protein
0.23	631	ABUW_RS10920	
	0.348903		DNA-3-methyladenine glycosylase
0.23	951	ABUW_RS03250	
	0.552785		PAAR domain-containing protein
0.23	675	ABUW_RS12485	
	0.367979		hypothetical protein
0.23	943	ABUW_RS09675	
	0.270794		outer membrane porin%2C OprD family
0.23	832	ABUW_RS17940	
	0.458499		tetratricopeptide repeat protein
0.23	305	ABUW_RS08505	
	0.526022		sulfate ABC transporter substrate-binding protein
0.23	298	ABUW_RS01375	
	0.291398		YfhL family 4Fe-4S dicluster ferredoxin
0.23	323	ABUW_RS14955	
	0.302560		class I SAM-dependent methyltransferase
0.23	129	ABUW_RS01035	
	0.410596		acyl-CoA thioesterase
0.23	986	ABUW_RS08195	
	0.346951		quinolinate synthase NadA
0.23	748	ABUW_RS15640	
	0.451734		response regulator transcription factor
0.24	909	ABUW_RS07395	
	0.324998		DNA replication/repair protein RecF
0.24	861	ABUW_RS00015	
	0.322092		Tol-Pal system beta propeller repeat protein TolB
0.24	852	ABUW_RS04870	
	0.274776		alpha/beta hydrolase
0.24	61	ABUW_RS08840	
	0.241519		polysaccharide biosynthesis tyrosine autokinase
0.24	785	ABUW_RS18660	
	0.595098		ABC transporter ATP-binding protein
0.24	843	ABUW_RS10245	
	0.363054		TonB-dependent receptor
0.24	895	ABUW_RS05870	
	0.344545		EamA family transporter
0.24	428	ABUW_RS01620	
	0.272681		bifunctional 3-demethylubiquinone 3-O-methyltransferase/2-octaprenyl-6-hydroxy
0.24	812	ABUW_RS18730	phenol methylase
	0.241518		hypothetical protein
0.24	783	ABUW_RS02205	
	0.388268		hypothetical protein
0.24	873	ABUW_RS07640	
	0.214809		LLM class flavin-dependent oxidoreductase
0.24	406	ABUW_RS07625	
	0.489146		phenylacetate--CoA ligase
0.24	946	ABUW_RS12280	
	0.256776		RsbU family protein phosphatase GigA
0.24	291	ABUW_RS15830	
	0.361250		LysR family transcriptional regulator
0.24	086	ABUW_RS16245	

	0.401530		response regulator transcription factor
0.24	15	ABUW_RS11805	
	0.374768		hypothetical protein
0.24	425	ABUW_RS05575	
	0.324162		DUF2061 domain-containing protein
0.25	742	ABUW_RS16845	
	0.373222		MgtC/SapB family protein
0.25	162	ABUW_RS06585	
	0.336177		RDD family protein
0.25	387	ABUW_RS07585	
	0.257626		AraC family transcriptional regulator
0.25	106	ABUW_RS06050	
	0.291869		hypothetical protein
0.25	205	ABUW_RS02455	
	0.283363		MFS transporter
0.25	831	ABUW_RS07760	
	0.371627		cob(I)yrinic acid a%2Cc-diamide adenosyltransferase
0.25	443	ABUW_RS03020	
	0.328156		YebC/PmpR family DNA-binding transcriptional regulator
0.25	155	ABUW_RS11315	
	0.475305		LysR family transcriptional regulator
0.25	574	ABUW_RS04075	
	0.320287		peptidase S41
0.26	611	ABUW_RS17735	
	0.352729		hypothetical protein
0.26	018	ABUW_RS04460	
	0.562781		GNAT family N-acetyltransferase
0.26	949	ABUW_RS18055	
	0.189037		nicotinate phosphoribosyltransferase
0.26	888	ABUW_RS00500	
	0.258157		cation transporter
0.26	171	ABUW_RS01320	
	0.457743		LysR family transcriptional regulator
0.26	205	ABUW_RS15350	
	0.303112		Lrp/AsnC family transcriptional regulator
0.26	788	ABUW_RS08000	
	0.422184		YajQ family cyclic di-GMP-binding protein
0.26	631	ABUW_RS02555	
	0.341208		LysR family transcriptional regulator
0.26	958	ABUW_RS14510	
	0.397788		hypothetical protein
0.26	383	ABUW_RS12975	
	0.191181		hypothetical protein
0.26	995	ABUW_RS20495	
	0.278597		serine O-acetyltransferase
0.26	34	ABUW_RS11490	
	0.190021		RNA polymerase-associated protein RapA
0.26	997	ABUW_RS05385	
	0.252180		Fur family transcriptional regulator
0.26	348	ABUW_RS18210	
	0.294321		Tim44 domain-containing protein
0.26	898	ABUW_RS04655	
	0.266649		DUF2797 domain-containing protein
0.26	897	ABUW_RS10510	
	0.310466		type I-F CRISPR-associated protein Csy1
0.26	148	ABUW_RS05345	
	0.192358		4-hydroxythreonine-4-phosphate dehydrogenase PdxA
0.27	874	ABUW_RS02430	
	0.236079		type 1 glutamine amidotransferase domain-containing protein
0.27	531	ABUW_RS09210	
	0.645840		benzoate 1%2C2-dioxygenase small subunit
0.27	035	ABUW_RS13155	
	0.483614		N-acetyltransferase
0.27	107	ABUW_RS11695	
	0.319365		glutathione peroxidase
0.27	205	ABUW_RS18150	
	0.543235		hypothetical protein
0.27	387	ABUW_RS11880	
	0.495746		methyltransferase
0.27	188	ABUW_RS04455	

	0.365697		protein rep
0.27	191	ABUW_RS19635	
	0.279131		FtsQ-type POTRA domain-containing protein
0.27	8	ABUW_RS00740	
	0.665913		hypothetical protein
0.27	842	ABUW_RS06150	
	0.175574		O-succinylhomoserine sulfhydrylase
0.27	767	ABUW_RS10450	
	0.180827		universal stress protein
0.27	489	ABUW_RS08095	
	0.195712		CysB family HTH-type transcriptional regulator
0.27	023	ABUW_RS04985	
	0.294838		NAD(P)H-dependent oxidoreductase
0.27	087	ABUW_RS03570	
	0.212071		RNA polymerase factor sigma-54
0.27	346	ABUW_RS15795	
	0.280395		MFS transporter
0.27	924	ABUW_RS08250	
	0.316867		hypothetical protein
0.27	833	ABUW_RS13000	
	0.200737		succinyldiaminopimelate transaminase
0.27	207	ABUW_RS11440	
	0.249454		ParA family protein
0.28	821	ABUW_RS11005	
	0.207068		CoA pyrophosphatase
0.28	846	ABUW_RS15720	
	0.358483		replication protein
0.28	988	ABUW_RS09660	
	0.266325		asparaginase
0.28	269	ABUW_RS16795	
	0.242337		arsenate reductase (glutaredoxin)
0.28	734	ABUW_RS17855	
	0.172160		7-cyano-7-deazaguanine synthase QueC
0.28	6	ABUW_RS04965	
	0.358725		D-alanyl-D-alanine carboxypeptidase PBP5/6
0.28	126	ABUW_RS05515	
	0.317688		D-amino acid dehydrogenase
0.28	078	ABUW_RS18450	
	0.484501		twin-arginine translocase subunit TatC
0.28	476	ABUW_RS16590	
	0.183824		PadR family transcriptional regulator
0.28	604	ABUW_RS08845	
	0.242188		indole-3-glycerol phosphate synthase TrpC
0.28	347	ABUW_RS05860	
	0.357669		AMP-binding protein
0.28	363	ABUW_RS18410	
	0.201745		peptidase M16
0.28	514	ABUW_RS08770	
	0.318465		sodium-dependent transporter
0.28	136	ABUW_RS00110	
	0.216509		BCCT family transporter
0.28	608	ABUW_RS05620	
	0.172827		MFS transporter
0.28	512	ABUW_RS06015	
	0.430132		hypothetical protein
0.29	075	ABUW_RS12630	
	0.555546		N-acetyltransferase
0.29	567	ABUW_RS12720	
	0.232183		hypothetical protein
0.29	357	ABUW_RS14190	
	0.126480		cell division protein FtsA
0.29	073	ABUW_RS00745	
	0.152799		YchF/TatD family DNA exonuclease
0.29	844	ABUW_RS10960	
	0.377122		YigZ family protein
0.29	338	ABUW_RS12815	
	0.296974		
0.29	663	sRNA27	
	0.158722		acyl-CoA desaturase
0.29	677	ABUW_RS18705	

	0.346779		hypothetical protein
0.29	496	ABUW_RS02590	
	0.236523		NIF3 1
0.29	276	ABUW_RS04930	
	0.526022		rhodanese-like domain-containing protein
0.29	298	ABUW_RS11745	
	0.177912		iron-sulfur cluster assembly protein IscA
0.29	897	ABUW_RS10715	
	0.256776		multidrug transporter MatE
0.29	291	ABUW_RS13110	
	0.169603		thioredoxin-disulfide reductase
0.29	898	ABUW_RS14820	
	0.272849		putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase
0.29	66	ABUW_RS10765	
	0.207545		hypothetical protein
0.29	676	ABUW_RS17765	
	0.422184		DUF4882 domain-containing protein
0.30	631	ABUW_RS09985	
	0.167123		Fe-S cluster assembly scaffold IscU
0.30	517	ABUW_RS10710	
	0.406174		DNA cytosine methyltransferase
0.30	386	ABUW_RS00425	
	0.104958		isocitrate lyase
0.30	276	ABUW_RS14030	
	0.372306		triacylglycerol lipase
0.30	52	ABUW_RS01595	
	0.568448		hypothetical protein
0.30	232	ABUW_RS02675	
	0.192098		peroxiredoxin
0.30	836	ABUW_RS04950	
	0.278597		
0.30	34	sRNA15	
	0.451857		DUF4902 domain-containing protein
0.30	33	ABUW_RS18380	
	0.246757		GntR family transcriptional regulator
0.31	573	ABUW_RS15195	
	0.185940		protein FilD
0.31	044	ABUW_RS15740	
	0.178475		bifunctional ADP-dependent NAD(P)H-hydrate dehydratase/NAD(P)H-hydrate epimerase
0.31	616	ABUW_RS11210	
	0.142822		hypothetical protein
0.31	667	ABUW_RS07945	
	0.136461		phospholipase D family protein
0.31	174	ABUW_RS10015	
	0.104300		P-II family nitrogen regulator
0.31	133	ABUW_RS17800	
	0.339519		hypothetical protein
0.31	599	ABUW_RS01790	
	0.287151		branched-chain amino acid transport system II carrier protein
0.32	277	ABUW_RS08655	
	0.244571		LysE family translocator
0.32	545	ABUW_RS15295	
	0.484893		ABC transporter permease
0.32	586	ABUW_RS07665	
	0.161438		FKBP-type peptidyl-prolyl cis-trans isomerase
0.32	562	ABUW_RS18665	
	0.291477		DUF421 domain-containing protein
0.32	924	ABUW_RS08895	
	0.099551		conjugal transfer protein TraG N-terminal domain-containing protein
0.32	063	ABUW_RS19555	
	0.201753		alpha/beta fold hydrolase
0.32	962	ABUW_RS17450	
	0.163802		Lon protease
0.32	435	ABUW_RS13920	
	0.304417		ethanolamine ammonia-lyase subunit EutC
0.32	846	ABUW_RS07895	
	0.185967		hypothetical protein
0.32	413	ABUW_RS02915	
	0.479259		GNAT family N-acetyltransferase
0.32	624	ABUW_RS09550	

	0.167681		hypothetical protein
0.32	359	ABUW_RS07000	
	0.675564		siderophore-interacting protein
0.32	677	ABUW_RS05710	
	0.150792		aldo/keto reductase
0.32	84	ABUW_RS01075	
	0.269529		RnfABCDGE type electron transport complex subunit B
0.32	272	ABUW_RS13945	
	0.137046		OsmC family peroxiredoxin
0.32	988	ABUW_RS11160	
	0.149737		DUF1173 domain-containing protein
0.33	627	ABUW_RS19045	
	0.588403		hypothetical protein
0.33	397	ABUW_RS19225	
	0.147092		[protein-Pil] uridylyltransferase
0.33	688	ABUW_RS11435	
	0.273146		DedA family protein
0.33	489	ABUW_RS18295	
	0.552662		
0.33	273	sRNA54	
	0.285015		paraquat-inducible protein A
0.33	541	ABUW_RS07315	
	0.163746		DUF4105 domain-containing protein
0.33	902	ABUW_RS16635	
	0.244215		
0.33	48	sRNA17	
	0.138081		helix-turn-helix domain-containing protein
0.33	476	ABUW_RS06185	
	0.106207		dioxygenase
0.33	405	ABUW_RS13930	
	0.084258		MBL fold metallo-hydrolase
0.33	285	ABUW_RS04515	
	0.175817		ATP-dependent Clp protease adapter ClpS
0.33	168	ABUW_RS08820	
	0.341220		hypothetical protein
0.33	03	ABUW_RS06180	
	0.129902		type 1 fimbrial protein
0.33	739	ABUW_RS09980	
	0.198521		TIGR01244 family phosphatase
0.34	494	ABUW_RS10310	
	0.171511		PLP-dependent aminotransferase family protein
0.34	022	ABUW_RS11635	
	0.188018		30S ribosomal protein S15
0.34	743	ABUW_RS17120	
	0.691326		hypothetical protein
0.34	255	ABUW_RS20485	
	0.155519		Fe-S biogenesis protein NfuA
0.34	533	ABUW_RS14165	
	0.073059		acetolactate synthase small subunit
0.34	388	ABUW_RS16305	
	0.173620		LysR family transcriptional regulator
0.34	546	ABUW_RS12670	
	0.114917		multifunctional CCA addition/repair protein
0.34	55	ABUW_RS05955	
	0.154843		NADH:flavin oxidoreductase/NADH oxidase
0.34	215	ABUW_RS03260	
	0.060106		OmpA family protein
0.34	858	ABUW_RS13250	
	0.163486		TonB-dependent receptor
0.34	062	ABUW_RS02950	
	0.068086		phosphoenolpyruvate carboxylase
0.34	636	ABUW_RS00155	
	0.181964		hypothetical protein
0.34	781	ABUW_RS02650	
	0.095441		ParA family protein
0.35	55	ABUW_RS18310	
	0.323953		1-aminocyclopropane-1-carboxylate deaminase/D-cysteine desulfhydrase
0.35	28	ABUW_RS15315	
	0.086158		hypothetical protein
0.35	789	ABUW_RS09995	

	0.125925		UDP-glucose 4-epimerase GalE
0.35	105	ABUW_RS18575	
	0.194989		tRNA glutamyl-Q(34) synthetase GluQRS
0.35	544	ABUW_RS17665	
	0.100854		LPS export ABC transporter periplasmic protein LptC
0.35	935	ABUW_RS12845	
	0.142822		DUF262 domain-containing protein
0.35	667	ABUW_RS01785	
	0.078554		DNA polymerase III subunit gamma/tau
0.35	787	ABUW_RS08185	
	0.532789		hypothetical protein
0.35	139	ABUW_RS19740	
	0.143971		aspartate 1-decarboxylase
0.35	977	ABUW_RS15050	
	0.156620		hypothetical protein
0.35	78	ABUW_RS09635	
	0.187731		zinc-binding alcohol dehydrogenase family protein
0.35	212	ABUW_RS16740	
	0.199442		nitronate monooxygenase
0.35	587	ABUW_RS12040	
	0.074245		acetyl-CoA C-acetyltransferase
0.35	722	ABUW_RS08155	
	0.225608		DNA helicase Rep
0.36	863	ABUW_RS14770	
	0.048169		molecular chaperone DnaK
0.36	967	ABUW_RS18890	
	0.408792		hypothetical protein
0.36	951	ABUW_RS11615	
	0.085981		hypothetical protein
0.36	903	ABUW_RS01460	
	0.279131		LuxR family transcriptional regulator
0.36	8	ABUW_RS18375	
	0.142822		Dyp-type peroxidase
0.36	667	ABUW_RS18230	
	0.138272		hypothetical protein
0.36	534	ABUW_RS05910	
	0.089699		tryptophan synthase subunit beta
0.36	476	ABUW_RS10390	
	0.397661		SDR family oxidoreductase
0.36	515	ABUW_RS13440	
	0.105155		PepSY domain-containing protein
0.36	888	ABUW_RS10595	
	0.260230		metal-dependent hydrolase
0.36	688	ABUW_RS01475	
	0.103078		DnaA regulatory inactivator Hda
0.37	961	ABUW_RS04820	
	0.053502		RNA polymerase sigma factor RpoD
0.37	518	ABUW_RS04230	
	0.085006		dCTP deaminase
0.37	591	ABUW_RS15255	
	0.072597		hypothetical protein
0.37	54	ABUW_RS04960	
	0.138081		PQQ-dependent sugar dehydrogenase
0.37	476	ABUW_RS00270	
	0.072836		hypothetical protein
0.37	018	ABUW_RS19995	
	0.397432		DUF1295 domain-containing protein
0.37	079	ABUW_RS07380	
	0.084886		threonine ammonia-lyase
0.37	65	ABUW_RS03475	
	0.050556		acetyl-CoA carboxylase carboxyltransferase subunit beta
0.37	853	ABUW_RS03065	
	0.105155		(p)ppGpp synthetase
0.37	888	ABUW_RS03770	
	0.253647		aldehyde dehydrogenase family protein
0.37	342	ABUW_RS05630	
	0.232549		hypothetical protein
0.37	71	ABUW_RS05125	
	0.291869		inovirus Gp2 family protein
0.37	205	ABUW_RS16215	

	0.102877		ferredoxin reductase
0.37	29	ABUW_RS18710	
	0.297739		tartrate dehydrogenase
0.37	302	ABUW_RS14935	
	0.059048		UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)
0.37	745	ABUW_RS05210	
	0.125925		FMN-binding glutamate synthase family protein
0.37	105	ABUW_RS08230	
	0.094928		tryptophan--tRNA ligase
0.37	344	ABUW_RS04315	
	0.191181		aromatic ring-hydroxylating dioxygenase subunit alpha
0.37	995	ABUW_RS13465	
	0.122490		DUF4760 domain-containing protein
0.37	92	ABUW_RS06475	
	0.363304		hypothetical protein
0.37	607	ABUW_RS07020	
	0.210520		protein-tyrosine-phosphatase
0.38	25	ABUW_RS03080	
	0.109004		rubredoxin
0.38	863	ABUW_RS14090	
	0.090923		NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
0.38	441	ABUW_RS06740	
	0.157959		phosphoethanolamine--lipid A transferase
0.38	074	ABUW_RS04050	
	0.035260		hypothetical protein
0.38	692	ABUW_RS14870	
	0.070219		DJ-1/PfpI family protein
0.38	026	ABUW_RS03500	
	0.108893		hypothetical protein
0.38	062	ABUW_RS18745	
	0.081531		NADPH:quinone oxidoreductase
0.38	848	ABUW_RS00945	
	0.130333		TonB-dependent siderophore receptor
0.38	356	ABUW_RS08765	
	0.258144		PepSY domain-containing protein
0.39	643	ABUW_RS08235	
	0.074245		FHA domain-containing protein
0.39	722	ABUW_RS17550	
	0.109453		2-C-methyl-D-erythritol 2%2C4-cyclodiphosphate synthase
0.39	904	ABUW_RS08415	
	0.054055		hydrolase
0.39	828	ABUW_RS06685	
	0.036373		single-stranded DNA-binding protein
0.39	864	ABUW_RS00975	
	0.047245		transketolase
0.39	573	ABUW_RS11165	
	0.063423		rRNA maturation RNase YbeY
0.39	974	ABUW_RS02270	
	0.086817		iron-containing alcohol dehydrogenase
0.39	022	ABUW_RS08200	
	0.084828		type I glutamate--ammonia ligase
0.39	411	ABUW_RS05895	
	0.084907		monofunctional biosynthetic peptidoglycan transglycosylase
0.39	861	ABUW_RS14120	
	0.037200		quinoprotein glucose dehydrogenase
0.39	204	ABUW_RS09285	
	0.083051		polyphosphate kinase 1
0.39	568	ABUW_RS14115	
	0.036896		ribonuclease R
0.39	116	ABUW_RS02180	
	0.147311		hypothetical protein
0.39	169	ABUW_RS01695	
	0.427949		hypothetical protein
0.39	778	ABUW_RS16205	
	0.179264		high frequency lysogenization protein HflD
0.39	951	ABUW_RS05495	
	0.102877		SDR family NAD(P)-dependent oxidoreductase
0.39	29	ABUW_RS00535	
	0.115936		DNA-binding response regulator PmrA
0.40	367	ABUW_RS04055	

	0.152046		3'-5' exonuclease
0.40	62	ABUW_RS02660	
	0.085652		hypothetical protein
0.40	989	ABUW_RS11870	
	0.062597		quinoprotein glucose dehydrogenase
0.40	394	ABUW_RS08585	
	0.115252		hypothetical protein
0.40	214493	ABUW_RS10475	
	0.214493		magnesium transporter
0.40	359	ABUW_RS01905	
	0.062597		DUF1315 family protein
0.40	394	ABUW_RS06635	
	0.281335		MotA/TolQ/ExbB proton channel family protein
0.40	51	ABUW_RS10840	
	0.152550		ABC transporter substrate-binding protein
0.40	71	ABUW_RS13800	
	0.036931		D-alanyl-D-alanine endopeptidase PBP7/8
0.40	203	ABUW_RS17715	
	0.543235		hypothetical protein
0.40	387	ABUW_RS19895	
	0.182634		nickel resistance MFS transporter NreB
0.41	632	ABUW_RS15960	
	0.052441		cell division protein FtsB
0.41	574	ABUW_RS08900	
	0.154937		aminodeoxychorismate lyase
0.41	383	ABUW_RS05015	
	0.024693		cysteine synthase A
0.41	029	ABUW_RS18050	
	0.129902		alanine racemase
0.41	739	ABUW_RS07535	
	0.047335		acyl carrier protein
0.42	849	ABUW_RS15085	
	0.320244		hypothetical protein
0.42	61	ABUW_RS00285	
	0.084907		IMP dehydrogenase
0.42	861	ABUW_RS00805	
	0.030950		HAD family hydrolase
0.42	643	ABUW_RS15070	
	0.106726		large conductance mechanosensitive channel protein MscL
0.42	041	ABUW_RS03230	
	0.047049		hypothetical protein
0.42	205	ABUW_RS00195	
	0.079722		response regulator transcription factor
0.42	171	ABUW_RS06600	
	0.123402		hypothetical protein
0.42	327	ABUW_RS13040	
	0.050428		cell division protein ZapA
0.42	735	ABUW_RS13900	
	0.048082		polyprenyl synthetase family protein
0.42	975	ABUW_RS04010	
	0.116056		type B 50S ribosomal protein L31
0.42	138	ABUW_RS16975	
	0.046121		AraC family transcriptional regulator
0.42	691	ABUW_RS09235	
	0.037425		recombinase family protein
0.42	906	ABUW_RS19440	
	0.037584		phosphate ABC transporter ATP-binding protein
0.42	5	ABUW_RS05470	
	0.048169		IcIR family transcriptional regulator
0.42	967	ABUW_RS12030	
	0.128655		glycerophosphodiester phosphodiesterase
0.42	13	ABUW_RS03015	
	0.313886		DUF3380 domain-containing protein
0.43	144	ABUW_RS02825	
	0.052284		bifunctional (p)ppGpp synthetase/guanosine-3'-bis(diphosphate) 3'-pyrophosphohydrolase
0.43	705	ABUW_RS01520	
	0.046820		DUF853 domain-containing protein
0.43	193	ABUW_RS01975	
	0.060975		accessory factor UbiK family protein
0.43	362	ABUW_RS17805	

	0.179871		polyketide cyclase
0.43	106	ABUW_RS13615	
	0.074554		TetR/AcrR family transcriptional regulator
0.43	535	ABUW_RS09410	
	0.087379		hypothetical protein
0.43	494	ABUW_RS19090	
	0.041339		glucose-6-phosphate isomerase
0.43	579	ABUW_RS18580	
	0.129590		hypothetical protein
0.43	992	ABUW_RS13105	
	0.257262		phage portal protein
0.43	466	ABUW_RS02870	
	0.046518		M61 family metalloproteinase
0.43	358	ABUW_RS05260	
	0.024488		DUF3336 domain-containing protein
0.43	331	ABUW_RS07095	
	0.073615		thiamine phosphate synthase
0.43	588	ABUW_RS05365	
	0.034813		DNA gyrase inhibitor YacG
0.43	413	ABUW_RS17005	
	0.098089		hypothetical protein
0.43	213	ABUW_RS20490	
	0.046135		exonuclease V subunit beta
0.43	728	ABUW_RS17135	
	0.144786		type 1 glutamine amidotransferase domain-containing protein
0.43	828	ABUW_RS07650	
	0.314266		nitroreductase family protein
0.44	527	ABUW_RS02215	
	0.056074		hypothetical protein
0.44	693	ABUW_RS15250	
	0.026057		UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase
0.44	999	ABUW_RS08490	
	0.094144		shikimate dehydrogenase
0.44	212	ABUW_RS01845	
	0.371563		helix-turn-helix transcriptional regulator
0.44	243	ABUW_RS01095	
	0.102877		transglycosylase SLT domain-containing protein
0.44	29	ABUW_RS19560	
	0.023476		conjugative relaxase
0.44	718	ABUW_RS19380	
	0.167117		type 1 glutamine amidotransferase domain-containing protein
0.44	62	ABUW_RS09200	
	0.037211		acyl-CoA desaturase
0.44	858	ABUW_RS03005	
	0.033453		LysE family translocator
0.44	371	ABUW_RS04690	
	0.270035		hypothetical protein
0.44	477	ABUW_RS09490	
	0.075557		DUF934 domain-containing protein
0.44	627	ABUW_RS03170	
	0.044390		pyruvate dehydrogenase (acetyl-transferring)%2C homodimeric type
0.45	943	ABUW_RS00770	
	0.037302		DUF3298 domain-containing protein
0.45	488	ABUW_RS04175	
	0.131440		hypothetical protein
0.45	775	ABUW_RS19120	
	0.231636		starvation protein A
0.45	429	ABUW_RS02415	
	0.111264		CoA transferase
0.45	864	ABUW_RS12200	
	0.030591		DsbA family oxidoreductase
0.45	401	ABUW_RS17415	
	0.019342		TetR/AcrR family transcriptional regulator
0.45	945	ABUW_RS10955	
	0.039888		ribose-5-phosphate isomerase RpiA
0.45	348	ABUW_RS08795	
	0.099928		hypothetical protein
0.45	343	ABUW_RS02935	
	0.527276		hypothetical protein
0.45	167	ABUW_RS07085	

	0.090963		phage tail tape measure protein
0.45	118	ABUW_RS06420	
	0.064652		hypothetical protein
0.46	785	ABUW_RS07775	
	0.339972		hypothetical protein
0.46	325	ABUW_RS19180	
	0.075300		GNAT family N-acetyltransferase
0.46	827	ABUW_RS12425	
	0.053253		SDR family oxidoreductase
0.46	179	ABUW_RS16035	
	0.035420		diacylglycerol kinase
0.46	004	ABUW_RS04485	
	0.064368		DUF1737 domain-containing protein
0.46	581	ABUW_RS00715	
	0.018432		hypothetical protein
0.46	585	ABUW_RS15675	
	0.130492		Y-family DNA polymerase
0.46	908	ABUW_RS08275	
	0.017347		hypothetical protein
0.46	774	ABUW_RS01325	
	0.386711		hypothetical protein
0.46	255	ABUW_RS13050	
	0.062597		LysR family transcriptional regulator
0.46	394	ABUW_RS11770	
	0.015062		OmpA family protein
0.46	143	ABUW_RS03195	
	0.208917		DUF1624 domain-containing protein
0.46	967	ABUW_RS18460	
	0.045780		helix-turn-helix domain-containing protein
0.46	694	ABUW_RS03680	
	0.361972		
0.46	908	sRNA24	
	0.022791		M48 family peptidase
0.46	506	ABUW_RS13315	
	0.179871		DUF159 family protein
0.46	106	ABUW_RS08580	
	0.084574		DUF1328 domain-containing protein
0.46	431	ABUW_RS00260	
	0.011417		Vi polysaccharide biosynthesis UDP-N-acetylglucosamine C-6 dehydrogenase TviB
0.46	075	ABUW_RS18645	
	0.189037		biopolymer transporter ExbD
0.46	888	ABUW_RS10850	
	0.043964		CoA transferase
0.47	716	ABUW_RS03150	
	0.097874		RnfH family protein
0.47	248	ABUW_RS14730	
	0.035907		hypothetical protein
0.47	351	ABUW_RS16220	
	0.305298		winged helix-turn-helix transcriptional regulator
0.47	112	ABUW_RS18455	
	0.058270		NAD(P)-dependent oxidoreductase
0.47	103	ABUW_RS09445	
	0.029616		GFA family protein
0.47	197	ABUW_RS13125	
	0.012204		multidrug efflux RND transporter outer membrane channel subunit AdeK
0.47	21	ABUW_RS04125	
	0.088222		hypothetical protein
0.47	214	ABUW_RS08395	
	0.087534		DUF1176 domain-containing protein
0.47	435	ABUW_RS03490	
	0.130119		type VI secretion system baseplate subunit TssF
0.47	642	ABUW_RS12515	
	0.028225		hypothetical protein
0.47	284	ABUW_RS04215	
	0.124043		hypothetical protein
0.47	934	ABUW_RS01155	
	0.036896		cell division protein ZipA
0.47	116	ABUW_RS15185	
	0.010510		DNA topoisomerase IV subunit A
0.47	022	ABUW_RS17965	

	0.050001		TonB-dependent receptor
0.47	932	ABUW_RS08035	
	0.204977		ATP-binding cassette domain-containing protein
0.47	197	ABUW_RS10085	
	0.061044		nitroreductase family protein
0.47	63	ABUW_RS08715	
	0.039719		hypothetical protein
0.47	001	ABUW_RS02720	
	0.068012		sorbose dehydrogenase family protein
0.48	752	ABUW_RS09260	
	0.012877		chaperonin GroEL
0.48	008	ABUW_RS04505	
	0.279672		TetR/AcrR family transcriptional regulator
0.48	176	ABUW_RS18085	
	0.242188		YaeQ family protein
0.48	347	ABUW_RS14380	
	0.113009		3-hydroxyisobutyrate dehydrogenase
0.48	961	ABUW_RS18415	
	0.036644		hypothetical protein
0.48	395	ABUW_RS00135	
	0.089383		amidohydrolase
0.48	287	ABUW_RS04895	
	0.050076		Y-family DNA polymerase
0.48	91	ABUW_RS19570	
	0.018651		type I methionyl aminopeptidase
0.48	34	ABUW_RS08660	
	0.220153		energy transducer TonB
0.49	369	ABUW_RS10465	
	0.175839		type I-F CRISPR-associated endonuclease Cas1
0.49	356	ABUW_RS05335	
	0.078172		OmpA family protein
0.49	514	ABUW_RS12490	
	0.083447		hypothetical protein
0.49	198	ABUW_RS08645	
	0.023445		type I-F CRISPR-associated helicase Cas3
0.49	798	ABUW_RS05340	
	0.041946		aminoacyl-tRNA hydrolase
0.49	649	ABUW_RS15045	
	0.059281		hypothetical protein
0.49	804	ABUW_RS06085	
	0.021526		glycine cleavage system protein GcvH
0.49	324	ABUW_RS11105	
	0.021506		response regulator
0.49	516	ABUW_RS03340	
	0.013133		UPF0149 family protein
0.49	656	ABUW_RS13890	
	0.142590		type-F conjugative transfer system pilin assembly protein TrbC
0.49	432	ABUW_RS19530	
	0.027769		aminodeoxychorismate/anthranilate synthase component II
0.49	974	ABUW_RS05880	
	0.033605		ATPase AAA
0.49	071	ABUW_RS13650	
	0.030707		DUF4258 domain-containing protein
0.49	022	ABUW_RS03890	
	0.044631		hypothetical protein
0.50	376	ABUW_RS01765	
	0.025926		Fic family protein
0.50	54	ABUW_RS14585	
	0.061911		quinone-dependent dihydroorotate dehydrogenase
0.50	776	ABUW_RS07035	
	0.028508		glycosyltransferase family 2 protein
0.50	165	ABUW_RS02905	
	0.111726		indoleacetamide hydrolase
0.50	419	ABUW_RS09475	
	0.053237		response regulator
0.50	791	ABUW_RS07345	
	0.126859		hypothetical protein
0.50	492	ABUW_RS04015	
	0.099912		rhombosortase
0.50	94	ABUW_RS02155	

	0.019949		hypothetical protein
0.50	756	ABUW_RS12725	
	0.059336		LysR family transcriptional regulator
0.50	36	ABUW_RS11285	
	0.028939		cell division protein
0.50	477	ABUW_RS18245	
	0.150544		HEAT repeat domain-containing protein
0.50	54	ABUW_RS10240	
	0.020028		hypothetical protein
0.50	06	ABUW_RS02325	
	0.043357		L%2CD-transpeptidase
0.51	616	ABUW_RS03395	
	0.105155		biopolymer transporter ExbD
0.51	888	ABUW_RS16645	
	0.132972		hypothetical protein
0.51	359	ABUW_RS06825	
	0.014024		ATP-dependent RNA helicase RhlB
0.51	779	ABUW_RS06725	
	0.023354		LysR family transcriptional regulator
0.51	212	ABUW_RS15485	
	0.053647		AI-2E family transporter
0.52	25	ABUW_RS05390	
	0.013012		3-deoxy-7-phosphoheptulonate synthase
0.52	193	ABUW_RS08835	
	0.013206		AraC family transcriptional regulator
0.52	322	ABUW_RS03145	
	0.008795		LysR family transcriptional regulator
0.52	181	ABUW_RS09145	
	0.008178		thiol:disulfide interchange protein DsbA/DsbL
0.52	114	ABUW_RS18725	
	0.387648		hypothetical protein
0.52	909	ABUW_RS19340	
	0.021397		type VI secretion system ATPase TssH
0.52	149	ABUW_RS12480	
	0.022240		DUF2239 family protein
0.52	946	ABUW_RS14055	
	0.035168		GGDEF domain-containing protein
0.52	166	ABUW_RS00680	
	0.023724		arginine--tRNA ligase
0.52	591	ABUW_RS18240	
	0.014610		methylated-DNA--[protein]-cysteine S-methyltransferase
0.52	489	ABUW_RS15650	
	0.066847		Fe-S cluster assembly protein IscX
0.52	938	ABUW_RS16435	
	0.051132		LemA family protein
0.52	059	ABUW_RS02625	
	0.204903		pseudouridylate synthase
0.52	155	ABUW_RS07840	
	0.015520		acyl-CoA thioesterase
0.52	142	ABUW_RS14400	
	0.152799		hypothetical protein
0.52	844	ABUW_RS13015	
	0.026531		hypothetical protein
0.52	552	ABUW_RS15055	
	0.155467		hypothetical protein
0.52	705	ABUW_RS16820	
	0.006207		1-(5-phosphoribosyl)-5-((5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase
0.53	677	ABUW_RS01205	
	0.033808		GGDEF domain-containing protein
0.53	328	ABUW_RS13725	
	0.008823		MFS transporter
0.53	07	ABUW_RS04465	
	0.004433		tryptophan synthase subunit alpha
0.53	734	ABUW_RS03060	
	0.278597		RND transporter
0.53	34	ABUW_RS00040	
	0.173791		hypothetical protein
0.53	09	ABUW_RS14270	
	0.024594		heme-binding protein
0.53	088	ABUW_RS10825	

	0.031715		LysR family transcriptional regulator
0.53	509	ABUW_RS11640	
	0.036362		hypothetical protein
0.53	137	ABUW_RS09585	
	0.041834		DUF454 domain-containing protein
0.53	23	ABUW_RS03390	
	0.012491		DNA primase
0.53	695	ABUW_RS14990	
	0.064989		hypothetical protein
0.53	739	ABUW_RS01330	
	0.006441		3-hydroxyacyl-ACP dehydratase FabZ
0.53	956	ABUW_RS08495	
	0.012582		capsule assembly Wzi family protein
0.54	83	ABUW_RS14070	
	0.062044		glycosyltransferase family 1 protein
0.54	138	ABUW_RS16445	
	0.063308		siderophore biosynthesis protein
0.54	141	ABUW_RS10640	
	0.234295		hypothetical protein
0.54	894	ABUW_RS19155	
	0.330732		damage-inducible protein CinA
0.54	434	ABUW_RS11865	
	0.023593		serine hydrolase family protein
0.54	757	ABUW_RS17400	
	0.012322		peptidase M48
0.54	51	ABUW_RS07050	
	0.011998		aminopeptidase N
0.54	622	ABUW_RS07955	
	0.007343		multidrug efflux SMR transporter
0.54	928	ABUW_RS15655	
	0.047249		type II secretion system protein E
0.54	012	ABUW_RS06590	
	0.022927		hypothetical protein
0.54	129	ABUW_RS01760	
	0.027893		phosphatidylglycerophosphatase A
0.54	137	ABUW_RS00450	
	0.160809		flavodoxin family protein
0.54	655	ABUW_RS01115	
	0.027495		peptidyl-prolyl cis-trans isomerase
0.54	153	ABUW_RS18855	
	0.006503		enol-CoA hydratase
0.55	852	ABUW_RS04935	
	0.007210		beta-ketoacyl-ACP synthase II
0.55	723	ABUW_RS14875	
	0.032476		NAD-dependent deacylase
0.55	711	ABUW_RS11110	
	0.056471		sel1 repeat family protein
0.55	476	ABUW_RS12635	
	0.029525		diphthine--ammonia ligase
0.55	336	ABUW_RS04955	
	0.010939		N-acetyltransferase
0.55	968	ABUW_RS11800	
	0.080346		acyl-CoA dehydrogenase
0.55	027	ABUW_RS11970	
	0.020523		hypothetical protein
0.55	761	ABUW_RS14545	
	0.004795		23S rRNA (uridine(2552)-2'-O)-methyltransferase RlmE
0.55	567	ABUW_RS04405	
	0.036731		hypothetical protein
0.55	404	ABUW_RS06435	
	0.039872		AraC family transcriptional regulator
0.56	423	ABUW_RS13430	
	0.054918		conjugal transfer protein TraB
0.56	377	ABUW_RS19485	
	0.005486		polysaccharide deacetylase family protein
0.56	161	ABUW_RS02900	
	0.050556		hypothetical protein
0.56	853	ABUW_RS01170	
	0.049701		1%2C6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD
0.56	209	ABUW_RS18680	

	0.169599		hypothetical protein
0.56	258	ABUW_RS19200	
	0.005499		helix-turn-helix domain-containing protein
0.56	937	ABUW_RS03895	
	0.007850		TIGR01244 family phosphatase
0.56	673	ABUW_RS02530	
	0.004550		transposase
0.56	738	ABUW_RS17905	
	0.026609		hypothetical protein
0.56	288	ABUW_RS04235	
	0.064527		OXA-51 family carbapenem-hydrolyzing class D beta-lactamase OXA-69
0.56	749	ABUW_RS11190	
	0.067912		acyltransferase
0.56	319	ABUW_RS00365	
	0.013802		TetR/AcrR family transcriptional regulator
0.56	074	ABUW_RS00940	
	0.028837		DUF2247 family protein
0.57	799	ABUW_RS09330	
	0.023511		YciK family oxidoreductase
0.57	136	ABUW_RS18740	
	0.459682		hypothetical protein
0.57	818	ABUW_RS03780	
	0.011297		cytochrome c assembly protein
0.57	238	ABUW_RS15220	
	0.003594		tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA
0.57	76	ABUW_RS07855	
	0.054695		hypothetical protein
0.57	415	ABUW_RS00780	
	0.149716		transporter substrate-binding domain-containing protein
0.57	638	ABUW_RS04555	
	0.035409		LysR family transcriptional regulator
0.57	201	ABUW_RS09000	
	0.009751		SGNH/GDSL hydrolase family protein
0.57	18	ABUW_RS08860	
	0.003880		OsmC family peroxiredoxin
0.57	619	ABUW_RS18255	
	0.053171		D-tyrosyl-tRNA(Tyr) deacylase
0.58	255	ABUW_RS00495	
	0.013348		TonB-dependent siderophore receptor
0.58	269	ABUW_RS10225	
	0.133814		hypothetical protein
0.58	582	ABUW_RS16140	
	0.015345		BrnA antitoxin family protein
0.58	961	ABUW_RS19610	
	0.021435		FAD-binding oxidoreductase
0.58	997	ABUW_RS09630	
	0.017816		organic hydroperoxide resistance protein
0.58	543	ABUW_RS15855	
	0.027585		CDF family Co(II)/Ni(II) efflux transporter DmeF
0.58	409	ABUW_RS18990	
	0.071354		hypothetical protein
0.58	632	ABUW_RS16225	
	0.006618		hypothetical protein
0.58	46	ABUW_RS14155	
	0.029009		replicative DNA helicase
0.59	839	ABUW_RS07540	
	0.156059		nuclease
0.59	22	ABUW_RS06145	
	0.004933		peptidyl-prolyl cis-trans isomerase
0.59	729	ABUW_RS07880	
	0.027283		alpha/beta fold hydrolase
0.59	513	ABUW_RS15155	
	0.063543		DUF4442 domain-containing protein
0.59	369	ABUW_RS02550	
	0.011992		APC family permease
0.59	733	ABUW_RS04205	
	0.007261		universal stress protein
0.59	917	ABUW_RS12805	
	0.011167		metal/formaldehyde-sensitive transcriptional repressor
0.59	994	ABUW_RS18995	

	0.048169		peptidase C39
0.59	967	ABUW_RS05985	
	0.006555		Do family serine endopeptidase
0.59	141	ABUW_RS05040	
	0.010675		TetR family transcriptional regulator
0.59	676	ABUW_RS08175	
	0.008187		hypothetical protein
0.59	724	ABUW_RS10370	
	0.006976		polyketide cyclase
0.59	727	ABUW_RS04110	
	0.021186		LysR family transcriptional regulator
0.59	235	ABUW_RS09560	
	0.041094		protein kinase
0.59	083	ABUW_RS07100	
	0.012256		transcriptional regulator
0.59	898	ABUW_RS07915	
	0.007411		type II secretion system protein GspE
0.60	194	ABUW_RS15860	
	0.009951		hypothetical protein
0.60	113	ABUW_RS19625	
	0.059217		YbjQ family protein
0.60	851	ABUW_RS04115	
	0.051042		molecular chaperone
0.60	347	ABUW_RS09970	
	0.055055		prepilin-type N-terminal cleavage/methylation domain-containing protein
0.60	723	ABUW_RS01570	
	0.006441		acetate kinase
0.60	956	ABUW_RS16500	
	0.155626		hypothetical protein
0.60	299	ABUW_RS11040	
	0.001781		PhoH family protein
0.60	558	ABUW_RS02275	
	0.010568		hypothetical protein
0.60	22	ABUW_RS11405	
	0.031958		NAD(P)/FAD-dependent oxidoreductase
0.60	216	ABUW_RS13435	
	0.001092		transposase
0.60	173	ABUW_RS17900	
	0.032497		hypothetical protein
0.60	833	ABUW_RS13870	
	0.009162		hypothetical protein
0.60	918	ABUW_RS17420	
	0.003299		lipoyl synthase
0.60	088	ABUW_RS06000	
	0.026609		UTRA domain-containing protein
0.60	288	ABUW_RS12100	
	0.011959		16S rRNA (uracil(1498)-N(3))-methyltransferase
0.60	757	ABUW_RS05970	
	0.001725		peptide-methionine (S)-S-oxide reductase MsrA
0.60	17	ABUW_RS16640	
	0.052241		DUF805 domain-containing protein
0.60	475	ABUW_RS00860	
	0.337350		hypothetical protein
0.60	43	ABUW_RS17065	
	0.002808		DEAD/DEAH box helicase
0.61	089	ABUW_RS09525	
	0.014971		TetR/AcrR family transcriptional regulator
0.61	942	ABUW_RS15300	
	0.033284		hypothetical protein
0.61	299	ABUW_RS07030	
	0.024339		uroporphyrinogen decarboxylase
0.61	104	ABUW_RS05810	
	0.020419		molecular chaperone
0.61	929	ABUW_RS07965	
	0.010206		FAD-binding protein
0.61	442	ABUW_RS01030	
	0.021416		crotonase/enoyl-CoA hydratase family protein
0.61	818	ABUW_RS14355	
	0.061649		hypothetical protein
0.61	543	ABUW_RS07520	

	0.483131		
0.61	267	sRNA74	
	0.003948		pyridoxamine 5'-phosphate oxidase
0.61	32	ABUW_RS00815	
	0.002128		hypothetical protein
0.61	888	ABUW_RS02405	
	0.053518		transcriptional regulator
0.61	17	ABUW_RS12580	
	0.008187		nucleoside-diphosphate sugar epimerase
0.61	724	ABUW_RS02890	
	0.002142		helix-turn-helix domain-containing protein
0.61	496	ABUW_RS10290	
	0.003407		TetR family transcriptional regulator
0.61	647	ABUW_RS18785	
	0.018631		DUF3800 domain-containing protein
0.61	436	ABUW_RS06395	
	0.113281		LysR family transcriptional regulator
0.62	048	ABUW_RS15530	
	0.013772		Rieske (2Fe-2S) protein
0.62	038	ABUW_RS08755	
	0.006872		mechanosensitive ion channel family protein
0.62	397	ABUW_RS00855	
	0.019332		hypothetical protein
0.62	963	ABUW_RS06255	
	0.001135		helix-turn-helix transcriptional regulator
0.62	012	ABUW_RS08345	
	0.002089		hypothetical protein
0.62	978	ABUW_RS03670	
	0.020372		NAD-dependent malic enzyme
0.62	085	ABUW_RS18235	
	0.004933		helicase
0.62	729	ABUW_RS07930	
	0.002487		pantetheine-phosphate adenylyltransferase
0.62	986	ABUW_RS14960	
	0.204977		hypothetical protein
0.62	197	ABUW_RS04600	
	0.002495		hypothetical protein
0.62	565	ABUW_RS09680	
	0.010134		excinuclease ABC subunit UvrB
0.62	313	ABUW_RS05140	
	0.059341		SGNH/GDSL hydrolase family protein
0.63	944	ABUW_RS11905	
	0.067832		
0.63	933	sRNA72	
	0.008795		response regulator
0.63	181	ABUW_RS15450	
	0.001953		FadR family transcriptional regulator
0.63	408	ABUW_RS13530	
	0.002638		site-specific DNA-methyltransferase
0.63	656	ABUW_RS14555	
	0.002339		phosphoglucosamine mutase
0.63	586	ABUW_RS00810	
	0.073961		hypothetical protein
0.63	289	ABUW_RS02630	
	0.002098		long-chain fatty acid transporter
0.63	019	ABUW_RS03565	
	0.008030		MarR family transcriptional regulator
0.63	597	ABUW_RS15850	
	0.095016		DUF2726 domain-containing protein
0.63	197	ABUW_RS18015	
	0.130259		fimbrial protein
0.63	792	ABUW_RS11250	
	0.020792		multidrug efflux RND transporter outer membrane channel subunit AdeC
0.63	916	ABUW_RS09610	
	0.008424		hypothetical protein
0.63	515	ABUW_RS02525	
	0.018271		ATP-binding protein
0.63	308	ABUW_RS00430	
	0.002998		hypothetical protein
0.63	424	ABUW_RS01780	

	0.001446		D-glycerate dehydrogenase
0.63	032	ABUW_RS07060	
	0.001959		3-isopropylmalate dehydrogenase
0.63	597	ABUW_RS16825	
	0.011029		30S ribosomal protein S21
0.63	092	ABUW_RS07075	
	0.004726		GntR family transcriptional regulator
0.64	546	ABUW_RS12170	
	0.003422		metallophosphatase
0.64	873	ABUW_RS04350	
	0.004426		alkene reductase
0.64	634	ABUW_RS00840	
	0.161592		DUF4442 domain-containing protein
0.64	748	ABUW_RS05410	
	0.017013		YafY family transcriptional regulator
0.64	51	ABUW_RS16895	
	0.011312		TIGR01666 family membrane protein
0.64	892	ABUW_RS01665	
	0.007091		BCCT family transporter
0.64	204	ABUW_RS05615	
	0.014496		LysR family transcriptional regulator
0.64	319	ABUW_RS10100	
	0.004386		alpha/beta fold hydrolase
0.64	736	ABUW_RS08635	
	0.005154		FadR family transcriptional regulator
0.64	644	ABUW_RS09155	
	0.020779		hypothetical protein
0.65	765	ABUW_RS13005	
	0.003692		endonuclease III
0.65	323	ABUW_RS13950	
	0.006214		metalloprotease
0.65	044	ABUW_RS04355	
	0.047822		AraC family transcriptional regulator
0.65	824	ABUW_RS07190	
	0.018651		hypothetical protein
0.65	272	ABUW_RS05520	
	0.005853		dihydropteroate synthase
0.65	588	ABUW_RS04415	
	0.000241		2-isopropylmalate synthase
0.65	353	ABUW_RS16550	
	0.016874		AraC family transcriptional regulator
0.65	624	ABUW_RS03055	
	0.147475		hypothetical protein
0.65	844	ABUW_RS06360	
	0.002366		DsbC family protein
0.65	674	ABUW_RS18985	
	0.014649		histidine-type phosphatase
0.65	447	ABUW_RS10555	
	0.001295		AraC family transcriptional regulator
0.65	01	ABUW_RS16805	
	0.001705		GGDEF domain-containing protein
0.65	907	ABUW_RS00930	
	0.004463		alpha-ketoglutarate-dependent dioxygenase AlkB
0.66	913	ABUW_RS17345	
	0.013191		hypothetical protein
0.66	618	ABUW_RS12935	
	0.036731		Cys-tRNA(Pro) deacylase
0.66	404	ABUW_RS10645	
	0.004227		membrane protein
0.66	121	ABUW_RS03435	
	0.020478		hypothetical protein
0.66	599	ABUW_RS09180	
	0.004463		alpha/beta fold hydrolase
0.66	913	ABUW_RS14455	
	0.000894		MerR family transcriptional regulator
0.66	395	ABUW_RS17105	
	0.002118		carbapenem-hydrolyzing class D beta-lactamase OXA-23
0.66	42	ABUW_RS02765	
	0.060085		hypothetical protein
0.66	97	ABUW_RS01345	

	0.003940		type II asparaginase
0.66	101	ABUW_RS11475	
	0.006987		hypothetical protein
0.66	19	ABUW_RS05205	
	0.002884		oxygen-insensitive NAD(P)H nitroreductase
0.67	022	ABUW_RS07870	
	0.000774		ABC transporter
0.67	337	ABUW_RS16970	
	0.006706		hypothetical protein
0.67	456	ABUW_RS03495	
	0.000378		ribosome recycling factor
0.67	585	ABUW_RS08455	
	0.005499		GGDEF domain-containing protein
0.67	937	ABUW_RS08595	
	0.000304		RNA polymerase-binding protein DksA
0.67	439	ABUW_RS17660	
	0.006855		amino acid transporter
0.67	477	ABUW_RS13855	
	0.008899		efflux system DNA-binding response regulator AdeR
0.67	155	ABUW_RS09595	
	0.019989		hypothetical protein
0.67	074	ABUW_RS16785	
	0.038513		AraC family transcriptional regulator
0.67	924	ABUW_RS09580	
	0.025892		DUF4062 domain-containing protein
0.67	232	ABUW_RS17020	
	0.000697		acyl-CoA dehydrogenase
0.67	765	ABUW_RS02980	
	0.002471		GHKL domain-containing protein
0.67	432	ABUW_RS06605	
	0.007494		pyrimidine/purine nucleoside phosphorylase
0.67	0.014264		ATP-dependent DNA helicase RecG
0.67	461	ABUW_RS01925	
	0.004373		AraC family transcriptional regulator
0.67	286	ABUW_RS15545	
	0.000816		hypothetical protein
0.68	273	ABUW_RS07950	
	0.000532		cell division protein ZapE
0.68	359	ABUW_RS10865	
	0.002927		response regulator
0.68	321	ABUW_RS16060	
	0.005343		MBL fold metallo-hydrolase
0.68	253	ABUW_RS06680	
	0.162426		FMN-binding negative transcriptional regulator
0.68	054	ABUW_RS11700	
	0.018295		hypothetical protein
0.68	411	ABUW_RS06730	
	0.002489		formate-dependent phosphoribosylglycinamide formyltransferase
0.68	766	ABUW_RS11430	
	0.062597		site-specific integrase
0.68	394	ABUW_RS12875	
	0.006613		general secretion pathway protein GspK
0.68	66	ABUW_RS10935	
	0.000426		ankyrin repeat domain-containing protein
0.68	947	ABUW_RS00665	
	0.002425		hypothetical protein
0.68	94	ABUW_RS03905	
	0.002415		1-acyl-sn-glycerol-3-phosphate acyltransferase
0.69	605	ABUW_RS02465	
	0.193498		biopolymer transporter ExbD
0.69	497	ABUW_RS10845	
	0.020423		enoyl-CoA hydratase
0.69	673	ABUW_RS12045	
	0.019158		DUF1232 domain-containing protein
0.69	492	ABUW_RS04640	
	0.065037		hypothetical protein
0.69	47	ABUW_RS16240	
	0.010594		acyltransferase
0.69	513	ABUW_RS14780	

	0.013650		2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
0.69	915	ABUW_RS07715	
	0.003103		hypothetical protein
0.69	586	ABUW_RS19230	
	0.001711		LysR family transcriptional regulator
0.69	886	ABUW_RS14940	
	0.000931		type IV secretion system protein TraC
0.69	417	ABUW_RS19505	
	0.023229		DUF4102 domain-containing protein
0.69	814	ABUW_RS03990	
	0.024870		cysteine hydrolase
0.69	526	ABUW_RS00870	
	0.001229		TonB-dependent receptor
0.70	537	ABUW_RS13745	
	0.000520		glycosyl transferase
0.70	809	ABUW_RS02895	
	0.000199		hypothetical protein
0.70	402	ABUW_RS07055	
	0.000435		helix-turn-helix domain-containing protein
0.70	732	ABUW_RS19595	
	0.038552		DMT family transporter
0.70	094	ABUW_RS13560	
	0.098776		ComEA family DNA-binding protein
0.70	305	ABUW_RS16025	
	0.001405		thioesterase family protein
0.70	903	ABUW_RS11965	
	0.001124		polyketide cyclase
0.70	099	ABUW_RS18470	
	0.009162		dicarboxylate/amino acid:cation symporter
0.71	918	ABUW_RS06645	
	0.058270		M23 family metalloproteinase
0.71	103	ABUW_RS13290	
	0.001485		Grx4 family monothiol glutaredoxin
0.71	328	ABUW_RS08675	
	0.006135		Paal family thioesterase
0.71	936	ABUW_RS11975	
	0.043478		DUF2147 domain-containing protein
0.71	079	ABUW_RS12745	
	0.019785		DUF4198 domain-containing protein
0.71	1	ABUW_RS07805	
	0.000446		hypothetical protein
0.71	856	ABUW_RS09695	
	0.000626		hypothetical protein
0.71	142	ABUW_RS17145	
	0.031971		hypothetical protein
0.71	364	ABUW_RS06315	
	0.000873		hypothetical protein
0.71	353	ABUW_RS17395	
	0.000500		glutathione synthase
0.71	495	ABUW_RS00720	
	0.031129		hypothetical protein
0.71	091	ABUW_RS06970	
	0.066482		ankyrin repeat domain-containing protein
0.71	439	ABUW_RS12445	
	0.006344		adenosine deaminase
0.71	17	ABUW_RS15615	
	0.081172		hypothetical protein
0.72	597	ABUW_RS09320	
	0.000165		SDR family NAD(P)-dependent oxidoreductase
0.72	271	ABUW_RS08380	
	0.002114		bacterioferritin
0.72	131	ABUW_RS15175	
	0.209891		hypothetical protein
0.72	929	ABUW_RS06345	
	0.013012		type II secretion system protein Gspl
0.72	193	ABUW_RS10945	
	0.000347		lipoyl(octanoyl) transferase LipB
0.72	129	ABUW_RS04220	
	0.022173		AraC family transcriptional regulator
0.72	714	ABUW_RS10120	

	0.136736		alkylphosphonate utilization protein
0.72	806	ABUW_RS03295	
	0.075300		hypothetical protein
0.72	827	ABUW_RS04090	
	0.001539		TetR/AcrR family transcriptional regulator
0.72	112	ABUW_RS17635	
	0.001839		hydroxyacylglutathione hydrolase
0.72	277	ABUW_RS07455	
	0.002686		glycosyltransferase family 25 protein
0.72	385	ABUW_RS02920	
	0.067195		chorismate mutase
0.72	767	ABUW_RS07995	
	0.000341		DUF3298 domain-containing protein
0.72	074	ABUW_RS16265	
	0.009712		efflux RND transporter periplasmic adaptor subunit
0.72	815	ABUW_RS03325	
	0.001050		arylesterase
0.73	672	ABUW_RS14140	
	0.010820		tRNA-dihydrouridine synthase C
0.73	733	ABUW_RS15225	
	0.055197		transcriptional regulator FeaR
0.73	379	ABUW_RS09085	
	0.007847		hypothetical protein
0.73	959	ABUW_RS19100	
	0.000110		response regulator
0.73	874	ABUW_RS02995	
	0.005691		membrane protein
0.73	871	ABUW_RS18925	
	0.003057		glutathione peroxidase
0.74	837	ABUW_RS11455	
	0.000377		lipopolysaccharide transport periplasmic protein LptA
0.74	655	ABUW_RS12840	
	0.001934		helix-turn-helix transcriptional regulator
0.74	186	ABUW_RS02695	
	0.015166		LysR family transcriptional regulator
0.74	228	ABUW_RS08145	
	0.075238		hypothetical protein
0.74	968	ABUW_RS20000	
	0.000711		hypothetical protein
0.74	951	ABUW_RS07620	
	0.013650		DUF2236 domain-containing protein
0.74	915	ABUW_RS18090	
	0.187332		hypothetical protein
0.75	152	ABUW_RS06480	
	0.000176		SDR family oxidoreductase
0.75	784	ABUW_RS05095	
	0.007288		hypothetical protein
0.75	424	ABUW_RS12625	
	0.000840		winged helix-turn-helix transcriptional regulator
0.75	712	ABUW_RS00875	
	0.067561		type 1 glutamine amidotransferase
0.75	303	ABUW_RS01985	
	0.000119		thioredoxin
0.75	535	ABUW_RS15910	
	0.013573		hypothetical protein
0.75	621	ABUW_RS19205	
	0.000253		BON domain-containing protein
0.75	932	ABUW_RS13830	
	0.000206		thiaminase II
0.76	804	ABUW_RS00960	
	0.002645		glutamate racemase
0.76	122	ABUW_RS17025	
	0.048169		membrane protein
0.76	967	ABUW_RS07355	
	0.004197		DUF2057 domain-containing protein
0.76	729	ABUW_RS08720	
			TetR/AcrR family transcriptional regulator
0.76	3.18E-05	ABUW_RS09625	
	0.011420		hypothetical protein
0.77	521	ABUW_RS19065	

	0.000382		transcriptional regulator
0.77	524	ABUW_RS04195	
	0.018090		BLUF domain-containing protein
0.77	841	ABUW_RS07175	
	0.003948		LysR family transcriptional regulator
0.77	397	ABUW_RS07125	
	0.000553		NAD(P)/FAD-dependent oxidoreductase
0.77	049	ABUW_RS10875	
	0.062900		hypothetical protein
0.77	599	ABUW_RS00215	
	8.21E-05	ABUW_RS18875	MBL fold metallo-hydrolase
0.77	0.004311		GatB/YqeY domain-containing protein
0.77	682	ABUW_RS07070	
	0.003353		HTH-type transcriptional repressor FabR
0.77	975	ABUW_RS05395	
	0.004827		methionine/alanine import family NSS transporter small subunit
0.77	941	ABUW_RS00115	
	0.000253		LysR family transcriptional regulator
0.77	882	ABUW_RS10200	
	0.000142		META domain-containing protein
0.78	555	ABUW_RS03010	
	0.000144		hypothetical protein
0.78	674	ABUW_RS11500	
	0.085652		GNAT family N-acetyltransferase
0.78	989	ABUW_RS13295	
	0.008846		ABC transporter ATP-binding protein
0.78	972	ABUW_RS13785	
	8.72E-05	ABUW_RS07695	flavin reductase family protein
0.78	0.064527		type II secretion system protein GspJ
0.78	749	ABUW_RS10940	
	0.000471		aminoacyl-histidine dipeptidase
0.78	792	ABUW_RS06675	
	0.001044		alpha/beta hydrolase
0.78	477	ABUW_RS16465	
	0.034212		esterase
0.79	79	ABUW_RS14080	
	0.002247		DUF2058 domain-containing protein
0.79	419	ABUW_RS11085	
	0.046517		hydroxyisourate hydrolase
0.79	807	ABUW_RS07335	
	0.044188		DUF2238 domain-containing protein
0.79	399	ABUW_RS05485	
	4.33E-05	ABUW_RS16745	SlyX family protein
0.80	0.000516		alginate biosynthesis protein
0.80	848	ABUW_RS17605	
	0.001737		LexA family transcriptional regulator
0.80	048	ABUW_RS13080	
	0.024688		ATP-binding cassette domain-containing protein
0.80	607	ABUW_RS19750	
	0.101841		hypothetical protein
0.80	698	ABUW_RS06265	
	0.000130		hydroxymethylpyrimidine/phosphomethylpyrimidine kinase
0.80	369	ABUW_RS15075	
	8.85E-05	ABUW_RS14150	alpha/beta hydrolase
0.80	0.034680		dipeptidase
0.80	481	ABUW_RS10035	
	0.045036		transporter
0.80	215	ABUW_RS12770	
	0.002335		amino-acid N-acetyltransferase
0.80	983	ABUW_RS18755	
	0.009525		hypothetical protein
0.80	595	ABUW_RS00915	
	0.000957		DUF4391 domain-containing protein
0.80	114	ABUW_RS14560	
	0.115583		N-acetyltransferase
0.80	536	ABUW_RS01125	
	0.001602		LysE family translocator
0.81	309	ABUW_RS01150	

	0.012644		DsbC family protein
0.81	985	ABUW_RS19490	
	0.005744		HAD-IB family hydrolase
0.81	009	ABUW_RS05180	
	0.064070		hypothetical protein
0.81	711	ABUW_RS01295	
			feruloyl-CoA synthase
0.81	9.44E-05	ABUW_RS13500	
	0.004393		
0.81	258	sRNA111	
	0.000430		haloacid dehalogenase
0.81	25	ABUW_RS08525	
	0.000707		phosphomannomutase/phosphoglucosyltransferase
0.81	813	ABUW_RS18570	
	0.000810		DUF1285 domain-containing protein
0.81	32	ABUW_RS17030	
	0.001628		flavin reductase
0.82	064	ABUW_RS15515	
	0.000477		bifunctional diguanylate cyclase/phosphodiesterase
0.82	874	ABUW_RS16295	
	0.079686		type II toxin-antitoxin system Phd/YefM family antitoxin
0.82	567	ABUW_RS05670	
	0.003057		type II toxin-antitoxin system RelE/ParE family toxin
0.82	837	ABUW_RS19215	
	0.000145		hypothetical protein
0.82	399	ABUW_RS03910	
	0.000319		metal-dependent hydrolase
0.82	865	ABUW_RS03050	
	0.000244		MacA family efflux pump subunit
0.82	342	ABUW_RS16335	
	0.003228		NirD/YgiW/YdeI family stress tolerance protein
0.82	534	ABUW_RS07170	
			Si-specific NAD(P)(+) transhydrogenase
0.82	4.61E-06	ABUW_RS06005	
	0.000558		ABC-F family ATP-binding cassette domain-containing protein
0.82	544	ABUW_RS08090	
	0.000959		DUF2786 domain-containing protein
0.82	085	ABUW_RS19110	
	0.010408		head morphogenesis protein
0.82	75	ABUW_RS13030	
	0.000421		TIGR04219 family outer membrane beta-barrel protein
0.82	972	ABUW_RS00105	
	0.005404		AraC family transcriptional regulator
0.82	12	ABUW_RS10870	
			2-nonaprenyl-3-methyl-6-methoxy-1%2C4-benzoquinol hydroxylase
0.83	5.12E-05	ABUW_RS07755	
	0.000596		PLP-dependent aminotransferase family protein
0.83	013	ABUW_RS08350	
			HlyC/CorC family transporter
0.83	1.76E-05	ABUW_RS14040	
	0.000204		MarR family transcriptional regulator
0.83	399	ABUW_RS09035	
			DUF2846 domain-containing protein
0.83	1.54E-05	ABUW_RS16520	
	0.000208		tyrosine recombinase XerC
0.83	823	ABUW_RS04695	
	0.006000		hypothetical protein
0.83	488	ABUW_RS05165	
			dihydrolipoyl dehydrogenase
0.84	1.99E-05	ABUW_RS02520	
	0.000118		ATP-binding protein
0.84	166	ABUW_RS07090	
	0.004667		copper resistance protein CopC
0.84	331	ABUW_RS16160	
	0.000304		AraC family transcriptional regulator
0.84	773	ABUW_RS07675	
			hypothetical protein
0.85	2.52E-05	ABUW_RS06280	
			DUF2520 domain-containing protein
0.85	1.17E-05	ABUW_RS13245	
	0.002030		CoA-acylating methylmalonate-semialdehyde dehydrogenase
0.85	54	ABUW_RS18420	
	0.000492		GntR family transcriptional regulator
0.85	36	ABUW_RS13475	

	0.001200		MFS transporter
0.85	746	ABUW_RS09440	
	0.138308		
0.85	308	sRNA9	
			phospholipase D
0.85	4.61E-05	ABUW_RS02955	
	0.002114		transcription elongation factor GreB
0.85	131	ABUW_RS04560	
			autotransporter domain-containing protein
0.85	8.84E-05	ABUW_RS16130	
	0.015707		LysE family translocator
0.86	735	ABUW_RS17095	
	0.001008		hypothetical protein
0.86	418	ABUW_RS17815	
	0.001252		gamma-glutamylcyclotransferase
0.86	682	ABUW_RS03235	
	0.003573		hypothetical protein
0.86	83	ABUW_RS10300	
			metal-dependent hydrolase
0.86	3.78E-05	ABUW_RS14845	
	0.042342		hypothetical protein
0.86	119	ABUW_RS10590	
	0.000165		phosphonate ABC transporter substrate-binding protein
0.86	931	ABUW_RS05455	
			BrnT family toxin
0.86	9.44E-05	ABUW_RS19605	
	0.000428		hypothetical protein
0.87	842	ABUW_RS02305	
	0.098578		hypothetical protein
0.87	456	ABUW_RS19545	
			hypothetical protein
0.87	8.72E-05	ABUW_RS19565	
	0.000981		LysR family transcriptional regulator
0.87	226	ABUW_RS08665	
			GGDEF domain-containing protein
0.87	1.32E-05	ABUW_RS10375	
	0.000215		UDP-glucose/GDP-mannose dehydrogenase family protein
0.87	797	ABUW_RS18585	
	0.002010		exo-alpha-sialidase
0.87	623	ABUW_RS12740	
			heavy metal sensor histidine kinase
0.88	8.85E-05	ABUW_RS16150	
	0.051588		SDR family oxidoreductase
0.88	993	ABUW_RS12015	
			peptidylprolyl isomerase
0.88	9.04E-06	ABUW_RS10680	
			potassium channel family protein
0.88	6.67E-05	ABUW_RS07790	
	0.044447		hypothetical protein
0.88	513	ABUW_RS08605	
	0.002147		hypothetical protein
0.88	219	ABUW_RS08535	
			magnesium transporter
0.88	1.96E-06	ABUW_RS17110	
			LysR family transcriptional regulator
0.88	2.81E-05	ABUW_RS05605	
	0.000304		hypothetical protein
0.88	439	ABUW_RS13645	
			OmpW family protein
0.88	7.69E-05	ABUW_RS06025	
			ribonuclease PH
0.88	9.83E-06	ABUW_RS18700	
			prephenate dehydratase
0.89	5.28E-05	ABUW_RS06660	
			hypothetical protein
0.89	9.96E-05	ABUW_RS16690	
	0.002362		regulatory or redox protein complexing with Bfr in iron storage and mobility (BFD)
0.89	206	ABUW_RS01510	
	0.013585		AsnC family transcriptional regulator
0.89	769	ABUW_RS11120	
	0.006561		hypothetical protein
0.89	266	ABUW_RS08060	
			hypothetical protein
0.89	4.92E-05	ABUW_RS01640	
			alkane 1-monooxygenase
0.89	6.53E-05	ABUW_RS10670	
	0.000264		LysR family transcriptional regulator
0.89	394	ABUW_RS11555	

0.89	4.55E-05	ABUW_RS07710	dihydroneopterin aldolase
	0.001110		rRNA pseudouridine synthase
0.89	555	ABUW_RS07825	
	0.058679		hypothetical protein
0.89	362	ABUW_RS19430	
			pirin family protein
0.90	4.23E-05	ABUW_RS05695	conjugal transfer protein TraN
	0.000109		
0.90	149	ABUW_RS19535	leucine efflux protein LeuE
			hypothetical protein
0.90	4.08E-05	ABUW_RS08135	hypothetical protein
	8.59E-05	ABUW_RS05135	
	0.001485		
0.90	328	ABUW_RS19815	AraC family transcriptional regulator
			PspC domain-containing protein
0.90	1.76E-05	ABUW_RS11100	two-component sensor histidine kinase
	5.80E-05	ABUW_RS01825	
	0.000333		LysR family transcriptional regulator
0.91	465	ABUW_RS07350	HAMP domain-containing histidine kinase
	0.002339		2'-5' RNA ligase
0.91	586	ABUW_RS00210	sensor histidine kinase efflux regulator BaeS
			SDR family NAD(P)-dependent oxidoreductase
0.91	1.11E-05	ABUW_RS02875	IclR family transcriptional regulator PobR
	0.015506		
0.91	545	ABUW_RS10575	ATP-dependent helicase
			class I SAM-dependent methyltransferase
0.91	9.35E-06	ABUW_RS02990	prepilin-type N-terminal cleavage/methylation domain-containing protein
	0.000645		
0.91	695	ABUW_RS18490	molecular chaperone DnaJ
	0.002691		type IV secretion protein Rhs
0.91	673	ABUW_RS12110	hypothetical protein
			hypothetical protein
0.91	9.88E-06	ABUW_RS12255	Nif3-like dinuclear metal center hexameric protein
			hydroxypyruvate isomerase
0.91	7.38E-05	ABUW_RS01700	hypothetical protein
	0.006214		alpha/beta hydrolase
0.91	044	ABUW_RS03190	chorismate lyase
			hypothetical protein
0.91	8.42E-06	ABUW_RS00180	
	0.001059		
0.91	849	ABUW_RS12690	transporter
	0.000699		hypothetical protein
0.92	993	ABUW_RS04100	
	0.000774		
0.92	337	ABUW_RS10750	
0.92	5.80E-07	ABUW_RS05945	
0.92	3.21E-05	ABUW_RS16075	
	0.000338		
0.92	754	ABUW_RS13895	
	0.000442		
0.93	687	ABUW_RS04800	
	0.003061		
0.93	177	ABUW_RS05900	
	0.000100		
0.93	35	ABUW_RS05105	
	0.004433		
0.93	734	ABUW_RS09640	
0.93	1.43E-05	ABUW_RS18515	
0.93	1.12E-05	ABUW_RS12050	
0.93	7.65E-06	ABUW_RS10705	
	0.064768		
0.94	69	ABUW_RS05280	
0.94	2.82E-06	ABUW_RS05305	
0.94	2.44E-05	ABUW_RS04790	
0.94	2.49E-06	ABUW_RS02290	
	0.000530		
0.94	894	ABUW_RS02135	

	0.000115		hypothetical protein
0.94	635	ABUW_RS14890	ClpXP protease specificity-enhancing factor
0.94	9.63E-05	ABUW_RS02410	RND transporter
0.95	2.52E-05	ABUW_RS17625	IclR family transcriptional regulator PcaU
0.95	4.57E-05	ABUW_RS08995	fatty acid desaturase
0.95	0.001742		peptide deformylase
0.95	194	ABUW_RS03580	sel1 repeat family protein
0.95	5.29E-05	ABUW_RS14260	hypothetical protein
0.95	0.000115		hypothetical protein
0.95	881	ABUW_RS03270	hypothetical protein
0.95	2.63E-05	ABUW_RS10650	DUF4142 domain-containing protein
0.95	1.60E-05	ABUW_RS02260	hypothetical protein
0.95	0.001252		3-deoxy-7-phosphoheptulonate synthase
0.95	682	ABUW_RS19115	hypothetical protein
0.95	8.64E-05	ABUW_RS13010	type VI secretion system-associated protein TagF
0.95	1.88E-06	ABUW_RS19150	D-serine ammonia-lyase
0.96	4.33E-06	ABUW_RS10545	ferredoxin family protein
0.96	2.88E-05	ABUW_RS08705	hypothetical protein
0.96	0.004218		urease subunit gamma
0.96	099	ABUW_RS12495	N-acetyltransferase
0.96	0.002845		hypothetical protein
0.96	523	ABUW_RS14195	hypothetical protein
0.96	0.000287		phosphatase PAP2 family protein
0.96	802	ABUW_RS12790	4'-phosphopantetheinyl transferase superfamily protein
0.96	1.97E-08	ABUW_RS16695	p-hydroxycinnamoyl CoA hydratase/lyase
0.96	0.011791		16S rRNA (guanine(527)-N(7))-methyltransferase RsmG
0.96	973	ABUW_RS14010	alpha/beta hydrolase
0.96	0.028686		hypothetical protein
0.96	229	ABUW_RS08545	hypothetical protein
0.96	0.047825		MFS transporter
0.96	014	ABUW_RS09295	TetR/AcrR family transcriptional regulator
0.96	0.001210		urease subunit beta
0.96	943	ABUW_RS04860	phage tail protein
0.96	0.001910		hypothetical protein
0.96	925	ABUW_RS16440	DUF1449 family protein
0.96	0.008653		DUF4850 domain-containing protein
0.97	267	ABUW_RS16385	carbonic anhydrase
0.97	5.83E-05	ABUW_RS13490	hypothetical protein
0.97	2.67E-06	ABUW_RS11010	hypothetical protein
0.97	0.001983		hypothetical protein
0.97	503	ABUW_RS06655	hypothetical protein
0.97	9.66E-06	ABUW_RS07630	hypothetical protein
0.97	7.52E-05	ABUW_RS11150	hypothetical protein
0.97	4.84E-05	ABUW_RS09380	hypothetical protein
0.97	0.000112		hypothetical protein
0.97	991	ABUW_RS05415	hypothetical protein
0.97	0.007103		hypothetical protein
0.97	327	ABUW_RS14005	hypothetical protein
0.97	0.000801		hypothetical protein
0.97	269	ABUW_RS02820	hypothetical protein
0.97	0.045531		hypothetical protein
0.97	946	ABUW_RS05680	hypothetical protein
0.98	3.03E-05	ABUW_RS08750	hypothetical protein
0.98	0.000942		hypothetical protein
0.98	182	ABUW_RS03485	hypothetical protein
0.98	1.23E-07	ABUW_RS14145	hypothetical protein
0.98	2.65E-06	ABUW_RS06975	hypothetical protein
0.98	0.002408		hypothetical protein
0.99	894	ABUW_RS12700	hypothetical protein

0.99	6.87E-07	ABUW_RS10785	3'(2')%2C5'-bisphosphate nucleotidase CysQ
0.99	4.55E-05	ABUW_RS14340	IcIR family transcriptional regulator
0.99	3.20E-07	ABUW_RS01485	TPM domain-containing protein
0.99	9.95E-05	ABUW_RS08785	TrkA family potassium uptake protein
1.00	5.04E-05	ABUW_RS12730	3-hydroxyacyl-CoA dehydrogenase
1.00	4.12E-08	ABUW_RS12795	hypothetical protein
1.00	6.71E-06	ABUW_RS11450	AraC family transcriptional regulator
1.00	1.49E-05	ABUW_RS10430	ribonuclease D
1.00	0.000124	ABUW_RS03585	PaaX family transcriptional regulator
1.00	026	ABUW_RS03585	hypothetical protein
1.00	1.52E-06	ABUW_RS08875	acyl-CoA dehydrogenase
1.00	9.89E-07	ABUW_RS06650	hypothetical protein
1.00	0.039872	ABUW_RS08055	uracil-DNA glycosylase family protein
1.00	423	ABUW_RS08055	YARHG domain-containing protein
1.00	0.000794	ABUW_RS10020	hypothetical protein
1.00	672	ABUW_RS10020	toxic anion resistance protein
1.00	1.27E-07	ABUW_RS10485	RidA family protein
1.00	0.000216	ABUW_RS18905	LysE family translocator
1.00	304	ABUW_RS18905	hypothetical protein
1.01	0.000166	ABUW_RS19165	hypothetical protein
1.01	444	ABUW_RS19165	DUF541 domain-containing protein
1.01	2.20E-07	ABUW_RS18010	response regulator
1.01	0.000942	ABUW_RS13060	heteromeric transposase endonuclease subunit TnsA
1.01	182	ABUW_RS13060	acyl-CoA dehydrogenase
1.01	6.24E-08	ABUW_RS14805	hypothetical protein
1.01	0.028225	ABUW_RS17040	hypothetical protein
1.01	284	ABUW_RS17040	
1.01	1.67E-06	ABUW_RS05420	
1.01	4.35E-07	ABUW_RS16145	
1.01	9.81E-08	ABUW_RS17910	
1.01	0.001659	ABUW_RS15600	
1.01	217	ABUW_RS15600	
1.01	2.94E-08	ABUW_RS19645	
1.01	0.162558	ABUW_RS19690	
1.01	239	ABUW_RS19690	
1.01	6.80E-05	ABUW_RS05030	
1.02	9.63E-05	ABUW_RS09345	
1.02	8.82E-06	ABUW_RS17570	
1.02	9.96E-05	ABUW_RS11460	
1.02	7.60E-05	ABUW_RS06830	
1.02	1.93E-05	ABUW_RS13805	
1.02	0.000142	ABUW_RS18005	
1.02	835	ABUW_RS18005	
1.02	0.069317	ABUW_RS00185	
1.02	114	ABUW_RS00185	
1.02	2.45E-08	ABUW_RS01895	
1.02	2.33E-06	ABUW_RS12890	
1.02	0.000285	ABUW_RS14835	
1.02	046	ABUW_RS14835	
1.02	3.27E-07	ABUW_RS17380	
1.02	0.025440	ABUW_RS17380	
1.03	784	ABUW_RS11895	
1.03	0.002073	ABUW_RS11895	
1.03	325	ABUW_RS08085	

1.03	2.71E-05	ABUW_RS18540	GntR family transcriptional regulator
1.03	1.08E-06	ABUW_RS08140	transaldolase
1.03	0.000428	ABUW_RS08420	hypothetical protein
1.03	522	ABUW_RS08420	GFA family protein
1.03	0.000193	ABUW_RS10480	serine protease
1.03	039	ABUW_RS10480	epoxyqueuosine reductase QueH
1.03	8.77E-05	ABUW_RS15120	hypothetical protein
1.03	2.30E-06	ABUW_RS12420	four-helix bundle copper-binding protein
1.03	0.059217	ABUW_RS13750	
1.03	851	ABUW_RS13750	
1.04	7.64E-07	ABUW_RS13120	
1.04	0.081910	ABUW_RS13120	
1.04	969	sRNA25	
1.04	8.86E-06	ABUW_RS01505	bacterioferritin
1.04	0.252180	ABUW_RS01505	pyrroloquinoline quinone precursor peptide PqqA
1.04	348	ABUW_RS19800	
1.04	1.75E-06	ABUW_RS06105	site-specific integrase
1.04	1.08E-05	ABUW_RS05965	EAL domain-containing protein
1.04	2.15E-08	ABUW_RS05245	peptidylprolyl isomerase
1.05	4.29E-07	ABUW_RS02285	lytic transglycosylase
1.05	5.62E-07	ABUW_RS14900	hypothetical protein
1.05	0.000253	ABUW_RS14900	Rha family transcriptional regulator
1.05	932	ABUW_RS02705	
1.05	0.000439	ABUW_RS02705	hypothetical protein
1.05	292	ABUW_RS02930	
1.05	0.008009	ABUW_RS02930	oxidoreductase
1.05	743	ABUW_RS02310	
1.05	6.75E-08	ABUW_RS15755	hypothetical protein
1.05	0.000170	ABUW_RS15755	TonB-dependent siderophore receptor
1.05	398	ABUW_RS00790	
1.05	0.000201	ABUW_RS00790	3'-5' exonuclease domain-containing protein 2
1.05	631	ABUW_RS01210	
1.06	2.03E-07	ABUW_RS19590	replication initiation protein
1.06	1.85E-05	ABUW_RS16255	aconitate hydratase AcnA
1.06	1.78E-07	ABUW_RS03115	SAM-dependent methyltransferase
1.06	0.010719	ABUW_RS03115	hypothetical protein
1.06	627	ABUW_RS02970	
1.06	6.93E-06	ABUW_RS17545	phosphoglycolate phosphatase
1.07	1.62E-06	ABUW_RS06500	alpha/beta fold hydrolase
1.07	6.20E-05	ABUW_RS11065	TetR/AcrR family transcriptional regulator
1.07	7.66E-07	ABUW_RS13200	KTSC domain-containing protein
1.07	0.009068	ABUW_RS13200	DUF4124 domain-containing protein
1.07	456	ABUW_RS16315	
1.07	9.27E-09	ABUW_RS13495	aldehyde dehydrogenase
1.07	1.11E-06	ABUW_RS01745	hypothetical protein
1.07	0.001034	ABUW_RS01745	hypothetical protein
1.08	152	ABUW_RS08640	
1.08	0.000569	ABUW_RS08640	enoyl-CoA hydratase
1.08	963	ABUW_RS12010	
1.08	2.98E-05	ABUW_RS11550	hydrolase
1.08	2.05E-05	ABUW_RS02300	DUF2789 domain-containing protein
1.08	1.32E-05	ABUW_RS17435	DUF1311 domain-containing protein
1.08	0.017586	ABUW_RS17435	DUF2314 domain-containing protein
1.08	401	ABUW_RS09350	
1.08	5.19E-05	ABUW_RS17305	hypothetical protein

	0.004163		acyl-CoA dehydrogenase
1.08	087	ABUW_RS12060	
1.09	6.19E-09	ABUW_RS10490	HIT family protein
1.09	2.23E-08	ABUW_RS01480	LemA family protein
	0.000122		anthranilate synthase component I
1.09	66	ABUW_RS17540	
1.09	7.78E-05	ABUW_RS10010	hypothetical protein
	0.007649		ATP-binding cassette domain-containing protein
1.10	935	ABUW_RS06545	
1.10	9.34E-07	ABUW_RS08975	hypothetical protein
1.10	1.64E-06	ABUW_RS14965	SsrA-binding protein SmpB
1.10	1.53E-06	ABUW_RS12710	type VI secretion system tip protein VgrG
	0.000230		hypothetical protein
1.10	977	ABUW_RS08540	
	0.000145		LysR family transcriptional regulator
1.10	399	ABUW_RS10175	
1.11	5.88E-06	ABUW_RS00100	glutathione S-transferase family protein
1.11	9.44E-05	ABUW_RS14235	hypothetical protein
1.11	5.62E-06	ABUW_RS00690	DUF2147 domain-containing protein
1.12	2.33E-06	ABUW_RS10580	HAD family hydrolase
1.12	5.44E-07	ABUW_RS05475	protease SohB
1.12	2.16E-05	ABUW_RS19445	hypothetical protein
	0.000624		Lrp/AsnC family transcriptional regulator
1.12	113	ABUW_RS05440	
1.13	7.82E-06	ABUW_RS16920	long-chain-acyl-CoA synthetase
	0.012373		UDP-2%2C3-diacylglucosamine diphosphatase
1.13	248	ABUW_RS07875	
	0.000216		YcxB family protein
1.13	304	ABUW_RS02220	
1.14	1.65E-07	ABUW_RS17455	DUF4442 domain-containing protein
	0.000155		SMP-30/gluconolactonase/LRE family protein
1.14	769	ABUW_RS09375	
1.14	2.68E-07	ABUW_RS20385	hypothetical protein
1.14	5.97E-06	ABUW_RS19210	helix-turn-helix transcriptional regulator
	0.004271		hypothetical protein
1.14	755	ABUW_RS08025	
1.14	1.20E-05	ABUW_RS19580	hypothetical protein
1.14	1.20E-07	ABUW_RS00045	hypothetical protein
	0.061098		flavodoxin
1.14	95	ABUW_RS12585	
	0.000474		peroxiredoxin
1.14	349	ABUW_RS14690	
1.15	3.25E-06	ABUW_RS19105	hypothetical protein
1.15	2.54E-10	ABUW_RS01955	metal-dependent hydrolase
1.15	1.20E-08	ABUW_RS13275	hypothetical protein
1.15	7.12E-06	ABUW_RS19170	hypothetical protein
1.15	8.88E-07	ABUW_RS09555	alpha/beta hydrolase
1.16	5.61E-08	ABUW_RS17340	transcriptional regulator
1.17	3.27E-09	ABUW_RS14590	hypothetical protein
1.17	7.46E-09	ABUW_RS11350	glutathione S-transferase
1.17	1.07E-06	ABUW_RS11425	tautomerase family protein
	0.010425		DUF971 domain-containing protein
1.17	328	ABUW_RS10235	
1.17	9.47E-05	ABUW_RS15680	HAD family hydrolase

	0.013026		
1.18	368	sRNA75	
	0.000138		site-specific integrase
1.18	545	ABUW_RS06750	
			N-acetyltransferase
1.18	8.90E-06	ABUW_RS08065	
	0.000116		antibiotic biosynthesis monooxygenase
1.18	214	ABUW_RS09270	
			outer membrane protein
1.18	2.52E-06	ABUW_RS14775	
			MFS transporter
1.19	4.77E-07	ABUW_RS00200	
	0.001151		diacylglycerol kinase
1.19	588	ABUW_RS04510	
			outer membrane lipoprotein chaperone LolA
1.19	1.73E-08	ABUW_RS04170	
	0.002876		GNAT family N-acetyltransferase
1.19	057	ABUW_RS07830	
	0.000198		hypothetical protein
1.19	835	ABUW_RS10005	
			alpha/beta fold hydrolase
1.19	8.90E-09	ABUW_RS10455	
			hypothetical protein
1.20	2.06E-06	ABUW_RS03975	
			alpha/beta hydrolase
1.20	2.40E-07	ABUW_RS18860	
			diguanylate cyclase
1.20	6.25E-08	ABUW_RS05130	
	0.002812		helix-turn-helix transcriptional regulator
1.20	244	ABUW_RS13020	
	0.004915		hypothetical protein
1.20	831	ABUW_RS09265	
			SgcJ/EcaC family oxidoreductase
1.20	5.02E-09	ABUW_RS04570	
			hypothetical protein
1.21	9.57E-11	ABUW_RS19585	
			hypothetical protein
1.21	2.05E-07	ABUW_RS02715	
			CAP domain-containing protein
1.21	5.23E-08	ABUW_RS04945	
			hypothetical protein
1.22	2.18E-07	ABUW_RS19050	
			ToIC family protein
1.22	6.49E-07	ABUW_RS04750	
			YbjQ family protein
1.22	6.15E-05	ABUW_RS04120	
			hypothetical protein
1.22	4.07E-07	ABUW_RS11180	
			acyltransferase
1.22	5.56E-07	ABUW_RS04035	
			KiA-N domain-containing protein
1.23	2.05E-07	ABUW_RS03925	
			ribonuclease E inhibitor RraB
1.23	1.38E-08	ABUW_RS18475	
			hypothetical protein
1.23	6.40E-07	ABUW_RS14570	
			MerR family transcriptional regulator
1.23	2.74E-10	ABUW_RS13865	
			phospholipase D family protein
1.23	3.79E-07	ABUW_RS02470	
			hypothetical protein
1.23	6.69E-10	ABUW_RS11835	
			hypothetical protein
1.23	2.44E-05	ABUW_RS03980	
			hypothetical protein
1.24	6.25E-07	ABUW_RS15440	
	0.156728		SRPBCC domain-containing protein
1.24	912	ABUW_RS14085	
			hypothetical protein
1.24	1.80E-10	ABUW_RS00660	
			WYL domain-containing protein
1.24	1.17E-06	ABUW_RS07510	
	0.000137		TonB-dependent siderophore receptor
1.24	025	ABUW_RS10520	
			threonylcarbamoyl-AMP synthase
1.24	7.92E-07	ABUW_RS15115	
	0.001206		hypothetical protein
1.24	519	ABUW_RS09545	
			hypothetical protein
1.24	9.86E-07	ABUW_RS01655	
			nucleoside-diphosphate sugar epimerase
1.24	9.94E-10	ABUW_RS10770	

1.24	2.42E-08	ABUW_RS05625	aromatic ring-hydroxylating dioxygenase subunit alpha
	0.002927		
1.25	173	sRNA86	
1.25	3.69E-07	ABUW_RS09690	zonular occludens toxin
1.25	1.11E-09	ABUW_RS04345	hypothetical protein
1.26	1.25E-06	ABUW_RS09275	hydrolase
1.26	3.18E-11	ABUW_RS08040	mechanosensitive ion channel
1.27	3.75E-05	ABUW_RS11300	hypothetical protein
1.27	1.88E-06	ABUW_RS12620	hypothetical protein
1.27	3.07E-11	ABUW_RS15230	hypothetical protein
1.27	1.47E-10	ABUW_RS14840	metal-dependent hydrolase
1.27	8.22E-11	ABUW_RS19600	sel1 repeat family protein
1.27	2.50E-05	ABUW_RS01920	ComF family protein
1.27	1.52E-05	ABUW_RS18870	hypothetical protein
1.28	1.45E-08	ABUW_RS01450	shikimate kinase AroK
1.28	1.14E-06	ABUW_RS10700	Rrf2 family transcriptional regulator
1.28	2.97E-05	ABUW_RS09325	hypothetical protein
1.28	6.09E-07	ABUW_RS05160	hypothetical protein
1.29	2.20E-07	ABUW_RS12800	O-methyltransferase
	0.000321		hypothetical protein
1.30	946	ABUW_RS16460	
			hypothetical protein
1.30	4.63E-12	ABUW_RS04390	DUF721 domain-containing protein
1.31	1.08E-08	ABUW_RS00760	TetR/AcrR family transcriptional regulator
1.31	1.02E-08	ABUW_RS18135	TetR/AcrR family transcriptional regulator
1.31	3.21E-08	ABUW_RS13405	OmpW family protein
1.31	5.96E-09	ABUW_RS08075	endonuclease
1.31	1.12E-05	ABUW_RS16775	gamma carbonic anhydrase family protein
1.31	6.48E-11	ABUW_RS05510	nucleoside triphosphate pyrophosphohydrolase
1.31	1.90E-05	ABUW_RS16030	hypothetical protein
	0.000165		
1.31	029	ABUW_RS02725	hypothetical protein
1.32	1.61E-09	ABUW_RS12245	XRE family transcriptional regulator
1.32	7.93E-07	ABUW_RS09650	hypothetical protein
1.32	2.34E-11	ABUW_RS01490	hypothetical protein
1.33	1.14E-05	ABUW_RS18750	hypothetical protein
1.33	8.43E-06	ABUW_RS11130	hypothetical protein
	0.000154		hypothetical protein
1.33	366	ABUW_RS15505	hypothetical protein
1.33	1.61E-06	ABUW_RS17460	MerR family transcriptional regulator
1.33	8.33E-09	ABUW_RS17405	hypothetical protein
	0.004680		
1.33	885	ABUW_RS03855	NAD(+) diphosphatase
1.33	8.52E-09	ABUW_RS13820	STAS domain-containing protein
1.34	8.99E-10	ABUW_RS01900	lipase secretion chaperone
1.34	9.08E-05	ABUW_RS01600	DMT family transporter
1.34	2.14E-06	ABUW_RS11265	hypothetical protein
1.35	4.30E-06	ABUW_RS17770	hypothetical protein
1.35	2.17E-11	ABUW_RS01370	

1.35	2.73E-11	ABUW_RS13240	glutathione S-transferase
1.35	4.83E-12	ABUW_RS10795	DUF159 family protein
1.35	5.14E-09	ABUW_RS09435	SDR family oxidoreductase
1.35	1.74E-07	ABUW_RS15260	multidrug transporter MatE
1.36	2.28E-08	ABUW_RS13225	glutathione S-transferase
1.37	5.72E-11	ABUW_RS19540	conjugal transfer protein TraF
1.37	0.055235		hypothetical protein
1.37	013	ABUW_RS04155	
1.37	1.16E-10	ABUW_RS01245	GNAT family acetyltransferase
1.38	6.12E-08	ABUW_RS10205	LysR family transcriptional regulator
1.38	0.001967		copper resistance protein CopD
1.38	675	ABUW_RS16165	
1.38	0.000894		phage virion morphogenesis protein
1.38	795	ABUW_RS02815	
1.39	1.57E-13	ABUW_RS05940	superoxide dismutase
1.39	4.47E-09	ABUW_RS03280	folate-binding protein YgfZ
1.39	4.63E-12	ABUW_RS00560	DUF924 domain-containing protein
1.39	5.29E-05	ABUW_RS10445	hypothetical protein
1.39	4.34E-07	ABUW_RS05240	deoxyribodipyrimidine photo-lyase
1.39	2.86E-09	ABUW_RS01810	putative DNA modification/repair radical SAM protein
1.40	8.67E-09	ABUW_RS15690	DUF2218 domain-containing protein
1.40	0.001538		hypothetical protein
1.40	008	ABUW_RS12215	
1.40	5.01E-05	ABUW_RS01815	DNA metabolism protein
1.40	4.19E-08	ABUW_RS15945	hypothetical protein
1.40	1.58E-09	ABUW_RS16540	TonB-dependent siderophore receptor
1.41	4.88E-05	ABUW_RS12685	hypothetical protein
1.41	1.87E-14	ABUW_RS16350	enoyl-ACP reductase
1.41	1.74E-09	ABUW_RS10000	catalase
1.41	7.46E-10	ABUW_RS12885	hypothetical protein
1.42	4.24E-12	ABUW_RS04365	universal stress protein
1.42	6.79E-11	ABUW_RS01650	flavodoxin family protein
1.42	2.81E-11	ABUW_RS02250	xanthine phosphoribosyltransferase
1.43	1.50E-09	ABUW_RS11560	GntR family transcriptional regulator
1.43	4.04E-08	ABUW_RS03370	alpha/beta fold hydrolase
1.43	0.003453		hypothetical protein
1.43	981	ABUW_RS13585	
1.43	0.000257		DUF488 domain-containing protein
1.43	306	ABUW_RS03290	
1.44	3.14E-13	ABUW_RS02255	DUF3108 domain-containing protein
1.44	9.57E-11	ABUW_RS05325	CYTH and CHAD domain-containing protein
1.44	1.18E-08	ABUW_RS07205	cyclase family protein
1.45	1.69E-11	ABUW_RS08390	hypothetical protein
1.45	6.91E-05	ABUW_RS05200	VIT family protein
1.45	0.000311		AraC family transcriptional regulator
1.45	189	ABUW_RS18145	
1.46	4.10E-08	ABUW_RS07500	hypothetical protein
1.46	1.99E-05	ABUW_RS06610	hemin uptake protein HemP
1.46	5.31E-10	ABUW_RS16815	DUF1311 domain-containing protein

1.46	2.31E-11	ABUW_RS01645	antibiotic biosynthesis monooxygenase
1.47	8.40E-14	ABUW_RS11220	biotin synthase
1.47	4.67E-10	ABUW_RS06400	ORF6N domain-containing protein
1.47	1.20E-09	ABUW_RS10760	glutathione S-transferase
1.47	3.41E-08	ABUW_RS03335	response regulator
1.48	3.70E-11	ABUW_RS13280	CinA family protein
1.48	4.96E-08	ABUW_RS09520	HD domain-containing protein
1.48	8.06E-09	ABUW_RS11495	hypothetical protein
1.48	6.21E-11	ABUW_RS13815	hypothetical protein
1.48	1.07E-11	ABUW_RS10095	molybdate ABC transporter substrate-binding protein
1.48	0.000347	129	glutamine synthetase
1.48	1.06E-14	ABUW_RS12900	DUF4882 domain-containing protein
1.51	8.29E-05	ABUW_RS12115	FMN-dependent NADH-azoreductase
1.51	1.37E-12	ABUW_RS10930	6-carboxytetrahydropterin synthase
1.51	2.93E-15	ABUW_RS04550	hypothetical protein
1.51	1.64E-10	ABUW_RS15920	hypothetical protein
1.51	6.77E-08	ABUW_RS11885	hypothetical protein
1.52	1.05E-10	ABUW_RS04830	CSLREA domain-containing protein
1.52	1.16E-10	ABUW_RS06670	hypothetical protein
1.52	5.68E-09	ABUW_RS10790	hypothetical protein
1.53	1.69E-16	ABUW_RS09425	fumarylacetoacetate hydrolase
1.53	3.20E-08	ABUW_RS17270	type IV-A pilus assembly ATPase PilB
1.54	0.000890	531	GFA family protein
1.54	2.88E-12	ABUW_RS13210	DUF1653 domain-containing protein
1.54	0.014370	487	sRNA28
1.54	1.28E-06	ABUW_RS03385	DUF1853 family protein
1.54	1.65E-13	ABUW_RS11410	hypothetical protein
1.54	3.37E-12	ABUW_RS12260	DUF2813 domain-containing protein
1.54	0.010520	643	hemerythrin
1.55	2.10E-10	ABUW_RS08695	hypothetical protein
1.56	2.98E-07	ABUW_RS03850	hypothetical protein
1.56	1.12E-15	ABUW_RS14025	copper resistance protein NlpE
1.56	3.74E-07	ABUW_RS11290	integrase
1.57	5.26E-06	ABUW_RS07785	hypothetical protein
1.57	0.001380	103	hypothetical protein
1.57	9.32E-06	ABUW_RS12880	hypothetical protein
1.57	3.74E-07	ABUW_RS12715	serine hydrolase
1.58	3.49E-09	ABUW_RS11070	helix-turn-helix transcriptional regulator
1.58	3.31E-15	ABUW_RS13205	O-methyltransferase
1.58	2.32E-14	ABUW_RS09535	hypothetical protein
1.59	8.50E-11	ABUW_RS06595	NirD/YgiW/YdeI family stress tolerance protein
1.60	4.29E-12	ABUW_RS04500	co-chaperone GroES
1.60	3.43E-13	ABUW_RS15940	hypothetical protein

1.61	7.68E-17	ABUW_RS19620	DIP1984 family protein
1.62	1.51E-07	ABUW_RS09470	LuxR family transcriptional regulator
1.63	6.91E-05	ABUW_RS02965	hypothetical protein
1.63	8.59E-10	ABUW_RS13380	hypothetical protein
1.64	4.36E-16	ABUW_RS03310	DUF1508 domain-containing protein
1.64	2.60E-05	ABUW_RS05285	hypothetical protein
1.64	1.38E-05	ABUW_RS19510	hypothetical protein
1.64	3.25E-15	ABUW_RS10885	orotidine-5'-phosphate decarboxylase
1.64	5.77E-15	ABUW_RS17640	hypothetical protein
1.65	3.66E-10	ABUW_RS10420	hypothetical protein
1.65	0.082379		
1.65	278	sRNA98	
1.65	1.79E-09	ABUW_RS19450	hypothetical protein
1.66	9.54E-07	sRNA87	
1.66	1.67E-06	ABUW_RS13910	hypothetical protein
1.66	0.000724		
1.67	016	ABUW_RS07835	type II toxin-antitoxin system RelB/DinJ family antitoxin
1.67	2.28E-13	ABUW_RS19055	hypothetical protein
1.68	4.28E-19	ABUW_RS06065	DUF962 domain-containing protein
1.68	4.55E-19	ABUW_RS14810	threonine export protein RhtC
1.68	1.60E-05	ABUW_RS11400	Crp/Fnr family transcriptional regulator
1.68	2.61E-15	ABUW_RS14745	class II glutamine amidotransferase
1.69	1.35E-18	ABUW_RS08685	CBS domain-containing protein
1.69	3.97E-11	ABUW_RS02790	alkaline phosphatase
1.69	1.11E-12	ABUW_RS12540	hypothetical protein
1.69	6.15E-13	ABUW_RS04360	MGMT family protein
1.69	0.000827		
1.69	641	ABUW_RS07410	N-acetyltransferase
1.70	5.16E-10	ABUW_RS11830	translesion error-prone DNA polymerase V autoproteolytic subunit
1.70	9.83E-15	ABUW_RS11155	polyisoprenoid-binding protein
1.70	0.000648		
1.70	372	ABUW_RS16110	RidA family protein
1.70	0.004172		
1.70	839	ABUW_RS12775	Lrp/AsnC family transcriptional regulator
1.70	6.90E-05	ABUW_RS02360	DUF4256 domain-containing protein
1.71	1.50E-23	ABUW_RS03915	Arc family DNA-binding protein
1.71	5.15E-08	ABUW_RS00410	HAD family hydrolase
1.71	1.79E-12	ABUW_RS07450	hypothetical protein
1.71	5.76E-08	ABUW_RS07440	TetR/AcrR family transcriptional regulator
1.71	9.60E-15	ABUW_RS18720	TetR/AcrR family transcriptional regulator
1.72	6.46E-21	ABUW_RS10925	uracil-DNA glycosylase
1.73	2.42E-10	ABUW_RS07490	DUF3426 domain-containing protein
1.74	1.76E-24	ABUW_RS11345	amino acid ABC transporter substrate-binding protein
1.74	2.78E-07	ABUW_RS18865	hypothetical protein
1.74	8.59E-10	ABUW_RS09645	hypothetical protein
1.74	3.03E-17	ABUW_RS08530	hypothetical protein
1.74	1.14E-06	ABUW_RS06270	hypothetical protein
1.76	3.03E-17	ABUW_RS08650	hypothetical protein

1.76	2.50E-08	ABUW_RS10315	MBL fold metallo-hydrolase
1.77	2.81E-16	ABUW_RS17410	hypothetical protein
	0.000714		hypothetical protein
1.78	436	ABUW_RS07635	
1.80	1.52E-12	ABUW_RS18030	MerR family transcriptional regulator
1.80	4.94E-12	ABUW_RS08410	hypothetical protein
1.81	3.74E-12	ABUW_RS15790	ribosome-associated translation inhibitor RaiA
1.82	1.51E-15	ABUW_RS08110	RDD family protein
1.82	1.09E-09	ABUW_RS04760	hypothetical protein
1.82	3.93E-12	ABUW_RS12910	right-handed parallel beta-helix repeat-containing protein
1.82	2.20E-09	ABUW_RS13480	MarR family transcriptional regulator
1.84	1.28E-19	ABUW_RS18485	DUF1003 domain-containing protein
1.86	2.25E-15	ABUW_RS08590	universal stress protein
1.86	2.80E-19	ABUW_RS10155	AraC family transcriptional regulator
1.86	1.20E-15	ABUW_RS14680	hypothetical protein
1.87	7.58E-08	ABUW_RS07290	hypothetical protein
	0.000209		metalloregulator ArsR/SmtB family transcription factor
1.87	209	ABUW_RS11530	
1.87	3.47E-25	ABUW_RS18820	NAD(P)H-dependent oxidoreductase
1.88	2.34E-20	ABUW_RS10895	integration host factor subunit beta
1.89	4.14E-21	ABUW_RS04825	rhombotarget A
	0.003572		hypothetical protein
1.90	877	ABUW_RS11230	
1.91	1.88E-11	ABUW_RS16880	DNA-binding transcriptional regulator HcaR
1.91	2.76E-08	ABUW_RS09960	hypothetical protein
1.91	6.10E-08	ABUW_RS01165	AraC family transcriptional regulator
1.94	4.51E-13	ABUW_RS15290	hypothetical protein
1.94	8.00E-20	ABUW_RS13220	hypothetical protein
1.97	4.63E-26	ABUW_RS08700	hypothetical protein
1.98	6.90E-18	ABUW_RS02985	hypothetical protein
1.99	4.64E-21	ABUW_RS15335	hypothetical protein
2.00	1.55E-15	ABUW_RS08690	DUF2750 domain-containing protein
2.01	4.01E-15	ABUW_RS09205	MerR family transcriptional regulator
2.03	1.04E-16	ABUW_RS14830	arginyltransferase
2.03	1.23E-14	ABUW_RS08045	hypothetical protein
	0.000536		hypothetical protein
2.03	656	ABUW_RS15455	
2.05	1.60E-18	ABUW_RS05330	DUF962 domain-containing protein
2.08	1.43E-18	ABUW_RS01690	hypothetical protein
2.08	7.30E-12	ABUW_RS11140	hypothetical protein
2.10	1.98E-22	ABUW_RS10890	DUF1049 domain-containing protein
2.11	1.41E-17	ABUW_RS06430	hypothetical protein
2.12	5.71E-15	ABUW_RS10675	AraC family transcriptional regulator
2.16	8.28E-09	ABUW_RS02355	GFA family protein
	0.016981		
2.17	311	sRNA105	
2.17	4.37E-10	ABUW_RS05675	TetR/AcrR family transcriptional regulator
2.18	1.04E-06	sRNA71	

2.19	6.90E-18	ABUW_RS03365	radical SAM protein
2.20	4.45E-32	ABUW_RS06425	hypothetical protein
2.26	7.68E-22	ABUW_RS05685	hypothetical protein
2.26	6.64E-22	ABUW_RS18520	hypothetical protein
2.27	3.80E-13	ABUW_RS01120	AraC family transcriptional regulator
2.37	1.74E-19	ABUW_RS11175	hypothetical protein
2.39	3.29E-07	ABUW_RS02710	hypothetical protein
2.41	1.27E-13	ABUW_RS16210	hypothetical protein
2.42	2.76E-19	ABUW_RS00205	2%2C5-didehydrogluconate reductase DkgB
2.44	3.95E-27	ABUW_RS13765	hypothetical protein
2.44	8.96E-24	ABUW_RS03380	entericidin A/B family lipoprotein
2.50	3.66E-17	ABUW_RS13915	5-formyltetrahydrofolate cyclo-ligase
2.52	2.01E-19	ABUW_RS13775	hypothetical protein
2.54	2.02E-36	ABUW_RS11270	hypothetical protein
2.54	9.51E-21	ABUW_RS07820	hypothetical protein
2.66	3.23E-47	ABUW_RS08610	MarR family transcriptional regulator
2.70	9.51E-21	ABUW_RS11305	TetR/AcrR family transcriptional regulator
2.73	2.07E-27	ABUW_RS16285	TetR/AcrR family transcriptional regulator
2.74	8.41E-07	ABUW_RS06275	hypothetical protein
2.77	3.35E-13	ABUW_RS03985	hypothetical protein
2.88	7.98E-20	ABUW_RS08240	TetR/AcrR family transcriptional regulator
3.09	2.42E-36	ABUW_RS09540	endonuclease/exonuclease/phosphatase family protein
3.13	6.72E-27	ABUW_RS14395	hypothetical protein
3.40	9.23E-49	sRNA106	
3.46	0.051966		hypothetical protein
	842	ABUW_RS19825	

