Mucoid Coating Provides a Growth Advantage to *Pseudomonas aeruginosa* at Oil-Water Interfaces

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Abstract: Chronic lung infection with bacterial biofilms is one of the leading causes of death in cystic fibrosis (CF) patients. Among many species infecting the lung airways, *Pseudomonas aeruginosa* is the major pathogen colonizing and persisting throughout the patient's life. The microorganism undergoes pathoadaptation, while switching from a non-mucoid to a mucoid phenotype, improving the mechanical properties of the resulting biofilms. Previous investigation of the dynamic rheological properties of non-mucoid (PANT) and mucoid (PASL) clinical *P. aeruginosa* isolates exposed to interfacial stresses demonstrated that the mucoid strains formed films with stronger resistance to bending and non-linear relaxation to compression and tension. We hypothesize that the mucoid switch provides a growth advantage to *P. aeruginosa* through the development of interfacial films with viscoelastic properties enabling cell survival. Here, we investigate physiological response of the mucoid and the non-mucoid *P. aeruginosa* at interfacial environments. Our results, both macroscopic and molecular, reveal that mucoid coating plays an important role in protecting the bacteria from interfacial stresses. Cell characterizations using electron and fluorescence microscopies showed higher proportion of dead non-mucoid cells compared to mucoid cells on interfacial exposure. For example, scanning electron microscopy (STEM) imaging showed that, 96.6% of non-mucoid cells were lysed while only 22.2 % of mucoid cells were lysed owing to interfacial stress. Furthermore, the transcriptional profiling of *P. aeruginosa* cells indicated the upregulation of pel, psl, and alginate genes encoding for exopolysaccharide biomaterials is associated with mucoid cells' ability to cope with the interfacial environments. Further characterization of real-time gene regulation at interfaces will further elucidate the effects of interfacial environment on the regulation of bacterial virulence.

1. INTRODUCTION

Cystic fibrosis (CF) is a life-threating genetic disorder caused by mutations in the cystic fibrosis transmembrane conductance regulator (*CFTR*) gene, encoding for the CFTR protein located in the membrane of epithelial cells in the lungs and pancreas.[1, 2] The CFTR protein acts as an ion channel that transports chloride, bicarbonate, and sodium in and out of the cells.[3] [4] Failure to control such transport disturbs the cell homeostasis, induces mucus build-up and causes the malfunction of the respiratory epithelial cells specialized in mucus clearance. Consequently, biofilm and chronic infections by opportunistic pathogens develops, leading to breathing obstruction and patient death. [3, 5]

Pseudomonas aeruginosa is a pathogenic Gram-negative bacterium frequently associated with recurrent CF infections.[6-9] Under anaerobic conditions, *P. aeruginosa* overproduces the extracellular polysaccharide (EPS) materials like alginate, which enables the microbe to persist in the respiratory tracts of CF patients.[6, 10] This phenotypic change, refer to as the mucoid switch,[7, 10, 11] occurs in the later stage of the disease.[7, 10] In addition to promoting cell adaptation under hypoxic conditions, this phenotypic switch contributes to bacterial survival through the secretion of a thick EPS matrix that shields against phagocytosis.[12, 13] Moreover, the mucoid phenotype provides a higher resistance to antimicrobials compared to the non-mucoid cells.[14-17] In fact, the mucoid switch is well-recognized as a defense mechanism of many microorganisms during pathogenesis and environmental stress. [11, 18-21]

While the physiology and gene expression of cells undergoing the mucoid switch have been widely investigated at solid surfaces,[11, 22, 23] very little is known about the biological implications of the switch at fluid interfaces.[24-26] In previous work,[27] analysis of the transcriptomes from *P. aeruginosa* strains from an early stage of interfacial confinement revealed significant expression of genes associated with stress response and DNA repair in PA14 compared to PAO1 cells. The differential transcriptional profiling indicated strain-dependent genetic response to interfacial confinement. More importantly, the upregulation of *alkB2*, a hydroxylase involved in C12–C16 alkane catabolism [28, 29], was associated with PAO1's ability to cope with the interfacial stresses, and deletion of this gene suppressed the formation of an elastic film in PAO1. Interestingly, PA14 lacked *alkB2* expression, and was unable to secrete psl polysaccharides or an elastic film at fluid interfaces. Thus, there is increasing evidence that interfacial confinement can impact bacteria and trigger cellular metabolism. However, it is unclear if the pathways driving these cellular responses in *P. aeruginosa* strains at fluid interfaces are universal. Because the mucoid switch also occurs at energy-rich interfaces we speculated that it might indicate a coping strategy of bacteria against the interfacial stress. We investigated rheological properties of the interfacial films formed by mucoid (PASL) and non-mucoid (PANT) *P. aeruginosa* strains at oil-water interfaces, and determined that mucoid cells form softer films with non-linear viscoelastic properties in contrast to the non-mucoid cells.[30] Such difference in the viscoelastic and the interfacial properties of both strains has been validated by others,[31, 32] leading to the hypothesis that *P. aeruginosa* cells might undergo morphological and metabolic adaptation during mucoid switch as a survival mechanism to interfacial stress.

In this study, we use complementary approaches including scanning transmission electron microscopy (STEM), scanning electron microscopy (SEM), and confocal microscopy to examine the physiological response of the mucoid and the non-mucoid *P. aeruginosa* at fluid interfaces. We reveal that physiological response of *P. aeruginosa* to interfacial stress vary between a mucoid and non-mucoid strain, and bacteria capable of secreting an EPS matrix are shielded from the physical stress of oil-water interfaces. Our transcriptional analysis indicates that *P. aeruginosa* exposed to interfacial confinement secrete more biomolecules in the form of pel, psl and alginate exopolysaccharides to cope with the interfacial stress. Our finding on the effects of fluid-interfaces on the bacterial phenotypical adaptation could provide new insights for developing the capability to manipulate both the metabolic and the interfacial properties of microorganisms. This would enable an evidence-based framework to rationally control the generation of microbial-based products by means of interfacial energy.

2. MATERIALS & METHODS

2.1. Bacterial culture and growth conditions

The bacterial isolates used for this study were a gift from Kevin Alby (University of Pennsylvania). We referred to the mucoid and non-mucoid strains of *P. aeruginosa* as PASL (*slimy*) and PANT (*non-slimy type*), respectively. The cells were cultured in Lysogeny broth (LB) medium containing 10 g/L tryptone, 5 g/L yeast extract, and 10 g/L NaCl. PANT cells were grown overnight and PASL cells were grown for 36 h in LB medium with shaking at 200 rpm to obtain cells in stationary phase. Cells were collected by centrifugation for 10 min at 6000 rpm, washed three times, and resuspended in 154 mM NaCl solution before each experiment.

2.2.Electron microscopy

Scanning electron microscopy was employed to analyze the architecture of interfacial films formed by PANT and PASL. The cells were aged on an 8 μL droplet at the hexadecane-water interface for 24 h. The droplet was then collected on a titanium coupon coated with cell adhesive protein Cell-Tak, and fixed in 2.5% glutaraldehyde for 12 h at room temperature. The samples were then washed in 154 mM NaCl solution followed by series of dehydrations in ethanol. The cells were introduced twice in a gradient of 50%, 70%, 90%, and 100% ethanol baths for 15 minutes each. After the final dehydration step, the samples were dried using critical point dryer with 100% ethanol and liquid CO_2 in a Leica Blazer CPD030 (Leica, IL). Imaging was performed using a Zeiss SIGMA 500 VP electron microscope at an operating voltage of 3 kV.

Scanning transmission electron microscopy (STEM) was utilized to analyze the phenotypic changes in cells after exposure to interfaces. Eight μL droplets of cells in hexadecane were aged for a period of 24 h and collected on ultrathin carbon-coated copper TEM grids previously treated with Cell-Tak. The samples were fixed in 2.5 % glutaraldehyde overnight followed by staining with uranyl acetate. High-angle annular dark-field (HAADF) STEM imaging was performed using a ThermoFisher Themis G2 200 S/TEM at an operating voltage of 200 kV and probe current of 51 pA. Under the conditions and magnifications used, no beam-induced damage to the bacteria was observed.

2.3. *Fluorescence Imaging*

Live/dead imaging was performed to evaluate the viability of PANT and PASL exposed to the water-hexadecane interface. Cells were exposed to interfaces through generation of oil in water emulsions. The emulsions were formed by mixing equal volumes of bacterial suspension and oil, which were then combined for 24 h with a gyratory rotation of 60 rpm. Emulsions formed were centrifuged at 15,000 g to separate the free-floating cell from the interfaces. The interfacial films were then stained with Syto-9 and (Live/dead™ Bacteria Viability Kit, Thermofisher Scientific, USA) for 15 minutes, and imaged using a Nikon A1 confocal microscope. Multiple images were acquired for triplicates experiments and the fluorescence intensity for the different channels were measured using ImageJ.

2.4. *Collection of the Interfacial films from a Pendant drop*

Interfacial films were formed by immersing a droplet containing 8 µL of bacteria suspended in 154 mM NaCl into a cuvette filled with 5 mL hexadecane. The bacteria are allowed to form an interfacial film at the interface of oil and water for a duration of 24 h. The droplet is then collected directly on either the titanium coupon for SEM or a carbon coated copper grid for STEM. Excess bacterial suspension was removed from inside the droplet and the film is further processed for imaging under electron microscopy, as described above.

2.5. *Transcriptome Analysis*

PANT and PASL cells exposed to hexadecane-water interfaces for 24 h were collected for total RNA extraction and transcriptomic analysis as previously described[25]. Briefly, PANT and PASL cultures grown in LB broth ($O.D_{600} = 1.5$) were washed and resuspended in 154 mM NaCl. The interfacial films were formed by introducing 10 mL of bacterial suspension to 10 mL of hexadecane in 50 mL glass vials and rotating at 60 rpm for 24 h. The bacterial cells attached to the hexadecane-water interfaces were collected in microcentrifuge tubes followed by centrifugation at 15,000 g for 2.5 min to remove the cells which were not attached to the interfaces.

Interfacial films were transferred to a bead beating vial for RNA extraction. Zirconia/Silica beads (Biospec Products, Bartlesville, OK) of 0.1 mm diameter were used to homogenize the interfacial films in the presence of a RLT lysis buffer (Qiagen, CA, USA) to lyse the cells prior to

RNA isolation. The untreated controls, collected from the overnight culture, were washed three times and resuspended in 154 mM NaCl, then introduced in 50 mL glass vials and rotated at 60 rpm for 24 h. The control samples were centrifuged and homogenized in the presence of lysis buffer prior to RNA isolation.

Total RNA extraction was carried out using the RNeasy Mini Kit (Qiagen, CA USA) following the manufacturer's instructions, and the extracts were measured and analyzed using a Qubit fluorometer (Thermo Fisher Scientific, MA USA) to evaluate the integrity of the nucleic acids. The content of the bacteria-laden interfaces from emulsions made with 25 mL cultures yielded up to 500 μL of total RNA at concentrations of 10–175 ng/μL and an average integrity number RIN=9.5. The RNA extracts were sent to the Microbial Genome Sequencing Center (Pittsburgh, PA USA) to be sequenced using 1x75 bp Illumina kit using the center's protocol (Illumina, WI USA).

The web-based platform Galaxy version 20.05.rc1 at *usegalaxy.org* was used to process the raw sequence reads and perform further analysis of the transcriptional profiles.[33] Briefly, raw reads were initially analyzed for their quality using FastQC version 0.72 and processed with Trimmomatic version 0.38.0 [34]. The trimmed reads were aligned and mapped with BWA version 0.7.17.4 using *P. aeruginosa* PAO1 as reference genome.[35] Last, the gene expression estimates were calculated with FeatureCounts version 1.6.4,[36] and the differential expression of the transcriptional profiles were determined using DESeq2 version 2.11.40.6.[37] The samples were prepared in triplicate for each experimental condition.

2.6.Real-time Polymerase chain reaction (RT-PCR)

To validate the RNA-seq data and evaluate the change in the expression of exopolysaccharide substances, quantitative PCR (RT-PCR) was performed. The relative expression of selected genes from *alginate*, *pel* and *psl* biosynthetic pathways were considered. Relevant primers were designed using NCBI Primer-Blast (Supplementary Information, **Table S1**). For the qPCR experiments, 10 ng of total RNA was reverse transcribed using iScript Reverse Transcription Supermix (Bio-Rad Laboratories, Inc., USA). The experiments were performed using iQ SYBR2x green supermix (Bio-Rad, Laboratories, Inc., USA) and CFX96^{TM} Thermocycler (Bio-Rad).

2.7.Statistical Analysis

All the experiments were conducted at least in triplicates and the standard errors were shown. Both control and interfacial films of mucoid and the non-mucoid strains were compared to each other. GraphPad prism Software (version 9.2.0) (San Diego, CA) was used to conduct t-tests to establish the significance of the percentage of live and dead cells in the control conditions and in the interfacial films of PANT and PASL. Differences with $p < 0.05$ were considered statistically significant. The following notations "ns", *, **, and *** describe statistical difference with *p values* corresponding to $p > 0.05$, $p < 0.05$, $p < 0.001$, and $p < 0.0001$, respectively.

3. RESULTS AND DISCUSSION

3.1.Electron microscopy

To characterize the morphology and film architecture of cells exposed to interfaces, scanning electron microscopy (SEM) imaging was performed on PANT and PASL cells (**Fig. 1**). Control cells were imaged by depositing 8 μL of bacterial suspension on titanium coupon. Interfacial films were obtained with a droplet of 8 μL bacterial suspension held at the tip of a needle immersed in hexadecane. Bacteria were allowed to adsorb to the droplet interface thereby forming an interfacial film which was collected on a titanium coupon after 24 h of interfacial confinement. Our results showed that control PANT cells maintained structural integrity and secreted less amounts of extracellular polymeric materials (**Fig. 1A**). Conversely, upon exposure to the interfaces, PANT cells experience some loss of membrane integrity and surface deformations (**Fig. 1B**). Similar deformation on the cell structure were reported for bacteria treated with reactive oxygen species, nanoparticles and other antimicrobials.[38, 39] Therefore, we anticipate that the interfacial stress might translate to physiological stress in bacteria.

However, the interfacial confinement of the mucoid *P. aeruginosa* cells increased EPS secretions. Unlike the PANT cells, the mucoid cells naturally form a film with a high content of extracellular polymeric materials (**Fig. 1C**). However, under confinement at hexadecane-water interface, a denser EPS matrix is secreted, suggesting that the cells remodel fluid interfaces with the extracellular biomaterials (**Fig. 1D**). *P. aeruginosa* commonly secrete an exopolysaccharide matrix containing bio molecules such including pel (pellicle), psl (polysaccharide synthesis locus), alginate, and some extracellular DNA. The mucoid cells are particularly known for secreting a high amount of alginate. We hypothesize that increase secretion of EPS by PASL cells under interfacial confinement might play a role such as shielding the cells from exposure to interfacial stress.

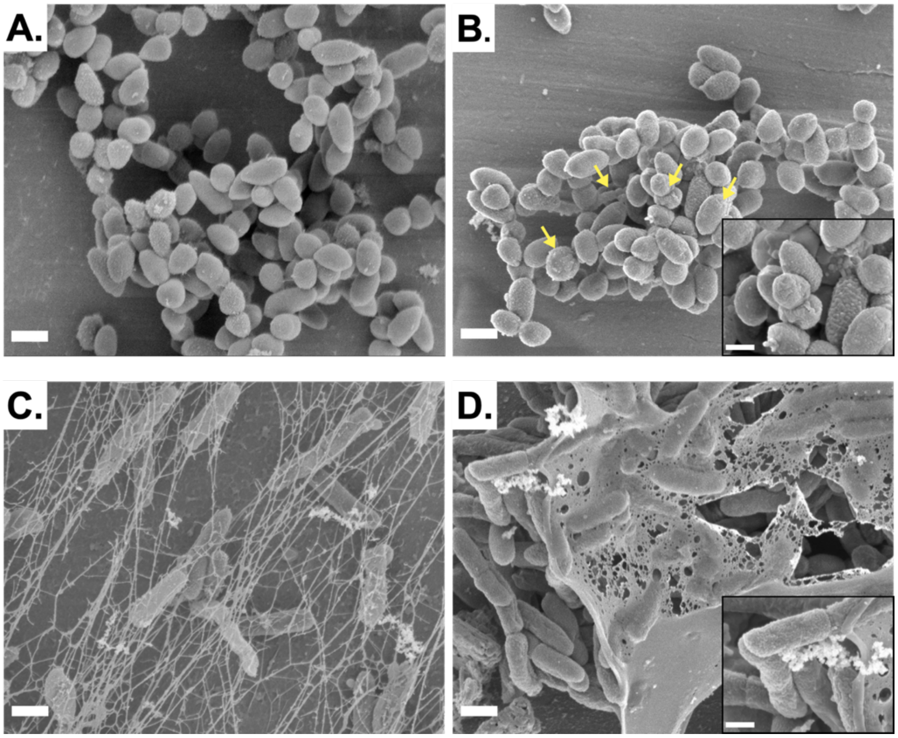

Figure 1. Scanning electron microscopy images showing (A) the control PANT cells; (B) the interfacial film of PANT; (C) the control PASL cells; and (D) the interfacial film of PASL. SB: 1 μm; (Inset SB: 500 nm).

To verify this hypothesis, STEM analyses were performed. The STEM technique negates the impact of dehydration and drying occurring during sample preparation by performing imaging under environmental condition. Further, by combining scanning and transmission microscopy, the structural integrity and the content of cells exposed to the interfacial environment can be assessed. Using STEM, the cell membranes were found to be intact in the control groups of PANT and PASL cells (**Fig. 2A & C**). However, the interfacial entrapment of the cells between hexadecane and water led to significant deformations. Most of the PANT cells were lysed or exhibited major membrane damage as illustrated in **Fig. 2B** and **Fig. 2E**.

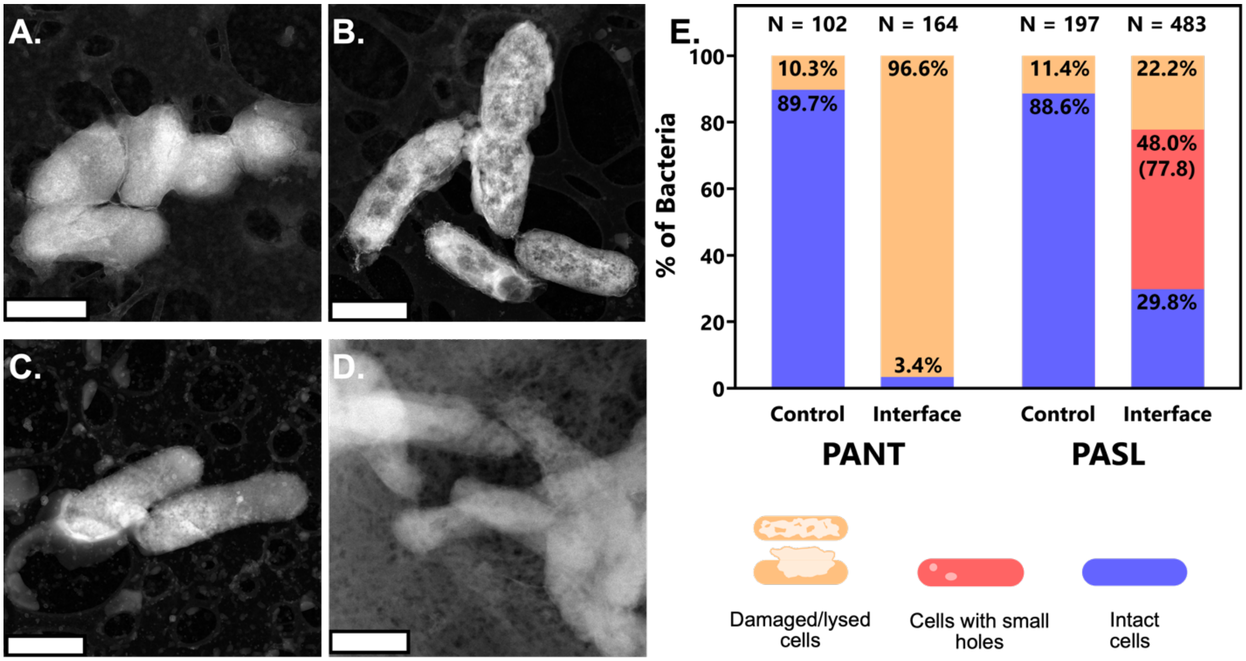

Figure 2. HAADF-STEM images of (A) the control PANT cells; (B) the PANT cells exposed to oil-water interface; (C) the control PASL cells; and (D) the PASL cells exposed to oil-water interface. (E) Proportion of damaged and intact bacteria counted over a large field of view is shown. SB: 1 μm

In contrast, a smaller proportion of PASL cells exhibited major structural damage compared to the control. Instead, the mucoid cells were found to be encased in high amounts of EPS, which presumably acted as a protective coating (**Fig. 2D**). A subset of the PASL cells exhibited minimal membrane damage, which appeared in a form of small holes. The amount of cells presenting membrane damage was quantified in the untreated control and the samples exposed to the interfacial environments (**Fig. 2E)**. Most of non-mucoid cells (~89.7% of 102 PANT cells) were found to be intact and 10.3% cells showed structural damage in the untreated control. However, upon exposure to the interfacial environment for 24 h, 96.6% PANT cells become lysed or exhibited major structural damage, while only 3.4% remained intact (N=164) (supplementary **Fig. S1)**. The mucoid cells had a comparable number of lysed cells in the control samples. Among 197 cells, only 88.6% were found structurally intact. However, a larger proportion of PASL cells exposed to the hexadecane-water interface remain intact. In contrast to PANT cells, 29.8% of PASL cells remained protected from the damaging exposure to interfacial environment, while 48% interfacial PASL cells displayed a partial damage presented as small holes on the cell membrane. These small holes (Supplementary **Fig. S1**) appeared qualitatively different from the structural damage experienced by the lysed PANT cells (**Fig. 2B**). Only 22.2 % of 483 interfacial PASL cells exhibited structural damage following interfacial exposure, which represented twice the proportion of damage cells found in the control mucoid sample. These results indicate that the interfacial environment might be detrimental to bacteria in general, and that the mucoid secretion might act like a protective layer for the mucoid cells.

3.2 Cell viability in interfacial films

To verify that the mucoid film acts as a protective layer to the *P. aeruginosa*, live/dead staining assay was performed to quantify the number of dead cells in all the samples exposed to the interfaces in comparison to the controls. Exponential cells stained with live/dead staining, dead cells stained with live/dead staining and unstained cells were used as imaging controls for confocal fluorescence microscopy (Supplementary **Fig. S2-4**). Emulsions of PANT and PASL cells were prepared by mixing equal parts of cell suspension and hexadecane followed by the application of gyratory motion for a duration of 24 h. Interfacial films were allowed to form on the oil-water emulsions for a duration of 24 h. The emulsions were then collected and centrifuged to separate the film formed at the interfaces. Interfacial films were further stained with live/dead staining kit and characterized using confocal fluorescence microscopy. The control PANT cells showed relatively high number of live cells (in green) compared to dead cells, represented in magenta (**Fig. 3A).** The average fluorescence intensity of the live control PANT cells corresponded to 200 a.u/μm^2, while that of the dead cells, represented in magenta, was significantly lower (*p=0.0035*). On the other hand, the control PASL cells showed comparable amount of live and dead cells (**Fig. 3B**), as demonstrated with the fluorescent intensity shown in **Fig. 3C** (*p*= 0.4048). However, a larger fraction of the non-mucoid films did not survive the interfacial confinement in contrast to the mucoid films (**Fig. 3D, E).** Quantitative analysis of fluorescence intensity compiled from an average of 24 confocal images revealed that the difference in the proportions of live and dead PANT cells embedded in the corresponding interfacial films was not statistically significant (**Fig. 3F**). On the other hand, the majority of the cells embedded in the mucoid film were viable (*p=0.0001*). These observations corroborate with the electron micrographs, which indicate that that stress at interfaces leads to higher damage in the non-mucoid cells compared to mucoid cells (**Fig. 1 & Fig. 2**).

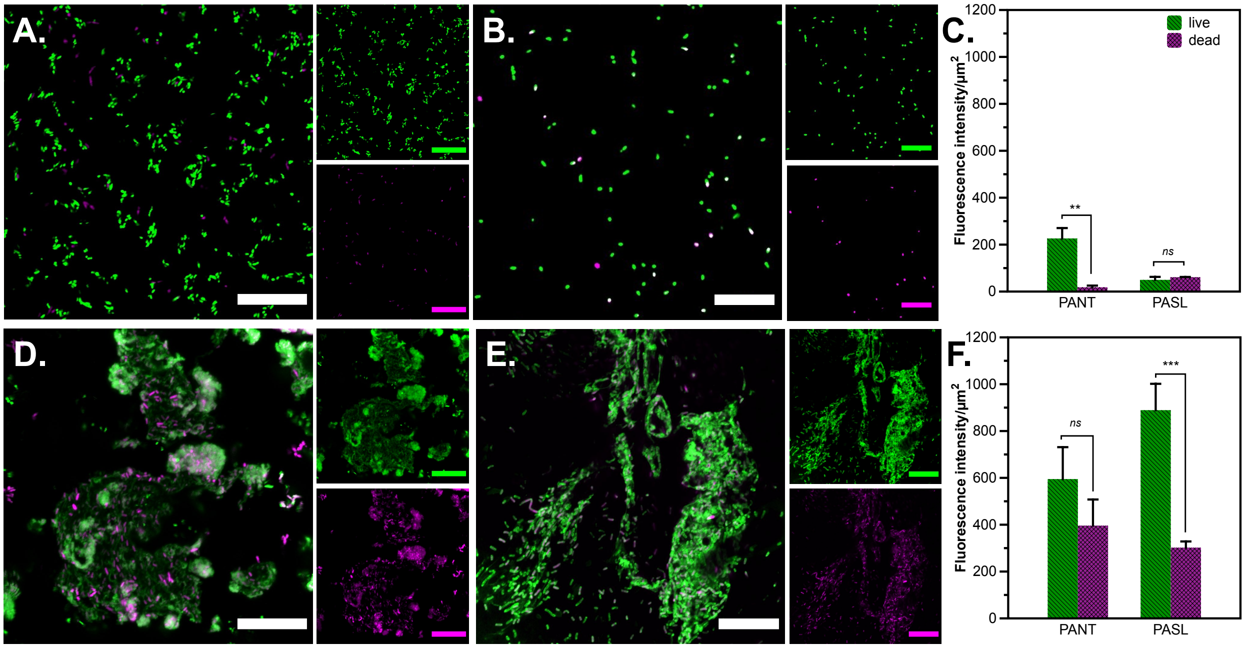

Figure 3. Representative confocal fluorescence images showing the effect of interfacial exposure on cell viability. (A, B) show the confocal microscopy images of control PANT cells and PASL cells respectively. (C) shows the quantitative analysis of the proportion of live and dead cells in control PANT and PASL cells. (D, E) show the confocal microscopy images of interfacial films of PANT and PASL respectively aged for a period of 24 h. (F) shows the quantitative analysis of the proportion of live and dead cells in the interfacial films. SB: 20 μm; (**: $p<0.005$; ***: $p<0.0001$)

3.3 Transcriptomic analysis

The change in the transcriptional profiling of PANT and PASL cells trapped at the oil-water interfaces for a period of 24 h were evaluated through RNA sequencing. The time point of 24 h was chosen for two reasons. First, the nonmucoid cells did not stabilized the oil-water emulsions as rapidly as the mucoid cells. Therefore, to compare both conditions, the emulsions used for RNA extraction needed to be exposed for an extended period, namely for 24 h. Second, the result of live dead staining indicated that a large proportion of both sample groups remain viable after 24 h. Therefore, emulsions for triplicate experiments, and their corresponding controls, were used for RNA sequencing. Gene expression greater than 1.5-fold change and *p value* <0.001 were considered significant. The differential gene expression of cells exposed to interfaces vs. their planktonic counterparts are shown in **Fig. 4.** The genes, which are significantly upregulated and downregulated are shown in blue and red, respectively. The gene expression with a *p value* >0.001 are presented in gray.

The transcriptional change of *P. aeruginosa* cells during interfacial film formation revealed that 38.2% and 40.2% of total genes expressed by PANT cells were significantly upregulated and downregulated, respectively. Interfacial confinement induced major transcriptional changes in PANT cells. A total of 413 genes were induced, and 1089 genes were repressed in PANT after interfacial entrapment at the hexadecane-water interfaces (supplementary **Fig. S6A**, **Table S2**). The most upregulated gene functions, besides hypothetical or unknown functions are transcription, amino acid transport and metabolism, and inorganic ion transport and metabolism (Supplementary **Table S2**). Upon exposure to interfacial environment, PANT cells expressed transcription (145 upregulated, 92 downregulated), amino acid transport and metabolism (112 upregulated, 160 downregulated), and inorganic ion transport and metabolism (95 upregulated, 69 downregulated) genes. A total of 135 genes (47 upregulated, 88 downregulated) involved in the cell wall/membrane/envelope biogenesis were observed in PANT cells exposed to interfaces. In addition, 72 genes (21 upregulated, 51downregulated) involved in replication, recombination and repair are significantly expressed under interfacial confinement.

On the other hand, interfacial confinement resulted in relatively fewer changes in gene expression of PASL cells, suggesting a lower transcriptional activity of the mucoid cells after film formation (Supplementary **Fig. S6B**, **Table S3**). Apart from hypothetical or unknown functions, genes corresponding to transcription (3 upregulated) and translation, ribosomal structure, and biogenesis (3 upregulated) were expressed by PASL cells exposed to interfaces.

The function of the top 10 genes induced or repressed in PANT and PASL cells differ strongly indicating differential metabolic pathways in response to interfacial entrapment at fluid interfaces (**Table 1** and **Table 2**). These results revealed that PANT has an extended response while coping with the interfacial stress compared to PASL cells. Paerucumarin – an iron binding protein involved in the modulation of biofilm formation – is significantly upregulated in PANT cells by 8.1-fold (**Table 1**). PANT cells also upregulated the Type VI pilus biosynthesis protein, which is associated with the Type 6 secretion (T6SS) by 8.2-fold under interfacial exposure (**Table 1**). T6SS is known to be activated by the bacteria subjected to outer membrane perturbations.[40] These results corroborate with our findings from electron microscopy where PANT showed loss in membrane integrity on exposure to interfacial environment. On the other hand, PhoP/Q and low Mg^{2+} inducible outer membrane protein H1 was found to be significantly downregulated by 2116.3

folds in PANT cells exposed to interfaces compared to its planktonic cells. These loss in membrane functions could be associated with the interfacial stress.

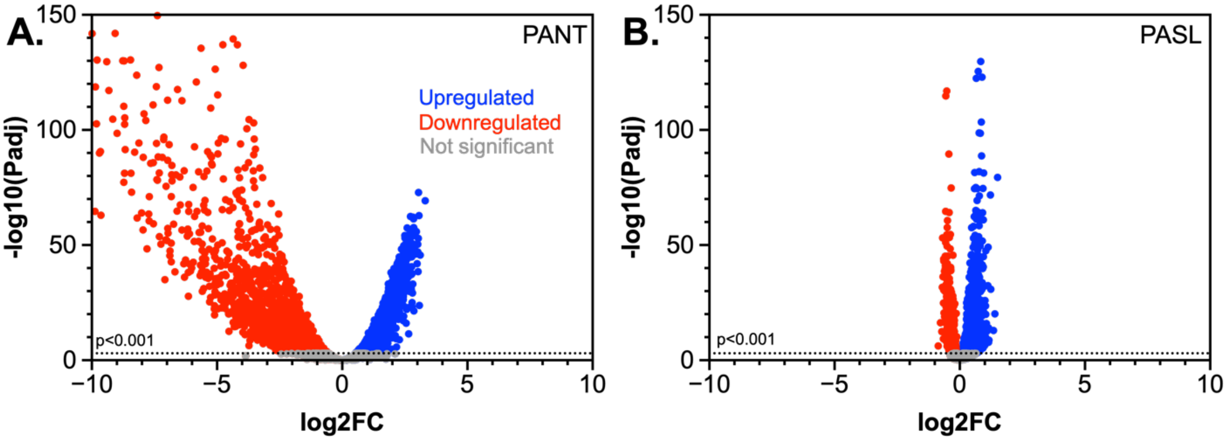

Figure 4: Volcano plots showing differential expression of genes between the planktonic cells and cells isolated form interfacial films of PANT and PASL analyzed by RNA sequencing (A) shows PANT cells; (B) shows PASL cells. $p<0.001$and a fold change of greater than 1.5 was considered significant. Significantly upregulated genes are indicated in blue and significantly downregulated genes are shown in red. The genes that did not show any significance are shown in gray.

While PANT cells exposed to interfaces expressed distinct genes compared to the planktonic cells, this was not the case in PASL cells. After interfacial exposure, no major differences were observed between the exposed PASL cells and the planktonic cells. *AlgU*, which is inherently upregulated in the mucoid phenotype, was also upregulated by 2.8-fold in PASL cells exposed to interfaces (**Table 2**). Cell division proteins and other ATP-dependent proteins were found to be upregulated in PASL cells exposed to interfaces. No significant downregulation of genes with fold change greater than 2 was observed in PASL under interfacial confinement for 24 h (**Table 2**).

From our complementary microscopic assessment (**Fig. 1-3**), we anticipated that the ability of cells to survive the interfacial environment strongly depended on their EPS secretions. Therefore, we analyzed the three major components of EPS in *P. aeruginosa*- alginate, pel and psl. The differential expression of alginate, pel and psl were analyzed to determine the effect of interfacial exposure on EPS secretions of mucoid and non-mucoid cells compared to their planktonic counterparts. Real time qPCR was also performed on selected genes from the biosynthetic pathways of alginate, pel and psl to validate the results obtained from RNA sequencing at the end of 24 h.

Alginate is the major exopolysaccharide produced by the mucoid strains, specifically the strains isolated from the lungs of CF patients. [41] Alginate protects the cells from harsh environment in the lungs of CF patients. It provides structural stability, helps in water and nutrient retention, resistance to antibiotics and opsonophagocytosis. [42-45] Thirteen alginate proteins are speculated to form a complex spanning through the inner membrane, periplasm, and the outer membrane of the cell. [46] Under interfacial confinement, PANT cells upregulated six of these 13 genes involved in the alginate biosynthetic pathway- *algI, algL, algX, algK, algJ, alg44* and downregulated four genes *algU, algR, algP, algQ* (Supplementary **Fig. S5**). This finding is not surprising since it has been demonstrated that alginate production is an induced response in *Pseudomonas* under environmental stress allowing bacterial survival and growth.[47, 48] Still, the mechanism and environmental factors responsible for conversion to mucoidy and alginate biosynthesis are not fully understood. AlgK, which acts as a scaffold protein and aids in the assembly of periplasmic components of the alginate biosynthetic pathway[46], was upregulated by PANT cells exposed to interfaces. In *P. aeruginosa*, alginate synthesis starts with the formation of a linear polymer of D-mannuronic acid units by the enzymes AlgA, AlgC, and AlgD. The monomeric units undergo polymerization using cytoplasmic membrane proteins Alg8 and Alg44. These two proteins are shown to be necessary for alginate production. [49, 50] The gene, *alg44* was found to be upregulated in PANT cells exposed to interfaces. Ploymannuronic acid from the inner membrane proteins is next modified to mature alginate polymer in the periplasm by O-acetylation complex. This O-acetylation complex is made up of the proteins AlgI, AlgJ, and AlgF; the epimerase AlgG; and AlgX protein, which has a potential role in alginate polymer modification. [51] Genes *algJ*, *algI*, and *algX* belonging to the O-acetylation complex were found to be upregulated in the PANT cells exposed to interfaces. The alginate polymer is later epimerized by *algG*, which converts the D-mannuronic acid units into L-guluronic acid units.

Reports have shown that mutants lacking *algK* compromised the localization of AlgE on the outer membrane of the bacteria [52, 53]. Most of these genes are associated with the late-stage alginate production. Based on the phenotypical assessment of PANT and PASL, we hypothesized that the slimy-mucoid phenotype exhibited by PASL resulted from alginate overproduction, contrasting with PANT, which showed a non-mucoid-like phenotype. Our results indicate that, at the interface PASL overexpressed alginate regulatory genes and genes involved with the production of alginate precursors (Supplementary **Fig. S5**). Specifically, PASL highly upregulated *algU. AlgU* is one of the main RNA polymerase sigma factors responsible for inducing alginate biosynthesis. In fact, *algU* participates in the mucoid switch widely described in *Pseudomonas*.[54] *AlgU* is sequestered by *mucA* in the non-mucoid phenotypes. Mutations in *mucA* can no longer sequester *algU* which binds to alginate biosynthetic operon, *algD* switching to a mucoid phenotype.

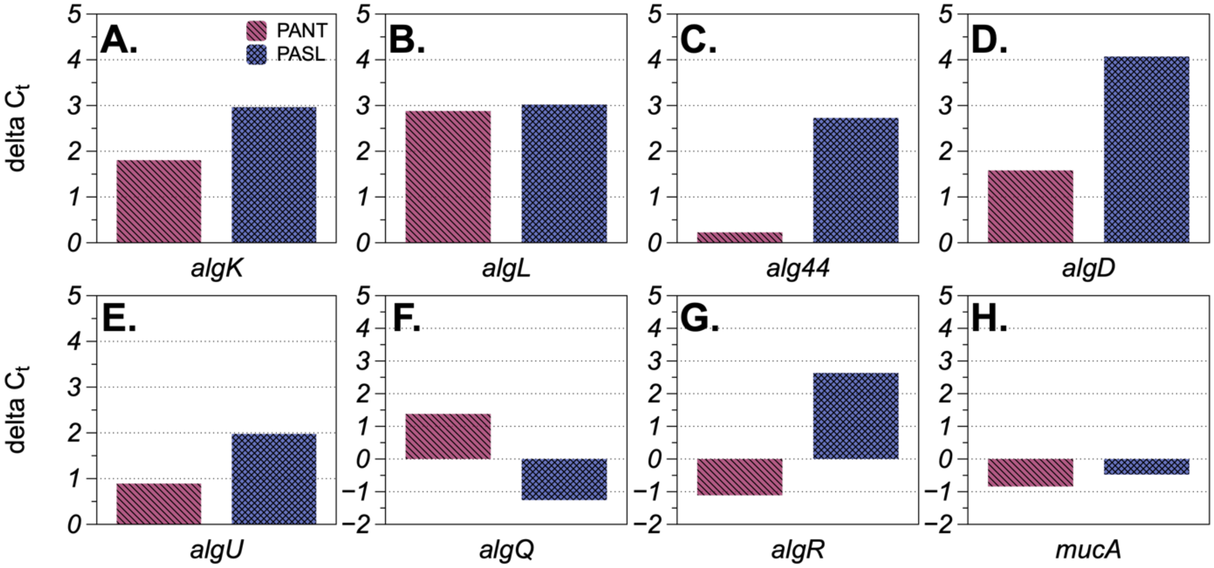

Figure 5: Gene expression analysis for alginate biosynthetic pathway using qPCR. Average delta Cq values of genes expressed by the cells exposed to interfaces vs. control cells are shown above (A.) *algK* (B.) *algL* (C.) *alg44* (D.) *algD* (E.) *algU* (F.) *algQ* (G.) *algR* and (H.) *mucA*.

The data obtained from RNA-seq were further validated using RT-PCR to characterize the expression of genes involved in alginate biosynthetic pathway (*algK, algL, alg44, algD,* and *algU).* In interfacial PANT cells, *algK, algL, alg44, algD, algU,* and *algQ* genes were upregulated compared to control PANT **(Fig. 5 A-F)** whereas in interfacial PASL cells, *algK, algL, alg44, algD, algU,* and *algR* genes were upregulated compared to control PASL (**Fig. 5 A-E, G)**. On the other hand, *algR* and *mucA* genes were downregulated in PANT cells at interfaces (**Fig. 5 G & H)** whereas *algQ* and *mucA* genes were downregulated in PASL cells at interfaces (**Fig. 5 F & H)**. Although, mRNA expression data from RT-PCR and RNA-seq data are not always overlapping, RT PCR data suggest adaptive behavior of PANT in response to interfacial stress.

Pel polysaccharide is mainly responsible for the ability of cells to form pellicles at the air-water interfaces. It is a glucose rich polysaccharide and is synthesized by the pel gene cluster (*pelA-F*).

Pel is also found to contribute to the biofilm formation supporting the psl and alginate polymers. In PA14 cells pel is shown to be responsible for cell-cell interactions and for providing antibiotic resistance.[55] *PelD* and *pelE*, which are involved in the transportation of pel through the inner membrane, were found to be upregulated in PANT cells exposed to interfaces. Ueda *et al*,[56] have shown that PelD is essential to produce pel polymer and is functionally similar to Alg44 from the alginate biosynthetic pathway. The genes encoding the outer membrane proteins PelB and PelC and which are expected to be involved in the transport of pel polymer out of the cell are upregulated by the PANT cells under interfacial confinement (Supplementary **Fig. S5**). Finally, PelA – involved in the feedback mechanism to control the synthesis of pel polymer – is also found to be upregulated by PANT cells.

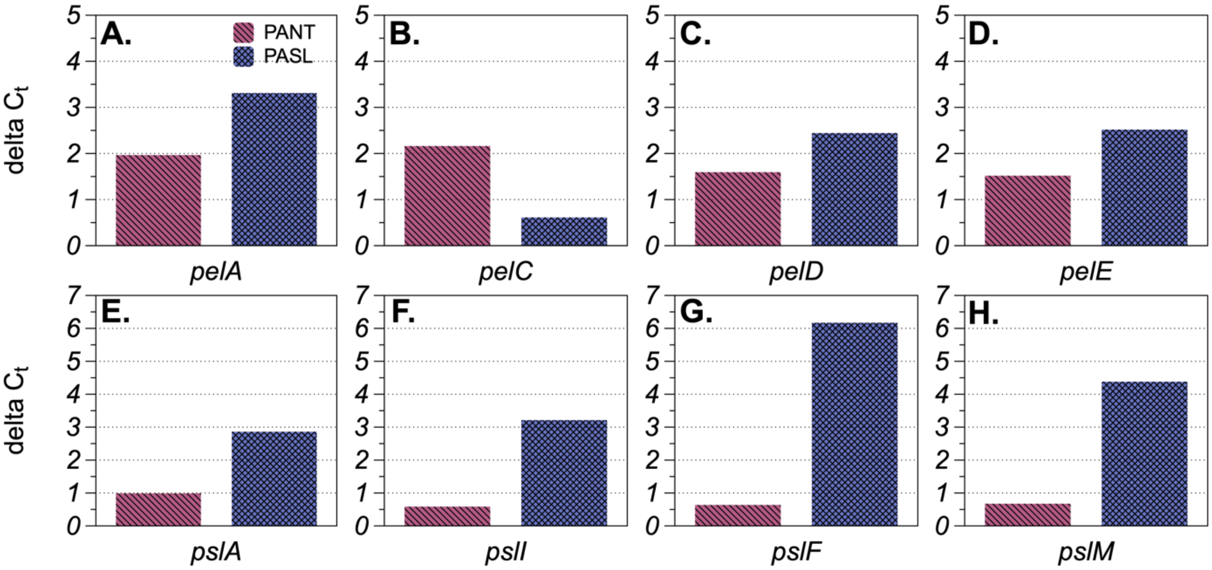

Figure 6: Gene expression analysis using qPCR. Average delta Cq values of genes expressed by the cells exposed to interfaces vs. control cells are shown above (A.) *pelA* (B.) *pelC* (C.) *pelD* (D.) *pelE* (E.) *pslA* (F.) *pslI* (G.) *pslF* and (H.) *pslM.*

In order to validate the expression of *pel* genes in PANT and PASL cells exposed to interfaces, RT-PCR analysis was performed on selected pel genes- *pelA, pelC, pelD* and *pelE* expressing proteins at different stages of pel biosynthetic pathway. Interestingly, both the PANT and PASL cells exposed to interfaces overexpress *pel* genes (**Fig. 6 A-D**). Furthermore, PASL cells showed relatively higher magnitude of upregulation of three of the four *pel* genes compared to PANT cells. Specifically, average differential Ct values of *pelA, pelD* and *pelE* expression in PASL cells were 1.6, 1.5, and 1.6 times higher than PANT cells. However, *pelC* expression in PASL showed about four times decrease in the differential Ct value compared to PANT cells. The overexpression of pel genes *(pelA, pelD* and *pelE)* indicates survival adaptation of PASL cells to interfacial stress by increasing the secretions of exopolysaccharide such as pel. In our analysis, all the *pel* genes tested were found to be upregulated by the PANT and PASL on interfacial exposure. *pelA, pelD* and *pelE* genes showed relatively higher expression in PASL cells compared to PANT cells. On the other hand, *pelC* was highly expressed in PANT compared to PASL cells. *P. aeruginosa* isolates from CF patients are known to show varying expressions of EPS owing to multiple mutations.[55] Recently, it has been reported that clinical isolates and *P. aeruginosa* grown in CF media form aggregates, and are associated with the secretion of pel and psl components.[57, 58] Thus, the growth environment of these bacteria determined their EPS composition. The upregulation of *pel* genes in PANT and PASL observed in our results can be attributed to the response of these cells to interfacial stress.

Table 1. Top 10 genes induced or repressed in PANT Interface vs. Control

Gene	**Description**	**Fold Change**
Upregulated		
PA2098	esterase	9.9
PA2092	major facilitator superfamily transporter	8.7
PA2161	hypothetical protein	8.5
PA1977	hypothetical protein	8.4
PA1497	transporter	8.3
PA1981	hypothetical protein	8.2
xphA	type VI pilus biosynthesis protein	8.2
PA2163	4-alpha-glucanotransferase	8.1
pvcD	paerucumarin biosynthesis protein PvcD	8.1
PA1701	hypothetical protein	7.9
Downregulated		
oprH	PhoP/Q and low Mg2+ inducible outer membrane protein H1	-2116.3
rplX	50S ribosomal protein L24	-1261.7
rpmJ	50S ribosomal protein L36	-1133.6
rplJ	50S ribosomal protein L10	-1102.7
rpmI	50S ribosomal protein L35	-1072.8
PA4739	hypothetical protein	-1052.4
PA4738	hypothetical protein	-1033.7
PA4463	hypothetical protein	-1018.6
rplW	50S ribosomal protein L23	-941.7
PA5482	hypothetical protein	-940.6

Table 2. Top 10 genes induced or repressed in PASL Interface vs. Control

Gene	**Description**	**Fold Change**
Upregulated		
algU	RNA polymerase sigma factor AlgU	2.8
PA2621	ATP-dependent Clp protease adapter protein Clp	2.6
ftsL	cell division protein FtsL	2.4
atpI	ATP synthase subunit I	2.2
clpP	ATP-dependent Clp protease proteolytic subunit	2.2
PA2737	hypothetical protein	2.2
PA0941	hypothetical protein	2.1
rpsL	30S ribosomal protein S12	2.1
PA4430	cytochrome b	2.1
nusG	transcription antitermination protein NusG	2.1
Downregulated		
PA2667	hypothetical protein	-1.8
PA2161	hypothetical protein	-1.7
mdcC	malonate decarboxylase acyl carrier protein	-1.6
PA0073	ABC transporter ATP-binding protein	-1.6
PA0072	hypothetical protein	-1.6
tonB2	transporter TonB	-1.6
PA1711	hypothetical protein	-1.6
PA0168	hypothetical protein	-1.6
PA1908	major facilitator superfamily transporter	-1.6
PA0150	transmembrane sensor	-1.6

The role of Polysaccharide synthesis locus (Psl) in biofilm formation is establishing cell-surface and intercellular adhesion. Psl cluster consists of 15 genes out of which pslA, pslB and pslD are found to be crucial in psl synthesis. [59, 60] In vivo studies have shown that psl provides survival advantage and targeting psl could eliminate persistent infections.[61] Other studies have also reported the role of psl in antibiotics resistance.[62] Therefore, psl not only provides biofilm structure but also has a role in providing survival advantage to *P. aeruginosa* and aids in colonizing different environments. Our results showed that the genes involved in the earlier stages of synthesis of psl polymer are upregulated by PANT cells exposed to interfaces. PslF, PslI, PslH, and PslC are predicted to be involved in the synthesis of precursor repeating units for psl polysaccharide. Two (*pslJ* and *pslK*) out of the five genes that are likely to make up the polymerization complex of psl are found to be upregulated by the *P. aeruginosa* cells (Supplementary **Fig. S5**). However, *pslD*, which is likely to be involved in the transport of the polymer through and out of the periplasmic space, did not show any significant differences in expression.

RT-PCR analysis was performed on selected psl genes- *pslA, pslI, pslF* and *pslM* expressing proteins at different stages of psl biosynthetic pathway[46]. Interestingly, both the PANT and PASL cells exposed to interfaces exhibited higher expression of *psl* genes (**Fig. 6 E-H**). Furthermore, PASL cells showed relatively higher upregulation of *psl* genes compared to PANT cells. Specifically, average differential Ct values of *pslA, pslI, pslF,* and *pslM* expression in PASL cells were 3–12 times higher than PANT expression of these genes. Such overexpression of *psl genes* indicates survival adaptation of PASL cells to interfacial stress by increasing the secretions of exopolysaccharides. Psl is generally found to be expressed in clinically isolated mucoid strains to protect against opsonization and complement activation.[63] Our results indicated that, *psl* genes were not only upregulated by the mucoid strain PASL, but also found to be upregulated by the nonmucoid strain PANT on interfacial exposure. These results further suggest that *Pseudomonas* upregulates the expression of EPS components under interfacial confinement.

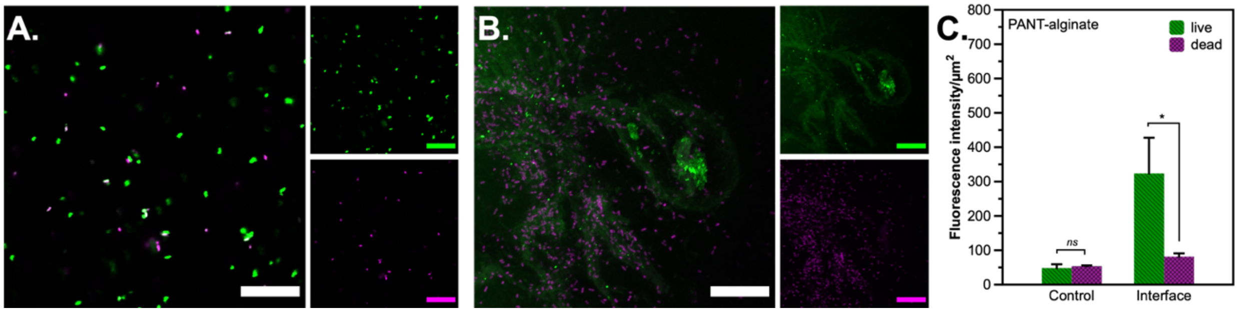

Figure 7. Representative confocal fluorescence imaging showing cell viability in the presence of alginate. (A) shows the confocal microscopy images of control PANT cells suspended in 5 mg/mL of alginate solution. (B) shows the confocal images of interfacial films of PANT suspended in alginate and exposed to hexadecane interfaces for a period of 24 h. (C) shows the quantitative analysis of proportion of live and dead cells in both the above conditions. SB: 20 μm (*: $p<0.05$).

To test the hypothesis that the EPS secretions provide growth advantage to bacteria at interfaces we performed confocal imaging of non-mucoid cells suspended in 5 mg/mL alginate solution. The concentration of alginate is chosen based on our previous reports, which demonstrate an improved mechanical properties of the resulting interfacial film.[30] Briefly, PANT cells were suspended in alginate and exposed to interfacial environment for a period of 24 h to form interfacial films. The control cells and the interfacial films are collected and stained using Syto-9 and propidium iodide to quantify the amount of live and dead cell population. Our results showed the proportion of live and dead cells remained similar on exposure to alginate in the control cells as shown in **Fig. 7 A**

& C. Conversely, alginate coating improved the viability of PANT cells under interfacial confinement (**Fig. 7B & C).** These results further strengthen our conclusion that mucoid coating composed of alginate, pel and psl biomaterials act as a protective layer that shield and allow *P. aeruginosa* to survive interfacial environments.

4. CONCLUSIONS

This study determined the effect of interfacial stress on the physiological changes of mucoid and non-mucoid cells on exposure to interfacial environment. The differential gene expression of mucoid and non-mucoid cells exposed to the interfacial environment were also evaluated. Our results showed that mucoid cells are better equipped to survive the interfacial environments compared to non-mucoid cells due to their ability to produce high amounts of EPS. Morphological characterization using electron microscopy showed that mucoid cells were enclosed in a polymer case that acted as a barrier to help shield the bacteria from interfacial stresses, enhancing survival. Lacking this protective layer, non-mucoid cells near-universally experienced extensive structural damage and lysing. Confocal imaging supported our electron microscopy findings, non-mucoid cells exhibiting a higher proportion of dead cells compared to mucoid cells at oil-water interfaces. When the non-mucoid cells are supplemented with alginate, high proportionof cells are found to be live in the interfacial films indicating that mucoid coating supports cell viability. To understand the gene expression of cells under these stressful environments, RNA sequencing was performed on mucoid and non-mucoid cells and compared to their respective planktonic cells. Transcriptomic analysis of the cells revealed that non-mucoid cells upregulated many genes involved in the EPS production especially in the alginate biosynthetic pathway. Gene expression of selected genes from RNA-sequencing analysis were also confirmed using qPCR analysis. On the other hand, no significant differences in the gene expression were observed in the mucoid cells upon exposure to interfaces. Overall, our results indicated that the non-mucoid cells experience extreme stress and thereby upregulate the genes involved in the EPS production to alter their phenotype into one more equipped to survive the interfacial environments.

Supporting information

Primer design; STEM analysis of interfacial films; Fluorescence microscopy of the Controls; Transcriptomic analysis of PANT and PASL cells

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Author Contributions

The manuscript was written through the contributions of all authors. All authors have given approval to the final version of the manuscript.

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Notes

The authors declare no competing financial interest

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Supplementary Information for

Mucoid Coating Provides a Growth Advantage to *Pseudomonas aeruginosa* at Oil-Water Interfaces

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In this supplementary information, we include additional information of primer sets used in RT-PCR studies to determine the mRNA expression. We also include supplementary STEM figures contrast the morphological change in the non-mucoid and the mucoid *P. aeruginosa* cells following interfacial confinements. The volcano plots showing differential gene expression of *alginate*, *pel* and *psl* genes in PANT and PASL are discussed. The number of genes which showed a fold change of greater than 2 folds and which are upregulated and downregulated are represented based on functions. Controls for the confocal imaging are discussed in Fig. S4-6. The total list of genes which showed a fold change of greater than 2-fold and a false discovery rate (p<0.01) for PANT and PASL are listed in Table S2-3 and Table S4 respectively.

1- Primer design

Table S1: List of primers used in RT-PCR experiments

Gene	Primer	Primer sequence	Gene	Primer	Primer sequence
rplU	Forward	CGCAGTGATTGTTACCGGTG	***pelA***	Forward	CCTTCAGCCATCCGTTCTTCT
	Reverse	AGGCCTGAATGCCGGTGATC		Reverse	TCGCGTACGAAGTCGACCTT
algU	Forward	AAGACGATTCGCTGGGACGCT	***pelC***	Forward	GACCACGTAGGCCAGCTTC
	Reverse	AACGCAGCCGGCATCCTCG		Reverse	GCCGCTGCTCAATTATTCCC
algD	Forward	GCGACCTGGACCTGGGCT	***pelD***	Forward	ACTCGAAGGCATACAGGCAG
	Reverse	TCCTCGATCAGCGGGATC		Reverse	GCCGTTCTTCGTCTTCAACG
algR	Forward	TAGGGCAACTGGACGGCTAT	***pelE***	Forward	CGTCGCTGAACATCATGTCG
	Reverse	CGGATATCCAGCAGGACGA		Reverse	TCTTCAGCCTGGCCTTCTTC
algQ	Forward	TATCTCGGCTTCTCCATCGT	***pslA***	Forward	TTCAAGATCAAGCGCATCGTGGTG
	Reverse	GGGGGATCCTTCGAGATCGACCTGCTG		Reverse	GGGGGATCCTTCGAGATCGACCTGCTG
alg44	Forward	CCCAACCAGCAGATCACCAT	***pslI***	Forward	TCGACCTGTACATCAGCACC
	Reverse	AGAGCTTCTCGATGTTGCCC		Reverse	CTGACCCGATAGACCAGTGC
algL	Forward	TCGACGACGAGGAAACCTTC	***pslF***	Forward	GCCATCGACTGGAACCTGAA
	Reverse	CTTCTTCGCCTCGAGCATCT		Reverse	CCGAGCAGACCGAGTTTCTT
algK	Forward	CTACTACGACGGCAAGTGGG	***pslM***	Forward	GAGGAGGACATCGAGCAACC
	Reverse	TTCTGCGGATAGACCTTGCC		Reverse	CTCGAAGAAGGCCACCATGT
mucA	Forward	GCGGATGAACTCGAGTTG			
	Reverse	CACTGACGGCGGATTGTT			

2- STEM analysis of the Interfacial films

Scanning transmission electron microscopy (STEM) was utilized to analyze the phenotypic changes in cells after exposure to interfaces. Eight μL droplets of cells in hexadecane were aged for a period of 24 h and collected on ultrathin carbon-coated copper TEM grids previously treated with Cell-Tak. The samples were fixed in 2.5 % glutaraldehyde overnight followed by staining with uranyl acetate. High-angle annular dark-field (HAADF) STEM imaging was performed using a ThermoFisher Themis G2 200 S/TEM at an operating voltage of 200 kV and probe current of 51 pA. The results shown in **Fig. S1A** demonstrate that most of the *P. aeruginosa* PANT cells experienced membrane damage at fluid interface and released cell content. On the other end, the PASL cells were covered by exopolysaccharide matrix, which acted as a shield against the interfacial stress. Consequently, a smaller number of the PASL cells experienced membrane damage (**Fig. S1B**).

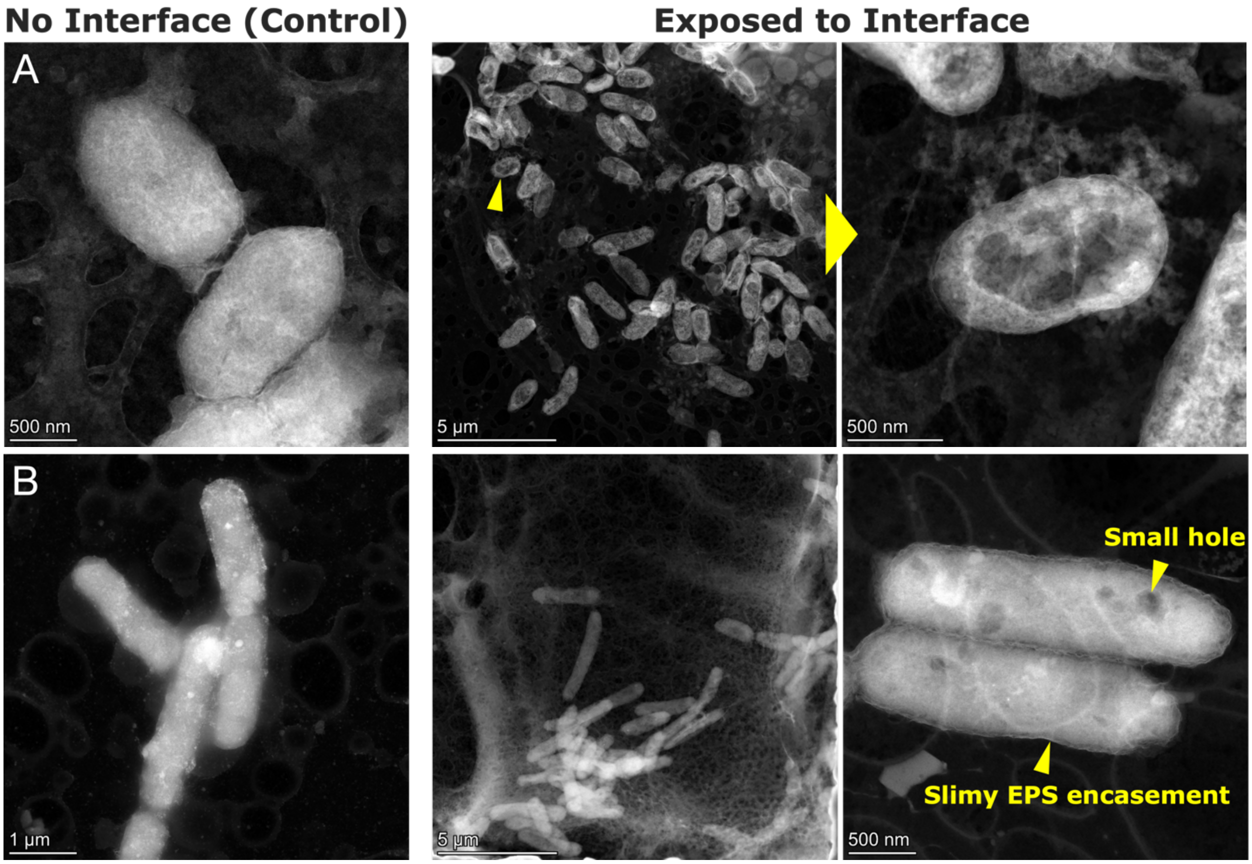


Figure S1: HAADF-STEM images of (A) control PANT cells and (B) the PASL cells are compared to their counterparts exposed to oil-water interface. The interfacial confinement severely damaged the membrane properties of the PANT cells. In contrast, PASL secreted an EPS matrix that contributed to lessening the detrimental effects of the interfaces.

3- Fluorescence microscopy of the Controls

To establish the staining procedures followed by confocal imaging, live-dead staining was performed on PANT and PASL cells derived from the exponential phase and cells subjected to thermal shock (dead cells). To confirm the absence of autofluorescence, cells were imaged without exposure to any stain. Syto-9 and propidium iodide (Live-dead staining kit) were used to stain the live and dead cells respectively.

i. Exponential cells (control):

Exponential phase cells of PANT were obtained by culturing the bacteria for a duration of 12 h. PASL cells were grown for a duration of 15 h to obtain the cells from exponential phase. The four image panels represent the live cells (in green), dead cells (in magenta), merged panel with live and dead cells and BF (brightfield). The bar plots to the right represent the quantitative analysis of fluorescence intensity of live and dead cells using imageJ.

As expected, the exponential phase cells of PANT (**Fig. S2A**) and PASL (**Fig. S2B**) showed relatively higher proportion of live cells compared to the dead cells.

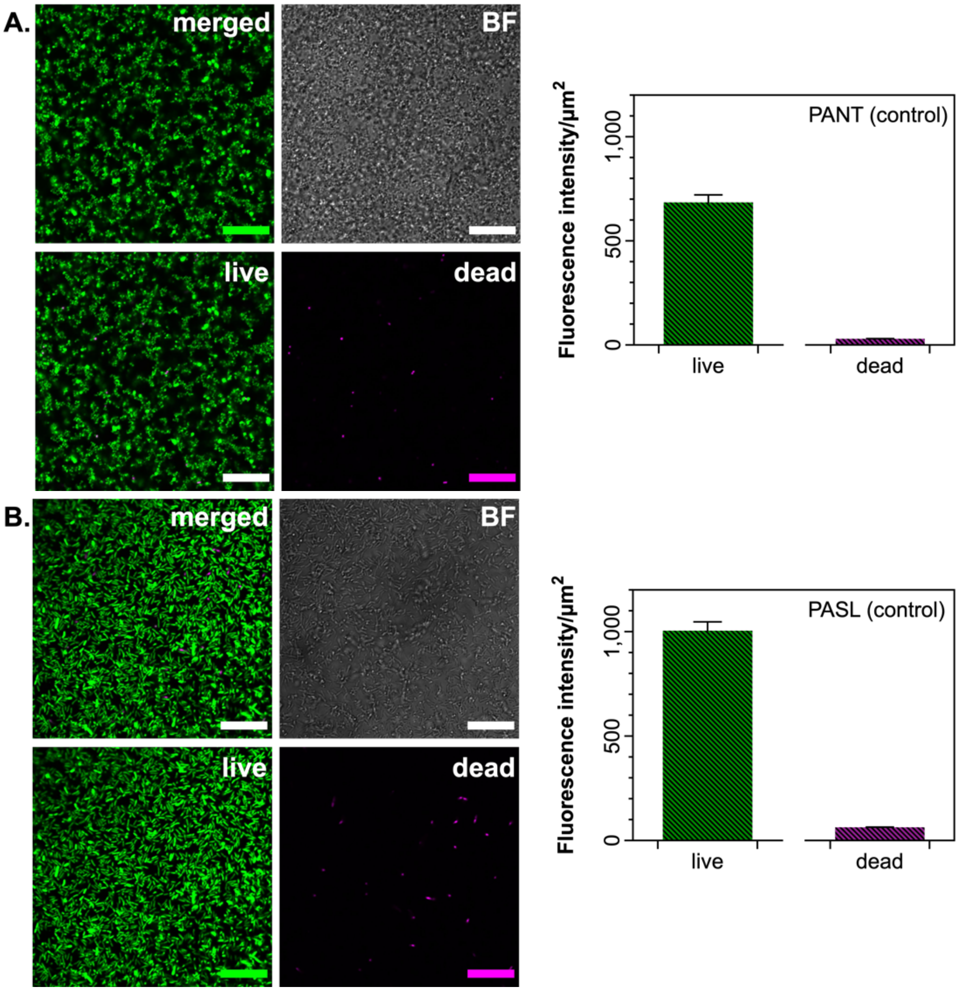


Figure S2: Live-dead staining of exponential cells of (A) PANT (B) PASL. PANT cells were grown for a period of 12 h and PASL cells were grown for a period of 15 h to reach exponential phase. Scale bar: 20

ii. Positive control:

Control for the dead cells were obtained by subjecting PANT and PASL cells to thermal shock at 80°C for a duration of 40 min. Subsequently, the cells were stained to analyze the quantity of live and dead cells in the samples. As mentioned above, the four image panels represent the live cells (in green), dead cells (in magenta), merged panel with live and dead cells and BF (brightfield). The bar plots to the right represent the quantitative analysis of fluorescence intensity of live and dead cells using imageJ. Our results showed that, thermal shock killed majority of cells which are stained with propidium iodide in magenta for both PANT (**Fig. S3A**) and PASL cells (**Fig. S3B**). This condition was performed to establish a positive control for the dead cells.

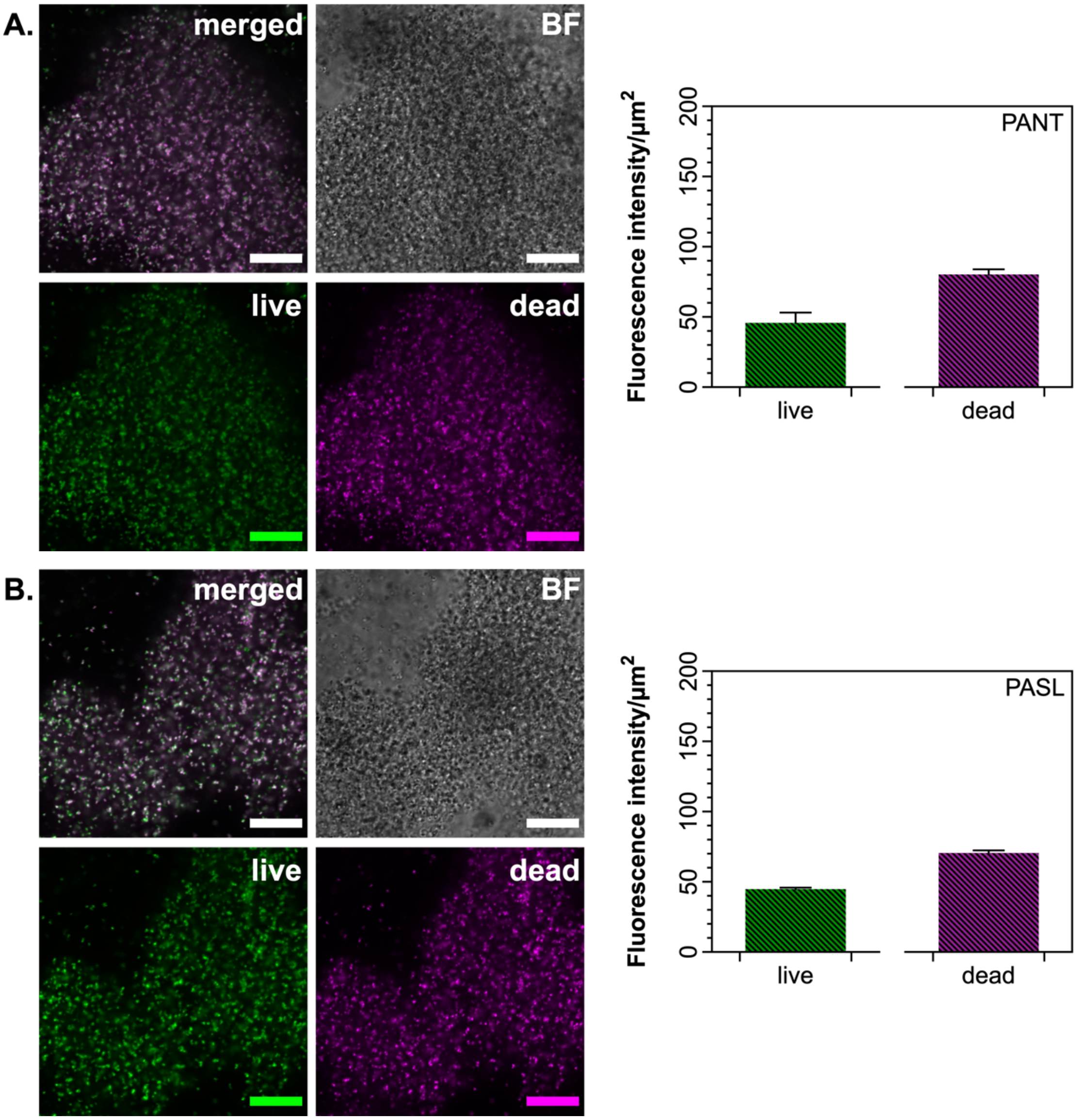


Figure S3: Live-dead staining of cells subjected to thermal shock (A) PANT (B) PASL. PANT cells were grown for a period of 12 h and PASL cells were grown for a period of 15 h to reach exponential phase. Here, thermal shock was used to kill the cells for positive control.

iii. No stain control:

To determine the autofluorescence from the samples at the imaging conditions, no stain control was analyzed. The data are represented below in **Fig. S4**. The top panel represents BF (brightfield), live and dead PANT cells. The bottom panel represents BF (brightfield), live and dead PASL cells. No auto fluorescence was observed at the imaging conditions in both the panels.

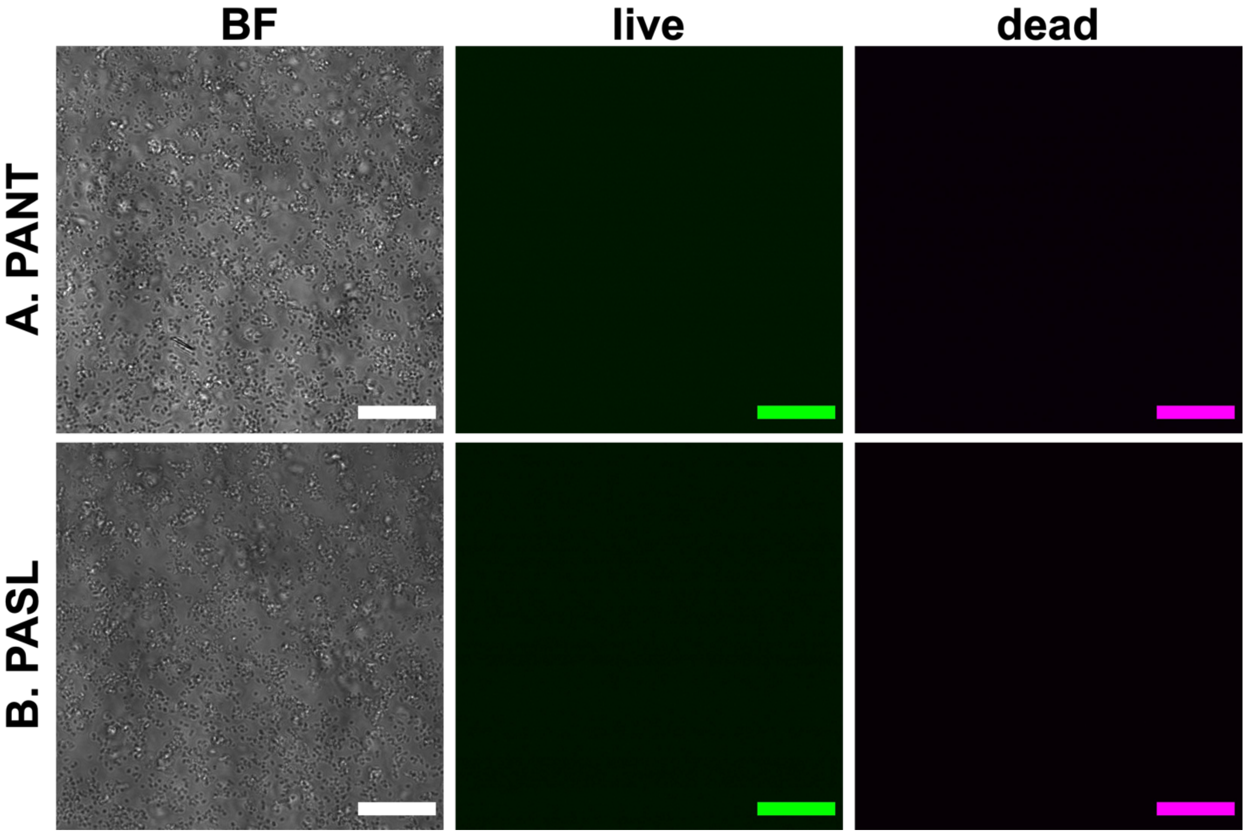


Figure S4: Representative confocal images of non-florescent *P. aeruginosa* (A) PANT (B) PASL. No fluorescent recorded through imaging of cells.

4- Transcriptomic analysis

Transcriptional profiling of PANT and PASL cells exposed to interfacial environment for a period of 24h was performed to determine differential gene expression on exposure to interfaces vs their planktonic counterparts. Our initial results from microscopic techniques (**Fig. 1-3**) revealed that cell viability at interfaces strongly depended on their EPS composition. Alginate, *pel* and *psl* are the three main extracellular polymeric substances (EPS) constituting the films of *Pseudomonas aeruginosa*. Therefore, gene expression of alginate, *pel* and *psl* genes was analyzed using RNA-seq. analysis as described in section 2.5. The genes that are significantly upregulated are shown in blue and the genes that are significantly downregulated are shown in red. The genes that did not show any significant differences are shown in grey. Transcriptomic analysis showed that PANT upregulated 6 genes (*algI, algL, algX, algK, algJ, alg44*) and downregulated 4 genes (*algU, algR, algP, algQ*) involved in alginate biosynthetic pathway (**Fig. S5A**). The genes upregulated are found to be involved in the later stages of alginate biosynthetic pathway[1]. PASL also showed upregulation of 3 genes (*algU, algZ and algR*) and downregulation of 3 genes (*algJ, alg44, algE*) (**Fig. S5D**). Interestingly the differential expression of alginate genes by PANT and PASL on interfacial exposure indicates that these two strains do not regulate the alginate biosynthetic pathway similarly on interfacial exposure. Pel genes *pelA, pelB, pelC* and *pelE* were also upregulated by PANT cells under interfacial confinement (**Fig. S5B**). On the contrary, PASL cells downregulated *pelB, pelC* and *pelE* genes along with *pelD* and upregulated *pelG* on interfacial exposure (**Fig. S5E**). *pslH*, *pslF, pslM, pslN, pslK* and *pslI* of the *psl* biosynthetic pathway were upregulated by PANT cells whereas *pslH*, *pslF, pslM, pslK, pslI and pslJ* were downregulated by PASL cells on interfacial exposure (**Fig. S5C&F**). *pslA,* the precursor component necessary for *pslI* synthesis was found to be upregulated by PASL cells on interfacial exposure. Similar results were obtained for pel and psl genes when tested using qRT-PCR. However, RNA-seq. indicated that PASL cells downregulated *pel* and *psl* genes on interfacial exposure which is complementary to our results from qRT-PCR where PASL genes upregulated the expression of *pel* and *psl* genes.

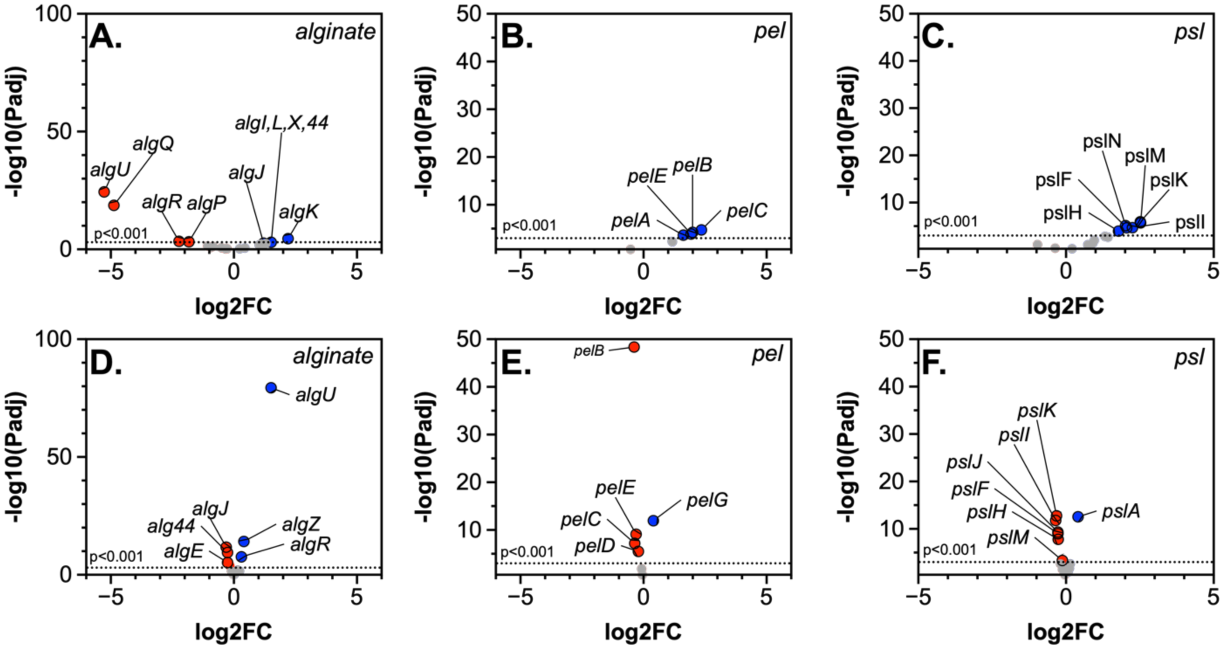
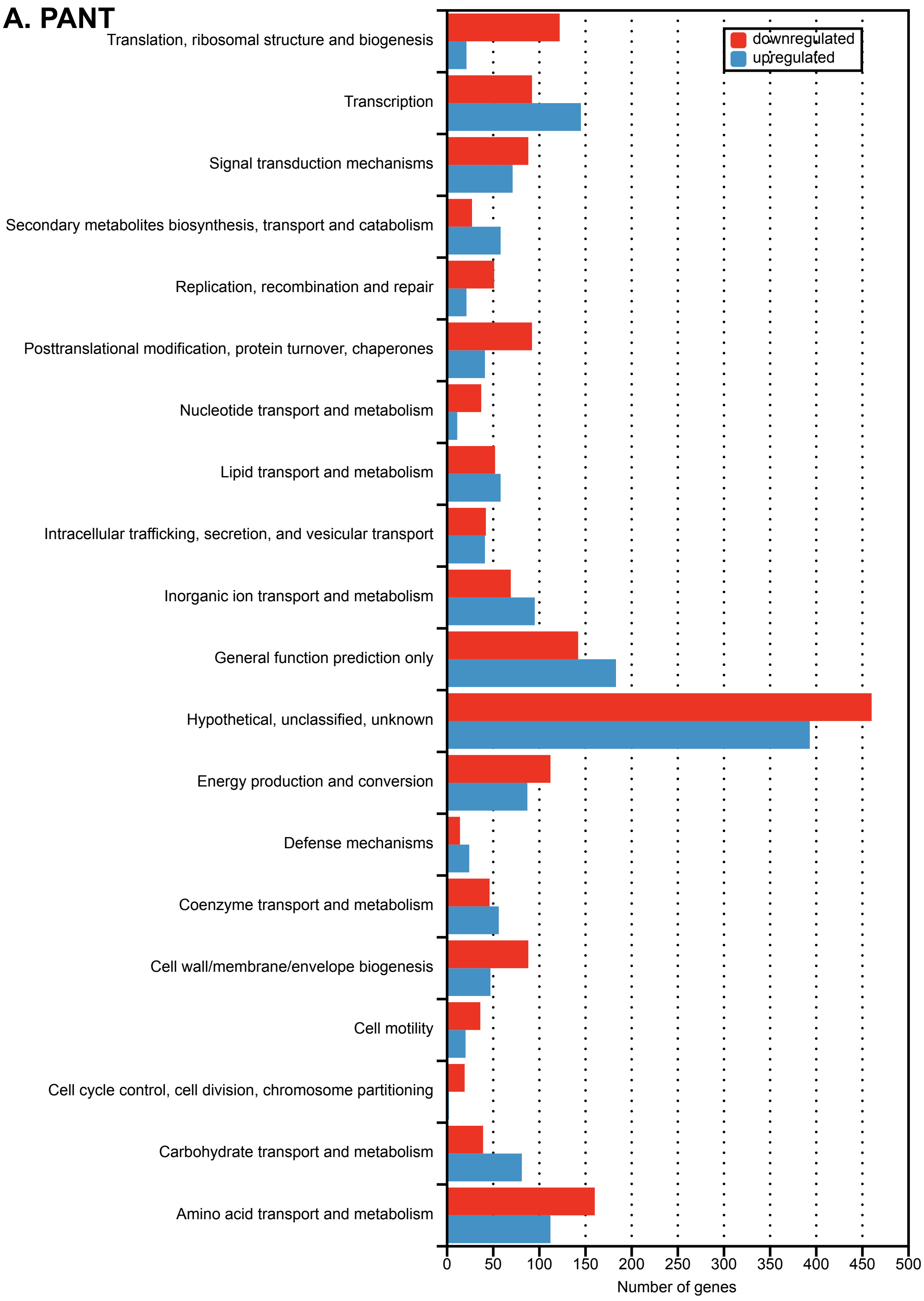


Figure S5: Volcano plot showing statistical significance (Padj) vs. fold change for genes differentially expressed due to interfacial exposure. (A) alginate genes by PANT (B) *pel* genes by PANT (C) *psl* genes by PANT (D) alginate genes by PASL (E) *pel* genes by PASL (F) *psl* genes by PASL.


A. PANT
Translation, ribosomal structure and biogenesis
Transcription
Signal transduction mechanisms
Secondary metabolites biosynthesis, transport and catabolism
Replication, recombination and repair
Posttranslational modification, protein turnover, chaperones
Nucleotide transport and metabolism
Lipid transport and metabolism
Intracellular trafficking, secretion, and vesicular transport
Inorganic ion transport and metabolism
General function prediction only
Hypothetical, unclassified, unknown
Energy production and conversion
Defense mechanisms
Coenzyme transport and metabolism
Cell wall/membrane/envelope biogenesis
Cell motility
Cell cycle control, cell division, chromosome partitioning
Carbohydrate transport and metabolism
Amino acid transport and metabolism
downregulated
upregulated
0
50
100
150
200
250
300
350
400
450
500
Number of genes

B. PASL

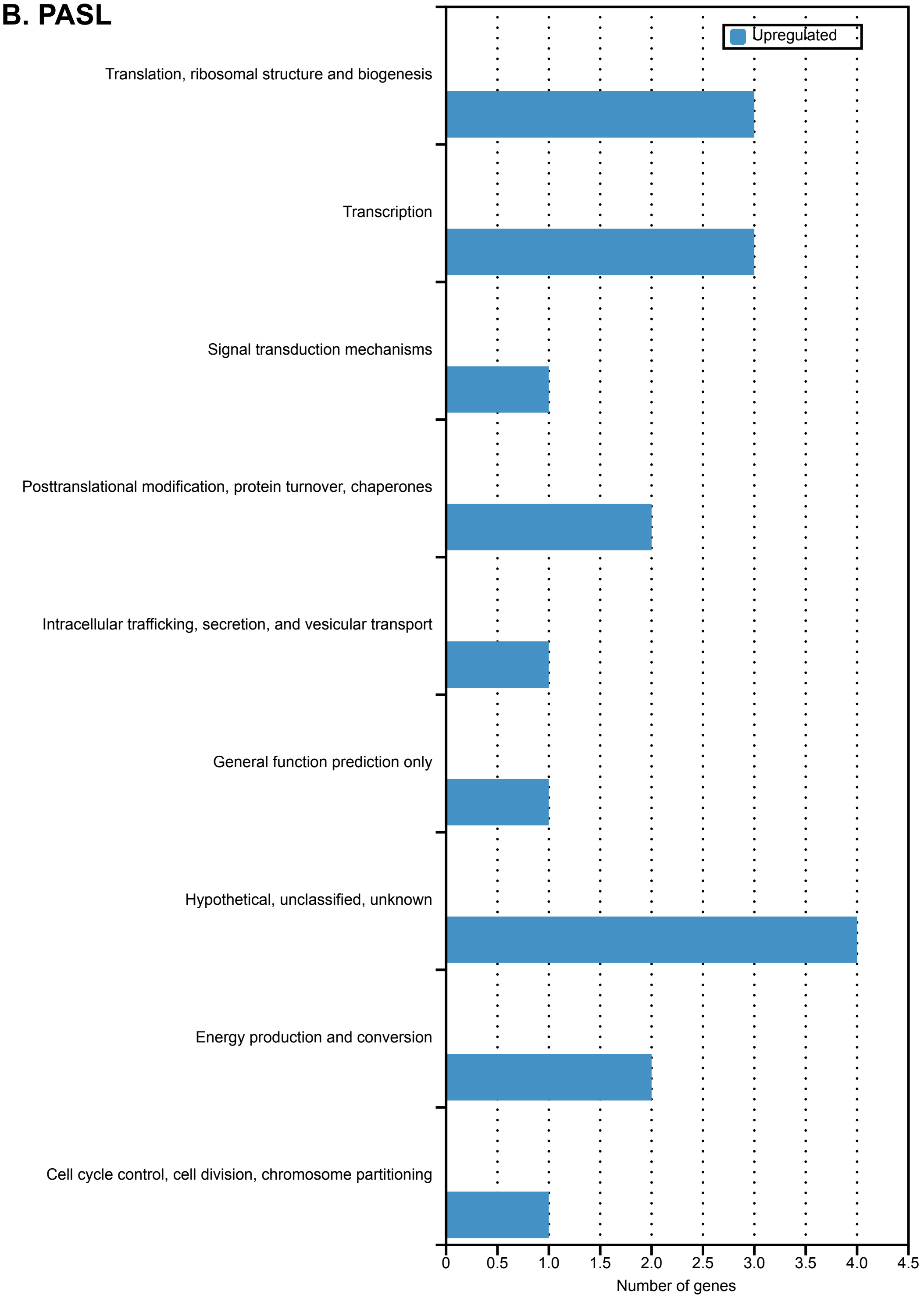


Figure S6: Transcriptional profile of (A) PANT (B) PASL after confinement at hexadecane-water interface for 24 h. The number of genes upregulated and downregulated are represented based on their functions.

Table S2. List of genes upregulated in PANT by at least 2-fold with a false discovery rate (FDR) <0.01 during exposure to hexadecane-water interface for 24 h versus the control.

Gene	Description	Fold Change	Padj-value
Amino acid transport and metabolism			
PA1977	hypothetical protein	8.37	1.69E-63
PA1497	transporter	8.25	1.57E-73
pqqH	peptidase	7.10	4.03E-50
PA1620	hypothetical protein	6.83	8.59E-48
PA2124	dehydrogenase	6.44	1.45E-30
PA1341	amino acid ABC transporter permease	6.28	3.77E-12
PA2202	amino acid permease	6.14	1.33E-37
phzC1	phenazine biosynthesis protein PhzC	6.03	3.71E-58
PA1214	hypothetical protein	5.99	2.09E-54
PA2084	asparagine synthetase	5.86	5.62E-40
PA2916	hypothetical protein	5.74	5.11E-38
PA1108	major facilitator superfamily transporter	5.70	1.73E-47
PA1267	hypothetical protein	5.63	2.16E-38
phzC2	phenazine biosynthesis protein PhzC	5.55	5.87E-50
PA1143	hypothetical protein	5.43	9.07E-42
PA1486	hypothetical protein	5.32	1.74E-35
PA1268	4-hydroxyproline 2-epimerase	5.18	1.33E-42
PA1346	hypothetical protein	4.94	7.15E-35
PA1566	hypothetical protein	4.74	2.31E-42
PA1966	hypothetical protein	4.65	6.07E-26
PA2062	pyridoxal-phosphate dependent protein	4.59	4.06E-27
PA1282	major facilitator superfamily transporter	4.57	2.55E-42
PA3175	formimidoylglutamase	4.56	3.38E-26
PA2203	amino acid permease	4.48	1.27E-28
PA2024	ring-cleaving dioxygenase	4.44	3.45E-19
PA3424	hypothetical protein	4.44	9.41E-37
PA0813	hypothetical protein	4.26	2.01E-31
PA3750	hypothetical protein	4.21	2.38E-31
hcnC	hydrogen cyanide synthase subunit HcnC	4.19	5.22E-25
PA2531	aminotransferase	4.17	2.03E-25
cobC	threonine-phosphate decarboxylase	4.04	1.29E-24
PA3956	hypothetical protein	3.99	5.75E-22
dauA	FAD-dependent catabolic D-arginine dehydrogenase DauA	3.83	3.35E-30
PA5084	oxidoreductase	3.65	3.35E-24

PA4165	transcriptional regulator	3.63	6.71E-26
pdxB	erythronate-4-phosphate dehydrogenase	3.58	6.46E-25
mdlC	benzoylformate decarboxylase	3.58	1.93E-23
PA1147	amino acid permease	3.58	1.34E-28
PA1255	trans-3-hydroxy-L-proline dehydratase	3.56	1.82E-17
PA4908	ornithine cyclodeaminase	3.53	7.38E-26
phnB	anthranilate synthase component II	3.51	4.20E-21
cpg2	glutamate carboxypeptidase	3.43	5.68E-23
PA0244	shikimate 5-dehydrogenase	3.39	7.22E-18
gltS	glutamate/sodium ion symporter GltS	3.36	3.62E-21
PA5341	hypothetical protein	3.32	8.24E-24
PA2035	thiamine pyrophosphate protein	3.29	1.89E-22
PA0268	transcriptional regulator	3.26	5.08E-27
PA1732	hypothetical protein	3.24	1.01E-19
PA1258	ABC transporter permease	3.20	3.65E-13
PA1129	glutathione transferase FosA	3.20	2.93E-14
phzE1	phenazine biosynthesis protein PhzE	3.16	3.94E-24
PA4510	hypothetical protein	3.15	1.29E-19
PA4509	hypothetical protein	3.10	4.84E-19
PA2943	phospho-2-dehydro-3-deoxyheptonate aldolase	3.08	2.17E-18
PA4860	ABC transporter permease	3.08	1.55E-18
PA3665	hypothetical protein	3.00	9.73E-19
PA2252	AGCS sodium/alanine/glycine symporter	2.99	1.08E-08
PA0851	hypothetical protein	2.93	1.38E-19
PA4926	hypothetical protein	2.93	7.41E-16
PA1254	dihydrodipicolinate synthetase	2.93	2.48E-10
PA5390	acetylornithine deacetylase	2.92	1.49E-16
PA4507	hypothetical protein	2.88	2.89E-14
dsdA	D-serine dehydratase	2.87	3.04E-15
PA0326	ABC transporter ATP-binding protein	2.87	1.99E-19
PA5093	histidine/phenylalanine ammonia-lyase	2.86	1.12E-20
braZ	branched-chain amino acid transport system 3 carrier protein	2.86	5.43E-17
PA0164	gamma-glutamyltranspeptidase	2.85	1.09E-17
PA2873	protein-glutamine gamma-glutamyltransferase	2.84	5.93E-21
PA4192	ABC transporter ATP-binding protein	2.80	5.25E-13
PA0361	gamma-glutamyltranspeptidase	2.79	1.10E-18
pvdH	diaminobutyrate--2-oxoglutarate aminotransferase	2.78	2.01E-11
PA2683	serine/threonine dehydratase	2.75	1.55E-17
PA5508	glutamine synthetase	2.71	1.41E-15
gcvT2	glycine cleavage system protein T2	2.71	4.34E-15

PA4677	hypothetical protein	2.71	8.06E-17
PA3749	major facilitator superfamily transporter	2.70	5.23E-18
PA2110	hypothetical protein	2.68	1.52E-07
PA1918	hypothetical protein	2.63	3.89E-09
PA1567	hypothetical protein	2.62	1.62E-12
ldh	leucine dehydrogenase	2.60	1.01E-12
hisQ	histidine ABC transporter permease HisQ	2.57	1.70E-07
PA4985	hypothetical protein	2.52	5.48E-13
PA0534	hypothetical protein	2.52	9.16E-14
chpE	chemotactic transduction protein ChpE	2.52	1.68E-12
PA5155	amino acid ABC transporter permease	2.48	1.76E-11
potA	polyamine transporter ATP-binding protein PotA	2.47	3.67E-11
dauB	NAD(P)H-dependent anabolic L-arginine dehydrogenase DauB	2.46	1.00E-13
PA4025	ethanolamine ammonia-lyase small subunit	2.42	4.32E-12
PA1028	oxidoreductase	2.40	2.30E-13
aruH	arginine:pyruvate transaminase AruH	2.39	2.52E-11
PA2835	major facilitator superfamily transporter	2.38	3.83E-11
PA0242	hypothetical protein	2.38	9.51E-14
soxA	sarcosine oxidase subunit alpha	2.38	4.20E-16
PA2111	hypothetical protein	2.37	1.07E-07
ureA	urease subunit gamma	2.37	3.65E-08
ilvA2	threonine dehydratase	2.33	2.73E-13
PA2058	ABC transporter	2.31	1.60E-11
PA0777	hypothetical protein	2.27	4.71E-08
PA1257	amino acid ABC transporter permease	2.24	1.99E-08
PA3125	hypothetical protein	2.22	2.03E-09
PA0902	hypothetical protein	2.22	5.44E-08
dapE	succinyl-diaminopimelate desuccinylase	2.18	4.98E-08
PA1819	amino acid permease	2.16	6.49E-11
gpuA	guanidinopropionase	2.12	5.18E-09
PA2079	amino acid permease	2.11	3.26E-07
PA3254	ABC transporter ATP-binding protein	2.10	1.06E-08
PA2929	hypothetical protein	2.10	5.98E-07
PA4804	amino acid permease	2.08	5.15E-10
sdaB	L-serine dehydratase	2.06	7.98E-09
PA2958	hypothetical protein	2.06	4.88E-09
PA3187	ABC transporter ATP-binding protein	2.05	3.04E-07
PA2842	hypothetical protein	2.04	5.05E-08
PA3667	cysteine desulfurase	2.03	3.19E-08
Carbohydrate transport and metabolism			

PA2092	major facilitator superfamily transporter	8.65	2.41E-46
PA2163	4-alpha-glucanotransferase	8.10	1.11E-47
PA1908	major facilitator superfamily transporter	7.79	1.58E-56
PA2472	major facilitator superfamily transporter	7.20	1.41E-55
PA1352	hypothetical protein	7.11	8.19E-63
PA1265	hypothetical protein	6.67	3.74E-41
PA1412	hypothetical protein	6.64	1.74E-56
PA2091	hypothetical protein	6.39	1.70E-45
PA2261	2-ketogluconate kinase	5.74	2.64E-45
PA2162	malto-oligosyltrehalose synthase	5.67	1.39E-33
PA2933	major facilitator superfamily transporter	5.61	1.52E-47
PA2172	hypothetical protein	5.05	2.79E-40
PA4903	major facilitator superfamily transporter	4.82	7.06E-34
PA3358	hypothetical protein	4.71	2.79E-38
PA1131	major facilitator superfamily transporter	4.70	3.14E-41
treA	trehalase	4.60	1.57E-23
PA3303	major facilitator superfamily transporter	4.55	3.04E-40
PA1993	hypothetical protein	4.48	1.93E-29
PA1144	major facilitator superfamily transporter	4.47	7.82E-36
PA3773	hypothetical protein	4.37	6.03E-39
PA1740	hypothetical protein	4.29	2.22E-30
PA2269	hypothetical protein	4.27	2.79E-26
PA1052	hypothetical protein	4.10	3.12E-26
PA4900	major facilitator superfamily transporter	4.09	2.98E-21
PA0811	major facilitator superfamily transporter	4.05	1.05E-34
arnD	4-deoxy-4-formamido-L-arabinose-phosphoundecaprenol deformylase ArnD	4.05	1.34E-23
PA4128	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	3.95	6.06E-32
PA2260	hypothetical protein	3.94	5.70E-17
PA0883	acyl-CoA lyase subunit beta	3.92	2.44E-18
glgB	1,4-alpha-glucan branching protein GlgB	3.91	1.89E-24
PA1313	major facilitator superfamily transporter	3.85	4.81E-29
PA4136	major facilitator superfamily transporter	3.83	2.91E-32
PA2152	trehalose synthase	3.77	4.46E-29
PA4355	major facilitator superfamily transporter	3.71	1.28E-28
PA0238	hypothetical protein	3.66	2.56E-18
PA1286	major facilitator superfamily transporter	3.65	3.87E-28
PA3760	N-acetyl-D-glucosamine phosphotransferase system transporter	3.62	9.38E-27
rbsA	ribose transporter RbsA	3.62	7.67E-17
PA2164	glycosyl hydrolase	3.57	1.14E-15
mucK	cis,cis-muconate transporter MucK	3.56	7.75E-26

PA2589	hypothetical protein	3.54	1.15E-23
fruK	1-phosphofructokinase	3.53	1.42E-27
PA1280	hypothetical protein	3.49	5.73E-23
PA1109	transcriptional regulator	3.48	8.14E-25
pgl	6-phosphogluconolactonase	3.40	8.62E-24
PA2210	major facilitator superfamily transporter	3.37	1.59E-19
PA2077	hypothetical protein	3.30	2.14E-19
PA0334	major facilitator superfamily transporter	3.22	4.72E-25
PA4779	hypothetical protein	3.19	1.08E-19
PA2006	major facilitator superfamily transporter	3.17	4.54E-21
fruI	PTS system fructose-specific transporter subunit FruI	3.17	9.30E-24
fruA	PTS system fructose-specific transporter subunit IIBC	3.17	2.37E-25
PA3024	carbohydrate kinase	3.13	1.25E-21
PA1236	major facilitator superfamily transporter	3.04	1.67E-21
glk	glucokinase	2.97	2.18E-20
PA3682	hypothetical protein	2.96	1.08E-19
PA2214	major facilitator superfamily transporter	2.95	1.30E-15
PA4096	major facilitator superfamily transporter	2.94	2.99E-14
PA3467	major facilitator superfamily transporter	2.87	8.46E-19
PA3222	hypothetical protein	2.81	1.94E-14
PA2165	glycogen synthase	2.78	3.15E-15
rbsK	ribokinase	2.77	1.76E-14
PA4120	transcriptional regulator	2.74	7.54E-15
PA5282	major facilitator superfamily transporter	2.73	2.40E-18
PA5219	hypothetical protein	2.73	1.15E-15
PA3780	hypothetical protein	2.73	4.10E-12
pslB	biofilm formation protein PslB	2.60	6.90E-14
PA1499	hypothetical protein	2.55	3.93E-11
PA0550	hypothetical protein	2.40	4.07E-12
PA3131	aldolase	2.39	4.00E-10
PA2414	L-sorbosone dehydrogenase	2.38	1.78E-09
bglX	beta-glucosidase	2.30	3.82E-13
PA3181	2-dehydro-3-deoxy-phosphogluconate aldolase	2.12	6.72E-08
PA3573	major facilitator superfamily transporter	2.10	2.36E-08
PA4113	sugar efflux transporter	2.09	8.41E-10
pslL	hypothetical protein	2.05	1.08E-06
PA3758	N-acetylglucosamine-6-phosphate deacetylase	2.04	3.10E-09
PA3189	sugar ABC transporter permease	2.04	9.15E-08
PA3781	transporter	2.03	2.03E-09
PA2262	2-ketogluconate transporter	2.02	5.57E-08

PA1046	hypothetical protein	2.01	5.68E-09
PA2151	alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase	2.00	2.18E-07
Cell cycle control, cell division, chromosome partitioning			
PA3638	tRNA(Ile)-lysidine synthase	2.83	2.30E-20
PA4478	hypothetical protein	2.24	2.26E-09
Cell motility			
PA0687	type II secretion system protein	5.19	7.24E-45
pscQ	type III secretion system protein	4.96	1.36E-34
PA2920	chemotaxis transducer	4.46	1.46E-34
cupC2	chaperone CupC2	4.31	1.85E-03
PA1697	type III secretion system ATPase	4.18	1.67E-28
PA0173	chemotaxis response regulator protein-glutamate methylesterase	4.04	3.73E-25
PA4844	chemotaxis transducer	3.95	8.99E-35
cupA2	chaperone CupA2	3.77	6.83E-18
PA1251	chemotaxis transducer	3.69	2.74E-22
cupB4	chaperone CupB4	3.68	1.40E-17
PA0686	type II secretion system protein HxcR	3.67	5.27E-28
PA4651	pili assembly chaperone	3.30	5.37E-21
PA0685	type II secretion system protein	3.19	1.41E-21
PA5072	chemotaxis transducer	3.06	1.73E-22
PA0078	hypothetical protein	3.00	8.25E-18
fliO	flagellar protein FliO	2.42	3.87E-11
pscC	type III secretion outer membrane protein PscC	2.39	4.77E-12
xcpS	type II secretion system protein F	2.36	4.31E-13
PA4652	hypothetical protein	2.36	3.71E-15
PA0178	two-component sensor	2.14	2.08E-10
PA2677	type II secretion protein	2.03	2.45E-07
Cell wall/membrane/envelope biogenesis			
pslI	biofilm formation protein PslI	6.15	8.85E-47
PA1435	resistance-nodulation-cell division (RND) efflux membrane fusion protein	5.19	1.59E-41
pslF	biofilm formation protein PslF	5.16	3.06E-37
PA3404	hypothetical protein	4.66	2.19E-36
opmQ	hypothetical protein	4.52	8.27E-32
PA3431	hypothetical protein	4.39	4.03E-30
pslH	biofilm formation protein PslH	4.18	2.69E-33
PA0842	glycosyl transferase family protein	4.15	4.80E-33
tonB2	transporter TonB	4.04	1.10E-14
PA0695	hypothetical protein	4.03	1.04E-20
PA0333	hypothetical protein	4.00	2.03E-37

hasE	metalloprotease secretion protein	3.97	3.29E-34
czcB	resistance-nodulation-cell division (RND) divalent metal cation efflux membrane fusion protein CzcB	3.89	1.33E-22
PA3677	resistance-nodulation-cell division (RND) efflux membrane fusion protein	3.79	9.51E-27
PA2548	hypothetical protein	3.65	5.17E-22
mexC	resistance-nodulation-cell division (RND) multidrug efflux membrane fusion protein MexC	3.53	7.39E-26
arnT	4-amino-4-deoxy-L-arabinose lipid A transferase	3.48	1.79E-26
lasA	protease LasA	3.45	5.06E-26
PA4188	hypothetical protein	3.35	2.43E-19
PA4818	hypothetical protein	3.26	8.52E-23
waaA	3-deoxy-D-manno-octulosonic acid transferase	3.17	5.52E-25
PA1408	hypothetical protein	3.12	2.99E-25
PA2684	hypothetical protein	3.09	7.23E-20
PA1874	hypothetical protein	3.05	3.00E-22
PA3402	hypothetical protein	3.05	5.87E-18
PA3759	aminotransferase	3.00	2.05E-19
PA0157	resistance-nodulation-cell division (RND) efflux membrane fusion protein	2.75	4.01E-19
PA3526	hypothetical protein	2.67	3.26E-17
ndvB	glycosyl transferase	2.65	5.19E-18
catB	muconate cycloisomerase I	2.63	2.82E-10
PA1385	glycosyl transferase family protein	2.60	1.17E-03
PA2865	glycosylase	2.57	1.66E-12
PA4591	hypothetical protein	2.56	3.28E-15
algI	alginate o-acetylase AlgI	2.55	2.15E-15
PA1171	transglycosylase	2.54	7.22E-09
pbpC	penicillin-binding protein 3A	2.51	2.51E-10
mexH	resistance-nodulation-cell division (RND) efflux membrane fusion protein	2.46	1.22E-11
PA4041	hypothetical protein	2.42	9.62E-11
PA4924	hypothetical protein	2.38	4.15E-11
alg44	alginate biosynthesis protein Alg44	2.38	1.67E-09
PA4819	glycosyl transferase family protein	2.34	5.58E-11
aprE	alkaline protease secretion protein AprE	2.33	1.25E-12
PA3523	resistance-nodulation-cell division (RND) efflux membrane fusion protein	2.29	2.88E-11
lpxK	tetraacyldisaccharide 4'-kinase	2.28	4.49E-11
pelF	pellicle/biofilm biosynthesis glycosyltransferase PelF	2.20	6.94E-10
pvdR	pyoverdine biosynthesis protein PvdR	2.20	1.98E-08

pslD	biofilm formation protein PslD	2.16	1.18E-07
mexE	resistance-nodulation-cell division (RND) multidrug efflux membrane fusion protein MexE	2.13	9.94E-10
Chromatin structure and dynamics			
aphA	acetylpolyamine aminohydrolase	2.35	2.26E-11
Coenzyme transport and metabolism			
PA1355	hypothetical protein	7.75	1.20E-47
PA1923	cobaltochelatase subunit CobN	7.11	5.05E-57
PA2263	2-hydroxyacid dehydrogenase	6.13	5.03E-33
PA2909	cobalt-precorrin-6x reductase	5.83	1.33E-35
PA2912	ABC transporter ATP-binding protein	5.43	1.30E-44
PA1417	hypothetical protein	5.38	1.14E-46
cobV	adenosylcobinamide-GDP ribazoletransferase	5.13	8.18E-40
PA2941	hypothetical protein	5.12	1.94E-37
cobD	cobalamin biosynthesis protein CobD	4.65	3.14E-39
cobJ	precorrin-3 methylase CobJ	4.62	6.28E-43
PA2942	magnesium chelatase	4.61	8.31E-40
phzG2	pyridoxamine 5'-phosphate oxidase	4.50	9.85E-28
moeA1	molybdenum cofactor biosynthesis protein A	4.42	1.17E-33
cobH	precorrin-8X methylmutase	4.42	1.60E-19
PA0209	2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	4.39	1.20E-26
cobL	precorrin-6y-dependent methyltransferase CobL	4.19	3.96E-30
phzG1	pyridoxamine 5'-phosphate oxidase	4.11	2.34E-18
PA1957	hypothetical protein	4.01	8.03E-21
cobU	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	3.98	9.93E-30
mobA	molybdenum cofactor guanylyltransferase	3.91	1.41E-24
aruI	hypothetical protein	3.61	1.15E-26
PA2650	hypothetical protein	3.55	1.08E-21
PA2108	thiamine pyrophosphate protein	3.49	3.01E-18
panE	2-dehydropantoate 2-reductase	3.48	1.11E-25
PA0510	uroporphyrin-III C-methyltransferase	3.47	9.24E-19
PA1958	transporter	3.39	4.60E-14
thiE	thiamine-phosphate pyrophosphorylase	3.38	9.43E-14
moaA1	molybdenum cofactor biosynthesis protein A	3.33	8.78E-20
rrmA	rRNA methyltransferase	3.30	8.88E-16
PA4286	hypothetical protein	3.24	8.92E-22
cobB	hydrogenobyrinate a,c-diamide synthase	3.24	1.64E-21
cbiD	cobalt-precorrin-5B C(1)-methyltransferase	3.23	4.44E-21
ispA	geranyltranstransferase	3.20	2.72E-20
PA0254	hypothetical protein	3.19	8.60E-21

PA4790	hypothetical protein	3.15	1.59E-20
PA2679	hypothetical protein	3.06	1.43E-18
phzE2	phenazine biosynthesis protein PhzE	3.01	1.18E-18
PA3119	hypothetical protein	2.95	8.41E-17
cobP	bifunctional adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase	2.91	3.99E-17
cobN	cobaltochelatase subunit CobN	2.90	3.81E-22
PA2212	4-hydroxythreonine-4-phosphate dehydrogenase	2.85	3.11E-14
pmtA	phospholipid methyltransferase	2.80	5.93E-15
ribD	riboflavin-specific deaminase/reductase	2.75	1.49E-16
cobQ	cobyric acid synthase	2.66	1.93E-16
PA4088	aminotransferase	2.64	9.44E-16
thiL	thiamine monophosphate kinase	2.57	3.22E-15
antC	anthranilate dioxygenase reductase	2.55	6.54E-07
pqqC	pyrroloquinoline-quinone synthase	2.54	1.44E-07
PA4917	hypothetical protein	2.53	4.06E-08
folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	2.42	5.15E-09
folA	dihydrofolate reductase	2.31	2.32E-11
PA5357	hypothetical protein	2.26	7.89E-11
PA0386	coproporphyrinogen III oxidase	2.18	6.74E-12
PA5228	5-formyltetrahydrofolate cyclo-ligase	2.17	1.02E-10
PA1598	3-methyl-2-oxobutanoate hydroxymethyltransferase	2.10	8.32E-07
thiD	phosphomethylpyrimidine kinase	2.07	4.79E-08
bioD	ATP-dependent dethiobiotin synthetase BioD	2.05	2.51E-09
GeneName	Description	FoldChange	Padj
Defense mechanisms			
PA1237	multidrug resistance efflux pump	6.78	6.63E-38
nosF	copper ABC transporter ATP-binding protein	5.38	2.29E-40
PA1231	hypothetical protein	5.13	6.39E-41
PA3360	secretion protein	5.12	5.13E-43
PA4821	transporter	4.62	4.65E-34
PA2836	secretion protein	4.55	9.27E-36
PA0073	ABC transporter ATP-binding protein	4.39	1.56E-34
PA0072	hypothetical protein	4.28	1.01E-33
PA1361	multidrug resistance protein PmpM	3.89	5.53E-29
PA1876	ABC transporter ATP-binding protein/permease	3.88	5.61E-34
PA4594	ABC transporter ATP-binding protein	3.48	5.30E-17
PA4593	ABC transporter permease	3.40	5.15E-26

pvdT	pyoverdine biosynthesis protein PvdT	3.37	6.35E-26
PA4064	ABC transporter ATP-binding protein	3.25	1.08E-18
PA5294	multidrug efflux protein NorA	3.25	2.75E-26
PA2228	hypothetical protein	2.73	1.19E-03
PA4222	ABC transporter ATP-binding protein	2.70	7.89E-14
PA1113	ABC transporter ATP-binding protein/permease	2.55	2.39E-15
PA0468	hypothetical protein	2.35	3.32E-13
PA1047	esterase	2.20	1.07E-09
PA0860	ABC transporter ATP-binding protein/permease	2.20	3.58E-11
PA2527	resistance-nodulation-cell division (RND) efflux transporter	2.15	5.72E-10
PA4347	hypothetical protein	2.12	3.31E-09
PA3136	secretion protein	2.09	6.40E-07
PA2987	lipoprotein-releasing system ABC transporter ATP-binding protein	2.08	2.60E-08
Energy production and conversion			
pvcD	paerucumarin biosynthesis protein PvcD	8.08	4.91E-51
napF	ferredoxin protein NapF	7.37	9.66E-50
PA2090	hypothetical protein	7.05	8.81E-34
pslM	FAD-binding dehydrogenase	6.60	4.04E-63
PA3208	hypothetical protein	4.91	1.04E-35
nosL	acessory protein NosL	4.90	1.85E-30
glcE	glycolate oxidase FAD binding subunit	4.76	2.03E-37
PA3025	FAD-dependent glycerol-3-phosphate dehydrogenase	4.76	6.56E-44
PA2125	aldehyde dehydrogenase	4.73	2.42E-24
napB	cytochrome C protein NapB	4.72	1.89E-18
PA1253	semialdehyde dehydrogenase	4.67	1.81E-37
PA2716	FMN oxidoreductase	4.61	1.12E-30
PA1880	oxidoreductase	4.55	2.48E-37
PA1416	hypothetical protein	4.55	7.39E-36
PA3328	FAD-dependent monooxygenase	4.48	2.78E-24
morB	morphinone reductase	4.48	1.22E-29
PA1600	cytochrome C	4.40	1.38E-35
PA1186	hypothetical protein	4.39	5.50E-35
PA2217	aldehyde dehydrogenase	4.33	4.44E-27
pelE	pellicle/biofilm biosynthesis protein PelE	4.29	5.33E-22
PA2936	hypothetical protein	4.28	2.33E-26
PA0521	cytochrome C oxidase subunit	4.14	2.42E-26
PA3415	branched-chain alpha-keto acid dehydrogenase subunit E2	4.10	1.92E-29
PA3444	alkanesulfonate monooxygenase	4.10	2.90E-23
PA3491	electron transport complex subunit C	4.08	7.35E-38

PA1146	iron-containing alcohol dehydrogenase	4.07	6.74E-35
PA1274	5,6-dimethylbenzimidazole synthase	4.05	2.42E-29
PA2477	thiol:disulfide interchange protein	4.04	2.77E-17
glcF	glycolate oxidase iron-sulfur subunit	3.99	4.29E-29
PA2691	hypothetical protein	3.91	1.26E-30
xylZ	toluate 1,2-dioxygenase electron transfer subunit	3.89	2.54E-22
PA4889	oxidoreductase	3.87	7.70E-32
PA5400	electron transfer flavoprotein subunit alpha	3.78	1.76E-31
PA1739	oxidoreductase	3.77	1.76E-17
PA1188	hypothetical protein	3.68	6.53E-29
PA3417	pyruvate dehydrogenase E1 component subunit alpha	3.64	1.36E-23
PA4189	aldehyde dehydrogenase	3.64	1.29E-19
vanB	vanillate O-demethylase	3.54	7.25E-25
PA1334	oxidoreductase	3.54	1.50E-26
nirC	cytochrome c55X	3.53	4.09E-08
PA0219	aldehyde dehydrogenase	3.52	2.32E-27
PA2715	ferredoxin	3.49	1.24E-14
PA4331	hypothetical protein	3.48	1.35E-26
mdcC	malonate decarboxylase acyl carrier protein	3.44	2.84E-17
PA2598	hypothetical protein	3.39	8.47E-21
PA3534	oxidoreductase	3.26	2.43E-23
pauA	pimeloyl-CoA synthetase	3.26	9.64E-24
PA2078	hypothetical protein	3.26	6.79E-19
PA4978	hypothetical protein	3.25	4.28E-24
PA3416	pyruvate dehydrogenase E1 component subunit beta	3.22	2.69E-20
PA0101	hypothetical protein	3.21	5.40E-26
PA3592	hypothetical protein	3.20	1.08E-21
PA3772	hypothetical protein	3.16	1.08E-18
PA0882	hypothetical protein	3.15	1.49E-22
PA0863	oxidoreductase	3.14	2.05E-18
PA5186	iron-containing alcohol dehydrogenase	3.12	7.57E-23
PA1487	carbohydrate kinase	3.10	1.32E-21
PA5401	hypothetical protein	3.06	2.83E-16
napE	nitrate reductase protein NapE	3.01	6.67E-05
fadH2	2,4-dienoyl-CoA reductase	2.97	1.29E-20
PA4859	ABC transporter permease	2.69	9.03E-19
PA4792	hypothetical protein	2.64	5.55E-13
PA3493	electron transport complex subunit G	2.58	1.46E-13
PA2600	hypothetical protein	2.49	3.31E-12

PA4150	dehydrogenase E1 component	2.48	4.97E-10
pntAA	NAD(P) transhydrogenase subunit alpha	2.46	2.51E-13
PA1601	aldehyde dehydrogenase	2.46	1.57E-15
PA3492	electron transport complex subunit D	2.45	9.90E-12
PA3256	oxidoreductase	2.41	5.58E-13
pqsL	monooxygenase	2.40	1.45E-13
lldA	L-lactate dehydrogenase	2.40	3.19E-11
PA1252	bifunctional Delta(1)-pyrroline-2-carboxylate/Delta(1)-piperideine-2-carboxylate reductase	2.37	1.19E-10
PA1734	hypothetical protein	2.36	4.04E-08
lpd3	dihydrolipoamide dehydrogenase	2.32	2.09E-12
PA4155	hypothetical protein	2.30	5.21E-11
PA4073	aldehyde dehydrogenase	2.30	7.06E-10
hpcC	5-carboxy-2-hydroxymuconate semialdehyde dehydrogenase	2.28	9.00E-10
PA1027	aldehyde dehydrogenase	2.28	2.41E-12
PA2714	molybdopterin oxidoreductase	2.25	2.39E-12
dgcB	dimethylglycine catabolism protein DgcB	2.20	2.77E-11
PA3490	electron transport complex subunit B	2.20	9.55E-08
PA2266	cytochrome C	2.19	1.03E-11
PA4899	aldehyde dehydrogenase	2.17	4.90E-10
PA2421	hypothetical protein	2.16	4.33E-06
PA2378	aldehyde dehydrogenase	2.13	3.77E-09
PA2482	cytochrome C	2.07	8.83E-09
PA4152	branched-chain alpha-keto acid dehydrogenase subunit E2	2.05	1.89E-08
narJ	respiratory nitrate reductase subunit delta	2.04	3.72E-05
Hypothetical, unclassified, unknown			
PA1981	hypothetical protein	8.20	1.31E-53
PA1960	hypothetical protein	7.21	4.25E-51
PA2370	hypothetical protein	7.21	9.09E-55
PA2048	hypothetical protein	6.93	7.79E-24
PA2368	hypothetical protein	6.91	2.71E-38
PA1547	hypothetical protein	6.57	1.66E-45
PA2369	hypothetical protein	6.16	1.47E-45
PA2157	hypothetical protein	5.91	9.51E-35
PA1849	hypothetical protein	5.86	9.17E-17
PA1259	hypothetical protein	5.85	2.59E-53
PA1270	hypothetical protein	5.64	7.37E-55
PA1232	hypothetical protein	5.64	8.50E-42
PA2362	hypothetical protein	5.56	4.66E-33

PA2363	hypothetical protein	5.48	1.94E-50
PA2412	hypothetical protein	5.48	8.16E-20
PA3320	hypothetical protein	5.36	1.33E-31
PA3436	hypothetical protein	5.30	1.94E-28
PA2198	hypothetical protein	5.12	1.13E-18
PA1495	hypothetical protein	5.12	8.91E-27
PA3456	tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein MnmC	5.11	1.72E-45
PA3765	hypothetical protein	4.98	3.52E-33
PA2154	hypothetical protein	4.92	2.15E-34
PA2360	hypothetical protein	4.52	7.16E-24
xqhA	secretion protein XqhA	4.48	6.10E-40
PA2181	glutamate--cysteine ligase	4.45	1.38E-35
PA3089	hypothetical protein	4.39	4.05E-34
PA4149	hypothetical protein	4.25	1.71E-34
PA1139	hypothetical protein	4.19	2.88E-25
PA4129	hypothetical protein	4.14	6.92E-26
PA2872	hypothetical protein	4.12	1.96E-32
PA2148	hypothetical protein	4.03	1.04E-16
PA3952	hypothetical protein	3.98	2.64E-14
PA1349	hypothetical protein	3.92	3.62E-19
PA2216	hypothetical protein	3.85	6.36E-21
PA1469	hypothetical protein	3.81	2.01E-23
PA1619	transcriptional regulator	3.80	4.49E-25
PA2946	hypothetical protein	3.79	6.90E-30
PA0801	hypothetical protein	3.79	3.19E-29
PA2045	membrane protein insertion efficiency factor	3.77	6.00E-18
PA0671	hypothetical protein	3.75	2.12E-22
PA4181	hypothetical protein	3.72	9.24E-19
popB	translocator protein PopB	3.70	1.21E-23
PA2844	hypothetical protein	3.67	3.61E-28
PA3904	hypothetical protein	3.61	1.29E-17
PA3388	S-adenosylmethionine-dependent methyltransferase RcsF	3.61	2.21E-17
PA0110	hypothetical protein	3.60	5.30E-27
PA2063	hypothetical protein	3.57	4.91E-22
PA1235	transcriptional regulator	3.55	3.00E-25
PA3681	hypothetical protein	3.55	2.57E-23
PA0339	hypothetical protein	3.46	2.73E-25
PA2361	hypothetical protein	3.43	2.34E-25
PA2839	hypothetical protein	3.42	2.64E-17
PA3275	hypothetical protein	3.40	9.96E-14

PA4219	hypothetical protein	3.39	3.73E-24
PA4364	hypothetical protein	3.38	7.35E-17
PA4362	hypothetical protein	3.35	2.38E-19
PA2367	hypothetical protein	3.32	4.67E-16
PA4828	hypothetical protein	3.29	1.11E-13
PA3282	hypothetical protein	3.28	4.37E-20
PA5391	hypothetical protein	3.27	7.37E-23
PA1424	hypothetical protein	3.23	9.01E-17
PA4634	hypothetical protein	3.23	3.06E-18
PA3091	hypothetical protein	3.23	4.40E-25
PA3305	hypothetical protein	3.22	3.86E-26
PA1114	hypothetical protein	3.21	3.50E-16
pelA	hypothetical protein	3.20	2.00E-23
exbB2	transporter ExbB	3.20	1.34E-25
PA0806	hypothetical protein	3.19	2.29E-15
PA1134	hypothetical protein	3.19	3.91E-15
PA0076	hypothetical protein	3.18	5.62E-21
PA4949	hypothetical protein	3.11	2.14E-22
PA0332	hypothetical protein	3.10	9.28E-20
PA0088	hypothetical protein	3.09	1.64E-25
PA0920	hypothetical protein	3.07	3.89E-23
PA3796	hypothetical protein	3.03	1.97E-17
PA3789	hypothetical protein	3.02	4.62E-23
PA3419	hypothetical protein	2.99	1.89E-17
PA4488	hypothetical protein	2.97	2.04E-20
PA4369	hypothetical protein	2.97	1.05E-16
PA1149	hypothetical protein	2.95	5.03E-13
PA0435	hypothetical protein	2.93	2.50E-20
PA0093	hypothetical protein	2.92	1.13E-19
PA4066	hypothetical protein	2.92	1.25E-12
PA0082	hypothetical protein	2.89	1.63E-14
PA0168	hypothetical protein	2.85	3.38E-17
PA2374	hypothetical protein	2.84	1.36E-12
PA0878	hypothetical protein	2.84	2.43E-18
PA2207	hypothetical protein	2.83	2.70E-12
PA2542	hypothetical protein	2.82	1.25E-21
PA2183	hypothetical protein	2.78	3.12E-05
PA4543	hypothetical protein	2.77	6.99E-18
PA3985	hypothetical protein	2.77	9.88E-17
PA3354	hypothetical protein	2.73	6.66E-13
PA3535	serine protease	2.71	8.65E-20

PA2075	hypothetical protein	2.70	2.30E-12
PA0097	hypothetical protein	2.70	2.28E-14
PA5543	hypothetical protein	2.63	5.58E-13
PA2880	hypothetical protein	2.63	3.47E-10
PA3606	hypothetical protein	2.63	1.55E-14
PA5114	hypothetical protein	2.62	3.31E-18
PA3294	hypothetical protein	2.58	4.58E-14
PA2066	hypothetical protein	2.58	1.24E-11
PA3453	hypothetical protein	2.58	2.27E-12
PA1975	hypothetical protein	2.56	1.12E-11
PA4927	hypothetical protein	2.54	6.85E-18
PA1357	hypothetical protein	2.52	2.60E-09
PA4835	hypothetical protein	2.51	7.37E-10
PA0312	hypothetical protein	2.49	4.71E-13
PA2845	hypothetical protein	2.48	3.03E-07
PA2229	hypothetical protein	2.48	2.75E-10
PA4319	hypothetical protein	2.48	1.84E-09
PA2366	uricase	2.46	1.55E-13
PA4095	hypothetical protein	2.46	2.27E-10
PA0089	hypothetical protein	2.45	4.54E-14
PA5407	hypothetical protein	2.44	1.35E-08
PA2465	hypothetical protein	2.43	1.73E-09
PA0812	hypothetical protein	2.43	2.49E-10
PA2496	hypothetical protein	2.42	2.36E-08
PA3893	hypothetical protein	2.41	5.05E-14
PA2917	transcriptional regulator	2.34	9.18E-12
PA4491	hypothetical protein	2.34	3.16E-14
PA0875	hypothetical protein	2.33	2.88E-14
PA4635	hypothetical protein	2.28	2.28E-10
PA1494	hypothetical protein	2.25	4.52E-12
PA1434	hypothetical protein	2.25	2.40E-09
PA3110	hypothetical protein	2.24	1.32E-07
PA3626	tRNA pseudouridine synthase D	2.24	1.48E-09
PA2134	hypothetical protein	2.22	4.38E-07
PA5395	hypothetical protein	2.19	7.09E-09
PA3403	hypothetical protein	2.16	1.24E-06
PA1909	hypothetical protein	2.13	1.88E-05
PA4177	hypothetical protein	2.12	5.79E-08
PA1513	hypothetical protein	2.11	7.94E-10
cdhC	carnitine dehydrogenase	2.09	5.15E-08
PA0255	hypothetical protein	2.09	2.70E-07

PA1599	transcriptional regulator	2.04	8.06E-08
PA5151	hypothetical protein	2.03	1.12E-07
PA0079	hypothetical protein	2.03	6.09E-09
PA4035	hypothetical protein	2.03	7.98E-09
icmF1	type VI secretion protein IcmF	2.02	1.75E-10
PA0841	hypothetical protein	2.01	2.02E-07
PA2161	hypothetical protein	8.45	1.76E-24
PA1701	hypothetical protein	7.94	1.26E-42
PA2107	hypothetical protein	7.25	4.17E-22
PA1891	hypothetical protein	6.98	6.89E-30
PA1348	hypothetical protein	6.94	7.18E-49
PA1952	hypothetical protein	6.83	2.73E-41
PA2087	hypothetical protein	6.77	3.40E-31
PA4298	hypothetical protein	6.73	5.14E-32
PA2724	hypothetical protein	6.06	1.48E-41
PA1702	hypothetical protein	5.94	8.87E-23
pelC	pellicle/biofilm biosynthesis outer membrane protein PelC	5.91	2.26E-33
PA2782	hypothetical protein	5.91	1.04E-44
PA1848	major facilitator superfamily transporter	5.84	5.35E-47
PA2655	hypothetical protein	5.66	9.61E-32
PA2947	hypothetical protein	5.49	2.68E-34
pscH	type III export protein PscH	5.46	1.76E-29
PA3307	hypothetical protein	5.41	5.39E-27
PA2538	hypothetical protein	5.38	1.11E-32
PA4360a	hypothetical protein	5.33	1.60E-26
PA2441	hypothetical protein	5.22	1.39E-26
arnE	4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnE	5.20	7.01E-28
PA2173	hypothetical protein	5.14	2.49E-19
GeneID:878090	unknown	5.13	3.57E-38
PA0683	type II secretion system protein	5.08	5.48E-37
PA3884	hypothetical protein	5.07	1.18E-29
PA2095	hypothetical protein	5.06	1.34E-30
PA3089a	1-aminocyclopropane-1-carboxylate deaminase	5.04	2.04E-41
PA3411	hypothetical protein	5.03	2.66E-25
PA3072	hypothetical protein	5.02	1.57E-32
pcrR	transcriptional regulator PcrR	4.99	2.22E-25
PA0855	hypothetical protein	4.99	2.05E-40
PA4062	hypothetical protein	4.91	2.01E-28
pcrG	type III secretion regulator	4.89	2.04E-21

pscB	type III export apparatus protein	4.89	1.24E-29
PA1711	hypothetical protein	4.86	1.37E-09
pscG	type III export protein PscG	4.85	8.37E-22
popN	type III secretion outer membrane protein PopN	4.80	3.16E-21
PA1896	hypothetical protein	4.78	1.06E-25
PA3963a	hypothetical protein	4.77	1.93E-29
aprI	alkaline proteinase inhibitor AprI	4.76	2.66E-24
pscP	translocation protein in type III secretion	4.75	2.43E-22
arnF	4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnF	4.58	6.00E-28
PA3414	hypothetical protein	4.57	1.15E-34
PA1578	hypothetical protein	4.54	1.63E-29
PA2375	hypothetical protein	4.50	1.89E-24
GeneID:882922	unknown	4.50	2.96E-37
PA2581.1	tRNA-Cys	4.49	1.98E-06
PA1595	hypothetical protein	4.49	1.79E-34
GeneID:878920	unknown	4.47	3.94E-25
PA4027a	hypothetical protein	4.47	2.45E-36
pscI	type III export protein PscI	4.44	4.93E-10
PA2068	major facilitator superfamily transporter	4.43	1.26E-30
PA2928	hypothetical protein	4.43	2.02E-33
PA1700	hypothetical protein	4.42	1.07E-19
PA1855	hypothetical protein	4.42	1.19E-14
PA0345	hypothetical protein	4.39	3.32E-33
PA2434	hypothetical protein	4.37	1.43E-25
PA2747a	hypothetical protein	4.34	1.52E-19
PA1743	hypothetical protein	4.34	2.11E-11
PA2895	hypothetical protein	4.32	6.63E-28
PA0213	phosphoribosyl-dephospho-CoA transferase	4.32	2.45E-23
PA1483a	hypothetical protein	4.27	4.30E-21
PA1289	hypothetical protein	4.27	3.30E-28
pscO	translocation protein in type III secretion	4.23	1.30E-22
PA2702	hypothetical protein	4.18	5.61E-22
PA4824	hypothetical protein	4.18	3.99E-31
PA4816	hypothetical protein	4.17	9.89E-32
PA4346	hypothetical protein	4.17	3.43E-23
PA2503	hypothetical protein	4.15	3.35E-26
PA3684	hypothetical protein	4.09	1.29E-14
PA1956	hypothetical protein	4.06	1.07E-21
PA0753	hypothetical protein	4.04	4.83E-20

PA4220	hypothetical protein	3.99	5.36E-20
PA4679	hypothetical protein	3.98	2.73E-24
PA2898	hypothetical protein	3.96	1.53E-14
PA0630	hypothetical protein	3.96	1.65E-21
PA1955	hypothetical protein	3.95	1.52E-18
PA3292	hypothetical protein	3.95	2.08E-10
PA5183	hypothetical protein	3.94	1.59E-25
PA1967	hypothetical protein	3.91	4.62E-17
pscD	type III export protein PscD	3.89	3.97E-24
PA2167	hypothetical protein	3.87	1.06E-13
PA2720	hypothetical protein	3.86	3.15E-24
PA1228	hypothetical protein	3.85	4.42E-19
PA1356	hypothetical protein	3.83	8.69E-25
PA2406	hypothetical protein	3.82	6.03E-20
PA0028	hypothetical protein	3.79	8.67E-27
PA1545	hypothetical protein	3.72	2.46E-19
PA0700	hypothetical protein	3.69	3.16E-18
PA0800	hypothetical protein	3.63	1.05E-19
PA3939	hypothetical protein	3.61	7.98E-21
PA2729	hypothetical protein	3.61	4.48E-23
PA2136	hypothetical protein	3.61	1.82E-12
GeneID:882576	unknown	3.58	7.85E-34
opdB	OpdB proline porin	3.56	1.21E-21
PA2937	hypothetical protein	3.55	2.28E-14
PA3730	hypothetical protein	3.53	1.84E-22
PA0720	helix destabilizing protein of bacteriophage Pf1	3.52	7.14E-16
PA1213	hypothetical protein	3.48	2.01E-24
PA3273	hypothetical protein	3.48	4.94E-16
PA0721	hypothetical protein	3.48	7.42E-04
PA5120	hypothetical protein	3.47	1.61E-20
PA0668.5	5S ribosomal RNA	3.46	5.88E-03
PA2030	hypothetical protein	3.46	1.25E-10
PA2852.1	tRNA-Ser	3.44	1.70E-03
PA5115	hypothetical protein	3.42	2.82E-21
PA1870	hypothetical protein	3.39	1.70E-10
PA1745	hypothetical protein	3.38	3.58E-18
PA4871	hypothetical protein	3.34	2.03E-25
PA0729.1	tRNA-Gly	3.33	1.50E-06
PA1245	hypothetical protein	3.33	2.11E-18
PA2420	porin	3.32	1.41E-17
toxA	exotoxin A	3.32	1.42E-26

PA2660	hypothetical protein	3.30	3.59E-15
PA1676	hypothetical protein	3.25	8.37E-12
PA2783	hypothetical protein	3.24	1.41E-21
PA3207	hypothetical protein	3.23	3.48E-18
PA4791	hypothetical protein	3.19	2.24E-23
PA2450	hypothetical protein	3.19	1.79E-15
PA3290	hypothetical protein	3.17	6.48E-21
PA0111	hypothetical protein	3.16	3.90E-19
PA2440	hypothetical protein	3.16	6.62E-15
PA2789	hypothetical protein	3.14	6.46E-17
PA2436	hypothetical protein	3.12	5.93E-15
PA0349	hypothetical protein	3.11	2.06E-20
PA0614	hypothetical protein	3.11	1.01E-16
PA2122	hypothetical protein	3.09	1.21E-17
PA3788	hypothetical protein	3.06	2.51E-16
PA3298	hypothetical protein	3.04	2.06E-08
PA0311	hypothetical protein	3.04	5.16E-18
pqqA	coenzyme PQQ synthesis protein A	3.03	8.10E-06
PA1019a	thioesterase	3.03	3.36E-14
PA3680	ribosomal RNA small subunit methyltransferase J	3.02	3.19E-15
PA1133	hypothetical protein	3.02	1.55E-13
PA2049	hypothetical protein	3.00	6.13E-14
PA3178	hypothetical protein	2.97	1.55E-12
PA3784	hypothetical protein	2.97	1.70E-15
PA1160	hypothetical protein	2.96	3.16E-15
PA0701a	AraC family transcriptional regulator	2.96	3.02E-18
PA2829	hypothetical protein	2.95	1.14E-13
algJ	alginate o-acetylase AlgJ	2.94	1.65E-17
PA3317	hypothetical protein	2.94	5.08E-14
PA2004	hypothetical protein	2.93	9.74E-15
PA3065	hypothetical protein	2.91	1.42E-17
PA3081	hypothetical protein	2.91	1.06E-14
PA1615	lipase	2.90	1.68E-09
PA3464	hypothetical protein	2.90	2.09E-19
PA0522	hypothetical protein	2.89	1.24E-08
PA3075	hypothetical protein	2.89	2.10E-18
PA3293	hypothetical protein	2.88	2.50E-16
PA2380	hypothetical protein	2.85	5.08E-08
PA0802	hypothetical protein	2.84	3.46E-12
PA3907	hypothetical protein	2.82	4.32E-15
PA2251	hypothetical protein	2.81	9.18E-10

PA0418	hypothetical protein	2.80	2.97E-21
PA0433	hypothetical protein	2.79	2.04E-11
PA1394	hypothetical protein	2.79	4.52E-06
pscK	type III export protein PscK	2.79	3.50E-10
PA2180	hypothetical protein	2.78	5.80E-13
vreA	hypothetical protein	2.77	2.19E-14
PA0189	porin	2.77	1.09E-17
PA4801	hypothetical protein	2.77	9.71E-14
PA2919	hypothetical protein	2.76	4.84E-09
pslJ	biofilm formation protein PslJ	2.74	7.62E-17
GeneID:879324	transcriptional regulator	2.74	7.64E-16
GeneID:880420	unknown	2.70	5.27E-06
GeneID:878139	unknown	2.69	8.45E-17
PA2027	hypothetical protein	2.68	2.11E-09
PA4823	hypothetical protein	2.65	1.79E-07
PA1825	hypothetical protein	2.65	1.40E-13
PA5381	hypothetical protein	2.65	5.81E-11
PA4877	hypothetical protein	2.64	9.91E-08
piv	endopeptidase IV	2.64	9.47E-13
PA3274	hypothetical protein	2.63	5.08E-09
PA3786	hypothetical protein	2.61	1.93E-13
PA0309	hypothetical protein	2.61	7.12E-14
PA3421	hypothetical protein	2.60	2.67E-13
PA5502	hypothetical protein	2.59	7.23E-16
PA5182	hypothetical protein	2.59	2.03E-13
PA4775	hypothetical protein	2.58	1.61E-16
PA3969a	hypothetical protein	2.57	8.45E-09
PA0049	hypothetical protein	2.56	3.45E-15
PA0788a	hypothetical protein	2.55	9.73E-07
PA4758.1	P32	2.55	1.67E-03
PA4586	hypothetical protein	2.53	1.09E-09
PA2894	hypothetical protein	2.51	9.38E-09
PA0631	hypothetical protein	2.49	1.58E-07
PA3485	hypothetical protein	2.48	5.62E-11
PA3016	hypothetical protein	2.47	2.35E-09
PA5412	hypothetical protein	2.47	2.18E-16
PA2274	hypothetical protein	2.46	2.38E-07
PA0697	hypothetical protein	2.43	2.08E-09
atuA	hypothetical protein	2.43	1.62E-11

PA4325	hypothetical protein	2.42	1.09E-10
PA1844	hypothetical protein	2.41	2.32E-06
PA0383	hypothetical protein	2.41	2.81E-15
PA4179	porin	2.41	7.03E-14
PA1036	hypothetical protein	2.37	5.25E-11
PA4826	hypothetical protein	2.37	1.19E-06
PA1117	hypothetical protein	2.36	8.99E-08
PA1474	hypothetical protein	2.35	3.80E-13
PA3905	hypothetical protein	2.34	2.22E-08
PA0568	hypothetical protein	2.33	2.70E-08
PA1233	hypothetical protein	2.33	9.10E-07
PA0096	hypothetical protein	2.33	5.10E-06
opdT	tyrosine porin OpdT	2.32	2.83E-11
PA1043	hypothetical protein	2.31	1.29E-08
exsD	hypothetical protein	2.31	6.04E-09
PA1951	hypothetical protein	2.30	3.77E-11
PA1465	hypothetical protein	2.30	1.02E-08
PA0466	hypothetical protein	2.29	1.72E-07
PA2031	hypothetical protein	2.29	2.59E-04
PA5113	hypothetical protein	2.29	3.79E-11
algX	alginate biosynthesis protein AlgX	2.28	1.61E-09
PA2140	metallothionein	2.27	3.25E-03
PA1052a	hypothetical protein	2.25	2.87E-07
PA4851	hypothetical protein	2.25	2.32E-09
PA1652	hypothetical protein	2.24	1.62E-09
popD	translocator outer membrane protein PopD	2.24	1.67E-10
PA1645	hypothetical protein	2.24	1.60E-07
PA1123	hypothetical protein	2.24	7.67E-07
PA2173a	hypothetical protein	2.23	2.30E-04
PA1889	hypothetical protein	2.23	5.97E-09
PA3359	hypothetical protein	2.21	2.61E-09
PA1496	potassium channel	2.20	1.05E-07
PA3850	hypothetical protein	2.20	2.02E-10
PA4071	hypothetical protein	2.19	2.04E-07
PA0377	hypothetical protein	2.19	1.69E-09
PA1929	hypothetical protein	2.18	9.65E-07
PA3069	hypothetical protein	2.18	1.06E-08
PA5318	hypothetical protein	2.18	3.53E-09
PA5156	hypothetical protein	2.16	1.49E-11
PA3386	hypothetical protein	2.16	1.72E-07
PA0599	hypothetical protein	2.15	2.68E-08

PA0696	hypothetical protein	2.15	2.68E-11
PA3960	hypothetical protein	2.13	5.08E-06
PA1624	hypothetical protein	2.12	1.58E-09
PA3318	hypothetical protein	2.11	1.54E-06
PA3906	hypothetical protein	2.11	1.15E-04
PA3720	hypothetical protein	2.10	2.56E-06
PA1872	hypothetical protein	2.09	3.87E-06
PA2117	hypothetical protein	2.09	4.66E-05
PA4724.1	hypothetical protein	2.09	6.35E-04
PA0850	hypothetical protein	2.08	5.81E-07
PA1578a	hypothetical protein	2.06	1.52E-04
PA1111	hypothetical protein	2.06	2.18E-06
PA1471	hypothetical protein	2.05	2.62E-04
algL	alginate lyase	2.05	2.73E-09
PA4684	hypothetical protein	2.04	8.40E-10
PA1865	Fanconi-associated nuclease	2.02	1.29E-07
armR	MexR antirepressor ArmR	2.01	6.51E-04
PA1892	hypothetical protein	2.00	6.51E-06
PA1332	hypothetical protein	2.00	3.85E-07
General function prediction only			
PA1266	oxidoreductase	7.10	7.11E-58
PA1921	hypothetical protein	6.91	9.71E-26
PA2689	hypothetical protein	6.84	1.42E-45
pslK	biofilm formation protein PslL	6.64	2.28E-50
PA2498	hypothetical protein	6.32	2.70E-37
PA2874	hypothetical protein	6.09	6.48E-50
PA2067	hydrolase	5.77	4.18E-32
PA2061	ABC transporter ATP-binding protein	5.75	8.18E-46
PA2156	hypothetical protein	5.73	1.23E-33
PA1211	hypothetical protein	5.60	2.19E-36
PA1329	hypothetical protein	5.52	7.14E-37
hcnA	hydrogen cyanide synthase subunit HcnA	5.47	2.93E-24
PA2680	quinone oxidoreductase	5.10	3.41E-39
hasD	transporter HasD	5.08	1.42E-41
PA0489	phosphoribosyl transferase	5.07	4.40E-39
algK	alginate biosynthesis protein AlgK	5.04	8.40E-43
PA1488	hypothetical protein	5.02	2.29E-41
PA1558	hypothetical protein	5.01	9.00E-37
PA2803	hypothetical protein	4.97	1.01E-34
PA3432	hypothetical protein	4.86	5.17E-28
PA1425	ABC transporter ATP-binding protein	4.85	8.68E-39

PA1907	hypothetical protein	4.82	4.85E-33
PA2099	short-chain dehydrogenase	4.76	3.05E-20
PA3209	hypothetical protein	4.71	4.51E-31
PA1885	hypothetical protein	4.68	3.64E-31
PA5144	hypothetical protein	4.68	1.10E-32
atuG	short-chain dehydrogenase	4.67	5.89E-32
PA2719	hypothetical protein	4.66	8.01E-35
PA4097	alcohol dehydrogenase	4.64	7.88E-40
PA2984	hypothetical protein	4.57	1.36E-42
PA3457	hypothetical protein	4.56	2.86E-36
PA2211	hypothetical protein	4.47	9.86E-27
PA2088	hypothetical protein	4.41	4.42E-29
PA1227	hypothetical protein	4.38	4.46E-35
PA3330	short-chain dehydrogenase	4.35	1.37E-28
PA2086	epoxide hydrolase	4.34	2.19E-19
PA0787	hypothetical protein	4.29	1.09E-35
PA2455	hypothetical protein	4.29	5.27E-19
PA2922	hydrolase	4.27	1.64E-32
PA1225	NAD(P)H dehydrogenase	4.25	5.08E-23
pelB	pellicle/biofilm biosynthesis protein PelB	4.25	5.90E-40
rhlC	rhamnosyltransferase	4.24	1.71E-32
PA0741	hypothetical protein	4.24	7.78E-26
PA2847	hypothetical protein	4.18	1.28E-29
PA2059	ABC transporter permease	4.14	1.87E-22
xylL	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	4.13	2.79E-15
aprD	alkaline protease secretion ATP-binding protein AprD	4.08	5.44E-32
PA2176	hypothetical protein	4.02	1.48E-16
PA4202	hypothetical protein	4.02	1.35E-16
nosY	membrane protein NosY	4.00	1.68E-30
PA2074	hypothetical protein	3.93	1.65E-05
PA2158	alcohol dehydrogenase	3.93	1.43E-21
PA3272	ATP-dependent DNA helicase	3.86	9.45E-39
PA2141	hypothetical protein	3.85	5.09E-13
PA1680	hypothetical protein	3.84	4.07E-22
PA2448	hypothetical protein	3.81	1.09E-24
phzF2	trans-2,3-dihydro-3-hydroxyanthranilate isomerase	3.80	5.93E-22
PA4783	hypothetical protein	3.78	7.11E-31
phzF1	trans-2,3-dihydro-3-hydroxyanthranilate isomerase	3.75	6.52E-28
PA1451	hypothetical protein	3.75	2.60E-25

PA5132	hypothetical protein	3.72	7.02E-29
PA3287	hypothetical protein	3.71	1.30E-23
PA2778	hypothetical protein	3.69	6.42E-17
PA3036	hypothetical protein	3.68	5.51E-24
PA0086	hypothetical protein	3.67	1.41E-29
PA1330	short-chain dehydrogenase	3.65	2.09E-23
PA1503	hypothetical protein	3.64	4.27E-18
PA4365	transporter	3.61	3.52E-17
pslC	biofilm formation protein PslC	3.60	1.58E-17
PA2529	hypothetical protein	3.56	2.00E-23
PA2168	hypothetical protein	3.56	3.51E-14
PA2060	ABC transporter permease	3.53	4.76E-19
PA1612	hypothetical protein	3.50	2.25E-21
PA1360	hypothetical protein	3.50	9.53E-24
PA4802	hypothetical protein	3.46	8.14E-23
PA2271	acetyltransferase	3.44	1.25E-18
PA2745	hydrolase	3.43	9.44E-18
PA2712	hypothetical protein	3.40	6.63E-24
PA4312	hypothetical protein	3.39	8.76E-18
PA2197	hypothetical protein	3.39	1.60E-21
hcnB	hydrogen cyanide synthase subunit HcnB	3.38	4.61E-22
PA0136	ABC transporter ATP-binding protein	3.38	6.41E-20
PA0790	hypothetical protein	3.34	8.48E-24
PA2201	hypothetical protein	3.33	4.32E-16
PA2502	hypothetical protein	3.30	3.11E-25
pvdQ	acyl-homoserine lactone acylase PvdQ	3.25	1.15E-23
PA5466	hypothetical protein	3.25	2.09E-22
PA0881	hypothetical protein	3.24	1.35E-21
PA2192	hypothetical protein	3.23	3.80E-13
PA3259	hypothetical protein	3.20	2.43E-18
PA5352	hypothetical protein	3.20	8.06E-17
PA2875	hypothetical protein	3.19	1.34E-21
PA2454	hypothetical protein	3.18	3.92E-14
PA0440	oxidoreductase	3.14	2.76E-19
PA3132	hydrolase	3.13	9.84E-19
PA4098	short-chain dehydrogenase	3.13	6.24E-16
PA3074	hypothetical protein	3.12	6.99E-21
PA0480	3-oxoadipate enol-lactonase	3.12	4.40E-17
PA3618	hypothetical protein	3.10	5.88E-19
PA0278	hypothetical protein	3.10	1.36E-18
PA4344	hydrolase	3.08	1.44E-23

PA3423	transcriptional regulator	3.05	8.37E-19
PA0344	hypothetical protein	3.02	4.69E-19
PA3586	hydrolase	2.99	1.12E-15
PA2635	hypothetical protein	2.98	5.48E-14
PA4986	oxidoreductase	2.98	1.10E-21
PA3941	hypothetical protein	2.98	1.82E-17
PA0629	hypothetical protein	2.94	1.42E-17
PA1316	major facilitator superfamily transporter	2.93	1.81E-17
PA1839	RNA methyltransferase	2.92	7.48E-15
PA1917	hypothetical protein	2.92	2.75E-08
PA5145	hypothetical protein	2.88	6.45E-18
PA0810	haloacid dehalogenase	2.88	3.80E-17
PA5430	hypothetical protein	2.84	2.18E-14
PA3693	hypothetical protein	2.83	1.54E-14
PA3073	hypothetical protein	2.83	9.95E-17
nirQ	denitrification regulatory protein NirQ	2.82	7.26E-12
cdhB	carnitine dehydrogenase	2.79	7.90E-11
PA1824	hypothetical protein	2.78	3.12E-12
ldhA	D-lactate dehydrogenase	2.77	7.00E-14
PA2530	hypothetical protein	2.74	1.74E-14
PA0063	hypothetical protein	2.73	3.59E-19
PA1893	hypothetical protein	2.72	2.53E-18
PA3071	hypothetical protein	2.70	4.68E-16
PA1470	short-chain dehydrogenase	2.69	2.19E-11
PA1972	hypothetical protein	2.69	1.19E-15
PA3241	hypothetical protein	2.68	1.23E-17
PA3957	short-chain dehydrogenase	2.68	6.26E-13
PA0751	hypothetical protein	2.64	2.46E-15
PA0891	hypothetical protein	2.63	8.57E-15
pqqB	coenzyme PQQ synthesis protein B	2.63	1.52E-13
PA3324	short-chain dehydrogenase	2.59	2.74E-14
PA4162	short-chain dehydrogenase	2.59	5.79E-13
ppkA	serine/threonine protein kinase PpkA	2.58	6.21E-15
PA3368	acetyltransferase	2.58	1.35E-11
PA0137	ABC transporter permease	2.55	2.81E-12
PA1024	nitronate monooxygenase	2.55	1.63E-13
eddB	extracelullar DNA degradation protein EddB	2.54	3.97E-14
PA0562	hydrolase	2.53	5.49E-15
PA2275	alcohol dehydrogenase	2.52	5.09E-13
PA1407	hypothetical protein	2.52	1.27E-12
hprA	glycerate dehydrogenase	2.46	7.31E-13

PA3668	hypothetical protein	2.45	4.56E-12
PA4803	hypothetical protein	2.45	3.26E-08
nirJ	heme d1 biosynthesis protein NirJ	2.45	2.08E-10
PA3829	hypothetical protein	2.44	1.27E-13
PA3332	hypothetical protein	2.44	1.83E-08
PA0237	oxidoreductase	2.43	9.22E-12
PA3856	hypothetical protein	2.43	3.15E-10
PA5031	short-chain dehydrogenase	2.43	2.03E-11
phzB2	phenazine biosynthesis protein PhzB	2.39	2.24E-05
PA4962	hypothetical protein	2.38	2.09E-11
PA4832	short-chain dehydrogenase	2.38	2.29E-09
PA3958	hypothetical protein	2.38	2.12E-11
PA1411	hypothetical protein	2.36	2.01E-11
pmbA	PmbA protein	2.35	5.95E-12
PA4612	hypothetical protein	2.34	2.96E-11
PA1402	hypothetical protein	2.33	1.99E-10
PA1418	sodium:solute symport protein	2.32	2.13E-12
PA2804	hypothetical protein	2.31	1.56E-08
PA0138	ABC transporter permease	2.30	4.74E-10
PA1450	hypothetical protein	2.29	8.69E-12
PA3949	hypothetical protein	2.27	3.19E-12
PA3214	hypothetical protein	2.27	6.96E-10
pqqE	coenzyme PQQ synthesis protein E	2.26	1.45E-09
pcaD	3-oxoadipate enol-lactonase	2.23	2.36E-09
PA2418	quercetin 2,3-dioxygenase	2.22	1.64E-08
PA4350	hypothetical protein	2.19	1.58E-06
PA4475	hypothetical protein	2.19	9.53E-12
PA1943	hypothetical protein	2.18	4.76E-09
PA3429	epoxide hydrolase	2.17	2.48E-10
PA2188	alcohol dehydrogenase	2.17	2.47E-06
PA1649	short-chain dehydrogenase	2.16	1.13E-06
PA0201	hypothetical protein	2.13	5.59E-08
PA3109	hypothetical protein	2.13	3.59E-06
PA0246	major facilitator superfamily transporter	2.13	2.15E-11
PA4323	hypothetical protein	2.12	1.70E-10
PA3425	hypothetical protein	2.08	1.04E-05
gpuP	3-guanidinopropionate transporter	2.08	2.25E-09
PA3037	hypothetical protein	2.06	7.33E-06
PA4200	hypothetical protein	2.05	5.17E-08
PA3093	hypothetical protein	2.02	8.36E-08
PA4322	hypothetical protein	2.00	7.14E-09

PA1137	oxidoreductase	2.00	2.13E-07
Inorganic ion transport and metabolism			
PA2055	major facilitator superfamily transporter	6.70	1.52E-47
foxR	anti-sigma factor FoxR	6.49	3.82E-51
PA3409	transmembrane sensor	6.18	9.52E-37
PA2435	cation-transporting P-type ATPase	5.78	3.43E-51
PA1262	major facilitator superfamily transporter	5.67	9.12E-54
PA2135	transporter	5.41	6.28E-41
PA2914	ABC transporter permease	5.35	1.75E-44
fepD	ferric enterobactin transporter FepD	5.33	1.70E-30
PA3380	hypothetical protein	5.28	2.84E-24
PA3442	aliphatic sulfonates ABC transporter ATP-binding subunit	5.27	6.39E-34
PA1626	major facilitator superfamily transporter	5.21	1.42E-45
PA2701	major facilitator superfamily transporter	5.15	6.12E-49
PA3900	transmembrane sensor	5.14	1.28E-40
PA3448	ABC transporter permease	5.00	2.79E-37
PA2051	transmembrane sensor	4.98	1.58E-25
PA2906	oxidoreductase	4.95	6.23E-38
fepG	ferric enterobactin transporter FepG	4.84	8.20E-41
arsB	arsenite-antimonite efflux pump ArsB	4.81	5.11E-41
PA3314	phosphonates ABC transporter ATP-binding protein	4.50	4.22E-36
PA2913	hypothetical protein	4.45	1.13E-33
PA3315	phosphonates ABC transporter permease	4.26	4.47E-27
PA4289	transporter	4.18	3.26E-34
PA0273	major facilitator superfamily transporter	4.11	2.32E-28
PA0185	ABC transporter permease	4.07	6.82E-28
PA2033	hypothetical protein	4.06	1.41E-22
nasA	nitrate transporter	4.02	2.11E-30
PA3316	ABC transporter permease	4.02	2.82E-31
fepC	ferric enterobactin transporter FepC	3.95	1.05E-31
PA0525	denitrification protein NorD	3.95	8.99E-34
PA3376	phosphonate C-P lyase system protein PhnK	3.92	3.83E-28
PA3379	carbon-phosphorus lyase complex subunit	3.84	3.60E-23
xylX	toluate 1,2-dioxygenase subunit alpha	3.78	1.97E-21
vreR	sigma factor regulator VreR	3.78	2.52E-25
phnC	phosphonate ABC transporter ATP-binding protein	3.71	6.80E-24
PA1301	transmembrane sensor	3.65	3.23E-24
cynT	carbonic anhydrase	3.62	2.93E-20
pcoB	copper resistance protein B	3.61	1.05E-16

PA1549	cation-transporting P-type ATPase	3.60	4.14E-32
femA	ferric-mycobactin receptor FemA	3.58	1.09E-22
PA0471	transmembrane sensor	3.54	1.05E-27
nosD	copper-binding periplasmic protein	3.48	4.12E-24
PA0703	major facilitator superfamily transporter	3.40	6.99E-21
PA1922	TonB-dependent receptor	3.37	6.51E-23
PA2500	major facilitator superfamily transporter	3.36	8.33E-20
PA4513	oxidoreductase	3.32	5.05E-28
PA0809	divalent metal cation transporter MntH	3.31	4.09E-26
PA3375	ABC transporter ATP-binding protein	3.28	1.69E-21
PA4706	hemin importer ATP-binding subunit	3.24	1.73E-23
PA3936	taurine ABC transporter permease	3.22	3.26E-22
PA3937	taurine ABC transporter ATP-binding protein	3.11	1.38E-20
PA5216	iron ABC transporter substrate-binding protein	3.03	1.14E-23
PA4707	ABC transporter permease	2.99	9.50E-21
PA3373	hypothetical protein	2.97	3.10E-17
PA4709	hemin degrading factor	2.92	1.73E-19
cynS	cyanate hydratase	2.92	2.04E-11
fepB	iron-enterobactin transporter periplasmic binding protein	2.92	5.17E-15
PA2603	thiosulfate sulfurtransferase	2.91	4.24E-18
napD	nitrate reductase biosynthesis protein NapD	2.91	8.69E-09
PA2097	flavin-binding monooxygenase	2.88	3.77E-13
PA3374	hypothetical protein	2.84	7.75E-19
PA1209	hypothetical protein	2.83	3.73E-14
PA2057	hypothetical protein	2.80	8.49E-15
PA1548	hypothetical protein	2.75	4.09E-05
PA2089	hypothetical protein	2.66	4.84E-12
PA2662	hypothetical protein	2.64	1.24E-12
PA2777	hypothetical protein	2.64	9.44E-14
phuT	heme-transporter PhuT	2.63	8.49E-15
vanA	vanillate O-demethylase oxygenase	2.59	3.74E-09
PA0029	sulfate transporter	2.57	5.44E-17
PA3443	ABC transporter permease	2.54	1.85E-11
PA2384	hypothetical protein	2.52	4.71E-05
PA2408	ABC transporter ATP-binding protein	2.50	2.42E-12
PA3447	ABC transporter ATP-binding protein	2.48	2.47E-12
PA3378	hypothetical protein	2.47	8.92E-13
PA3920	metal transporting P-type ATPase	2.43	8.91E-09
PA4822	hypothetical protein	2.42	1.63E-11
PA2407	adhesion protein	2.40	1.13E-09
PA2596	hypothetical protein	2.40	1.23E-12

PA3449	hypothetical protein	2.39	7.35E-12
PA2070	hypothetical protein	2.36	9.29E-09
PA1364	transmembrane sensor	2.36	2.14E-11
modC	molybdenum ABC transporter ATP-binding protein ModC	2.30	3.38E-11
czcA	resistance-nodulation-cell division (RND) divalent metal cation efflux transporter CzcA	2.29	1.98E-11
PA1056	monovalent cation/H+ antiporter subunit D	2.28	1.42E-11
PA4045	hypothetical protein	2.27	8.41E-11
eddA	extracelullar DNA degradation protein EddA	2.26	4.60E-10
pfeA	ferric enterobactin receptor	2.26	1.50E-11
foxA	ferrioxamine receptor FoxA	2.24	1.09E-10
PA5311	major facilitator superfamily transporter	2.16	8.01E-11
PA5101	hypothetical protein	2.13	1.94E-09
PA3465	hypothetical protein	2.10	8.23E-10
hasR	heme uptake outer membrane receptor HasR	2.09	2.05E-10
PA2765	hypothetical protein	2.02	2.21E-07
PA2594	hypothetical protein	2.02	3.75E-05
PA0151	TonB-dependent receptor	2.01	7.07E-08
PA0103	sulfate transporter	2.00	4.39E-10
Intracellular trafficking, secretion, and vesicular transport			
xphA	type VI pilus biosynthesis protein	8.15	3.64E-39
PA1238	multidrug efflux pump outer membrane protein	6.53	1.20E-52
PA2837	hypothetical protein	5.94	7.52E-55
cupA5	chaperone CupA5	5.40	6.90E-18
czcC	outer membrane protein CzcC	5.22	6.34E-46
xcpZ	type II secretion system protein M	4.83	2.05E-33
opmD	hypothetical protein	4.81	2.40E-40
tadD	type II secretion system protein TadD	4.78	3.55E-35
xcpY	type II secretion system protein L	4.77	5.42E-43
PA0677	HxcW pseudopilin	4.77	5.49E-31
PA3340	hypothetical protein	4.76	1.92E-38
PA0678	HxcU pseudopilin	4.62	3.10E-30
PA3521	hypothetical protein	4.57	5.80E-30
PA0682	HxcX atypical pseudopilin	4.04	4.80E-33
PA0021	hypothetical protein	3.93	2.75E-25
oprN	multidrug efflux outer membrane protein OprN	3.90	1.91E-26
PA4144	hypothetical protein	3.76	1.13E-25
PA0684	type II secretion system protein	3.69	1.03E-21
cupA4	fimbrial subunit CupA4	3.59	3.53E-19
PA3894	hypothetical protein	3.54	3.22E-26
rcpC	hypothetical protein	3.50	2.11E-24

cupA3	usher CupA3	3.45	5.63E-25
PA0041	hemagglutinin	3.40	6.52E-28
PA1924	hypothetical protein	3.37	2.84E-08
PA5158	hypothetical protein	3.19	2.78E-21
cupA1	fimbrial subunit CupA1	3.09	1.54E-09
xcpW	type II secretion system protein J	3.04	1.17E-17
tadZ	hypothetical protein	2.99	1.71E-20
pscL	type III secretion system protein	2.98	4.52E-12
PA4718	hypothetical protein	2.94	1.84E-16
PA0040	hypothetical protein	2.79	3.69E-20
PA2463	hypothetical protein	2.71	3.78E-17
pcrD	type III secretory apparatus protein PcrD	2.61	1.60E-15
oprJ	multidrug efflux outer membrane protein OprJ	2.52	8.10E-16
PA0690	hypothetical protein	2.43	3.79E-18
xcpR	type II secretion system protein E	2.42	6.51E-14
xcpX	type II secretion system protein K	2.42	5.30E-10
exbB1	transporter ExbB	2.37	3.80E-09
tadB	type II secretion system protein TadB	2.33	2.69E-10
aprF	alkaline protease secretion protein AprF	2.32	9.97E-11
xcpV	type II secretion system protein I	2.31	1.87E-08
PA2462	hypothetical protein	2.06	1.54E-12
Lipid transport and metabolism			
PA2098	esterase	9.93	5.83E-70
atuE	isohexenylglutaconyl-CoA hydratase	6.76	5.07E-48
PA2539	hypothetical protein	5.53	9.08E-44
PA2597	hypothetical protein	5.33	6.05E-39
PA1021	enoyl-CoA hydratase	5.28	6.51E-44
PA1020	acyl-CoA dehydrogenase	4.83	2.46E-39
PA1628	3-hydroxyacyl-CoA dehydrogenase	4.80	1.25E-40
PA2155	cardiolipin synthase 2	4.78	5.41E-25
PA5384	lipolytic protein	4.55	8.34E-30
PA3589	acetyl-CoA acetyltransferase	4.52	4.40E-37
fabH2	3-oxoacyl-ACP synthase III	4.27	9.59E-33
PA3023	lipid kinase	4.26	4.74E-25
atuF	geranyl-CoA carboxylase subunit alpha	4.24	2.12E-28
mdcE	malonate decarboxylase subunit gamma	4.21	2.10E-23
PA1400	pyruvate carboxylase	4.09	1.29E-36
mmsB	3-hydroxyisobutyrate dehydrogenase	4.06	2.54E-25
PA3312	3-hydroxyisobutyrate dehydrogenase	4.06	6.21E-24
PA2927	hypothetical protein	3.94	2.58E-33
PA0214	acyl transferase	3.83	2.89E-25

PA3590	3-hydroxyacyl-CoA dehydrogenase	3.83	2.74E-31
PA4980	enoyl-CoA hydratase	3.72	3.32E-24
PA0190	acid phosphatase	3.58	2.31E-22
PA3911	hypothetical protein	3.54	5.94E-20
PA3591	enoyl-CoA hydratase	3.52	3.26E-16
azoR2	FMN-dependent NADH-azoreductase	3.50	5.95E-16
PA4349	hypothetical protein	3.49	8.22E-22
PA3593	acyl-CoA dehydrogenase	3.45	4.37E-28
PA0743	NAD-dependent L-serine dehydrogenase	3.40	1.20E-26
PA4008	hydrolase	3.37	3.97E-24
PA4788	hypothetical protein	3.31	4.62E-23
PA2841	enoyl-CoA hydratase	3.26	6.40E-21
PA3426	enoyl-CoA hydratase	3.16	5.05E-19
PA4339	phospholipase	3.14	2.76E-23
PA1827	short-chain dehydrogenase	3.10	2.13E-13
PA2940	acyl-CoA thiolase	3.10	2.28E-19
PA3568	propionyl-CoA synthetase	2.95	2.65E-22
cdhA	3-hydroxybutyryl-CoA dehydrogenase	2.89	9.22E-18
PA5102	hypothetical protein	2.86	5.55E-18
PA1629	enoyl-CoA hydratase	2.79	2.31E-12
PA1018	hypothetical protein	2.77	4.07E-15
PA0494	acetyl-CoA carboxylase biotin carboxylase subunit	2.60	1.08E-15
ygbP	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	2.60	2.13E-14
PA0744	enoyl-CoA hydratase	2.45	1.25E-12
PA1869	acyl carrier protein	2.41	6.45E-05
pcaF	beta-ketoadipyl CoA thiolase	2.40	2.96E-10
atuC	geranyl-CoA carboxylase subunit beta	2.40	1.17E-10
PA5089	hypothetical protein	2.27	5.22E-11
PA2540	hypothetical protein	2.26	4.15E-10
PA4011	hypothetical protein	2.25	1.26E-11
PA0308	hypothetical protein	2.22	1.79E-11
PA5188	3-hydroxyacyl-CoA dehydrogenase	2.16	6.92E-12
PA2002	hypothetical protein	2.16	2.06E-09
mdcA	malonate decarboxylase subunit alpha	2.15	3.57E-09
PA3925	acyl-CoA thiolase	2.15	2.35E-08
PA0227	CoA transferase subunit B	2.12	2.94E-06
PA3994	epoxide hydrolase	2.10	1.18E-08
PA2871	hypothetical protein	2.06	4.49E-08
PA2554	short-chain dehydrogenase	2.06	4.94E-04
PA1016	thiolase	2.04	2.70E-08

Nucleotide transport and metabolism			
PA2268	hypothetical protein	6.30	1.57E-38
pyrF	orotidine 5'-phosphate decarboxylase	3.57	1.38E-22
pcaB	3-carboxy-cis,cis-muconate cycloisomerase	3.05	8.21E-19
xdhA	xanthine dehydrogenase	2.75	2.28E-15
PA0144	hypothetical protein	2.72	1.19E-16
codB	cytosine permease	2.51	5.52E-16
tmk	thymidylate kinase	2.41	2.90E-10
PA2625	hypothetical protein	2.38	7.77E-07
PA0166	transporter	2.15	1.08E-09
PA3517	adenylosuccinate lyase	2.14	1.84E-10
PA1419	transporter	2.02	1.24E-07
xdhB	xanthine dehydrogenase	2.01	9.83E-07
Posttranslational modification, protein turnover, chaperones			
pqqF	coenzyme PQQ synthesis protein F	7.39	2.48E-57
PA2437	hypothetical protein	7.22	2.50E-58
PA2439	hypothetical protein	7.19	4.53E-62
PA2473	glutathione S-transferase	5.84	6.48E-35
PA2478	thiol:disulfide interchange protein DsbD	5.33	3.34E-49
PA2438	hypothetical protein	5.29	1.48E-41
PA4894	hypothetical protein	5.07	8.98E-40
nrdG	class III (anaerobic) ribonucleoside-triphosphate reductase activating protein NrdG	4.86	4.90E-36
ureF	urease accessory protein UreF	4.66	1.93E-23
ureD	urease accessory protein	4.60	8.03E-33
PA2371	ClpA/B-type protease	4.44	1.36E-24
PA0699	PpiC-type peptidyl-prolyl cis-trans isomerase	4.42	4.57E-34
PA3685	hypothetical protein	4.36	2.32E-28
PA0451	hypothetical protein	4.28	8.75E-32
PA0859	hypothetical protein	3.97	9.27E-19
PA0058	hypothetical protein	3.82	1.05E-28
PA5211	hypothetical protein	3.61	3.44E-24
PA0277	hypothetical protein	3.57	8.28E-20
PA2069	carbamoyl transferase	3.53	1.04E-25
PA2725	chaperone	3.31	3.74E-24
PA4170	hypothetical protein	3.31	2.98E-15
PA1242	hypothetical protein	3.19	5.64E-23
PA1662	ClpA/B-type protease	3.17	3.63E-20
PA0112	hypothetical protein	3.12	5.90E-15
ureE	urease accessory protein UreE	3.00	6.67E-14
PA1522	hypothetical protein	2.94	9.26E-18
PA2694	thioredoxin	2.93	2.12E-12

ccmA	cytochrome c biogenesis ATP-binding export protein CcmA	2.81	3.35E-17
PA5290	hypothetical protein	2.76	1.28E-19
dipZ	thiol:disulfide interchange protein	2.76	7.21E-18
PA0113	protoheme IX farnesyltransferase	2.73	2.94E-18
PA3365	chaperone	2.60	1.32E-14
dsbB	disulfide bond formation protein	2.48	6.54E-11
lipH	lipase chaperone	2.44	5.99E-11
PA0473	glutathione S-transferase	2.41	6.44E-12
fdhE	formate dehydrogenase subunit epsilon	2.40	4.63E-14
PA2726	radical activating enzyme	2.36	1.40E-10
PA1890	glutathione S-transferase	2.28	9.27E-09
clpV1	secretion protein ClpV1	2.27	4.24E-14
PA1068	heat shock protein	2.23	3.90E-13
PA0467	hypothetical protein	2.17	1.89E-08
PA3871	PpiC-type peptidyl-prolyl cis-trans isomerase	2.04	9.36E-08
Replication, recombination and repair			
PA2750	hypothetical protein	5.42	4.80E-33
pslN	hypothetical protein	4.63	1.03E-35
ada	O6-methylguanine-DNA methyltransferase	4.43	8.45E-26
recO	DNA repair protein RecO	4.05	1.04E-22
PA1782	serine/threonine-protein kinase	3.92	9.25E-33
PA3564	hypothetical protein	3.89	2.19E-28
PA3596	methylated-DNA--protein-cysteine methyltransferase	3.61	6.37E-28
PA0670	hypothetical protein	3.53	4.30E-22
PA4392	hypothetical protein	3.44	5.13E-12
PA0799	helicase	2.88	1.90E-20
PA4172	nuclease	2.81	2.06E-16
PA3961	ATP-dependent helicase	2.80	3.84E-18
recD	exodeoxyribonuclease V subunit alpha	2.71	2.28E-20
alkA	DNA-3-methyladenine glycosidase II	2.47	9.57E-10
sss	site-specific tyrosine recombinase XerC	2.47	3.15E-14
polB	DNA polymerase II	2.41	7.87E-10
priA	primosome assembly protein PriA	2.29	2.15E-14
xseA	exodeoxyribonuclease VII large subunit	2.21	2.46E-10
PA3470	hypothetical protein	2.16	5.10E-08
recC	exodeoxyribonuclease V subunit gamma	2.12	4.92E-11
mttC	secretion protein MttC	2.11	4.72E-08
holB	DNA polymerase III subunit delta'	2.01	1.10E-05
RNA processing and modification			
rtcA	RNA 3'-terminal-phosphate cyclase	3.54	6.71E-29

Secondary metabolites biosynthesis, transport and catabolism			
PA2034	hypothetical protein	6.47	2.16E-40
pvcB	paerucumarin biosynthesis protein PvcB	5.99	1.46E-41
PA1219	hypothetical protein	5.91	3.66E-44
PA2411	thioesterase	5.42	2.68E-28
pcpS	4'-phosphopantetheinyl transferase	5.27	4.53E-42
pvcC	paerucumarin biosynthesis protein PvcC	4.74	1.59E-35
PA2475	cytochrome P450	4.69	3.39E-29
pvdL	peptide synthase	4.69	4.89E-43
PA1220	hypothetical protein	4.53	3.74E-38
PA3329	hypothetical protein	4.47	7.97E-24
PA2858	hypothetical protein	4.34	1.73E-39
PA4089	3-ketoacyl-ACP reductase	4.32	1.08E-22
PA1215	hypothetical protein	4.32	3.37E-32
PA4148	short-chain dehydrogenase	4.21	3.17E-29
PA3327	non-ribosomal peptide synthetase	4.18	1.64E-40
phzD1	phenazine biosynthesis protein PhzD	4.10	1.13E-25
PA1379	short-chain dehydrogenase	4.06	8.69E-25
PA2857	ABC transporter ATP-binding protein	3.88	9.36E-27
phzD2	phenazine biosynthesis protein PhzD	3.79	1.57E-21
PA2471	hypothetical protein	3.78	1.14E-18
PA4786	3-ketoacyl-ACP reductase	3.77	8.76E-28
PA3774	acetylpolyamine aminohydrolase	3.72	1.84E-28
gtdA	gentisate 1,2-dioxygenase	3.65	3.09E-23
PA3679	hypothetical protein	3.59	8.87E-31
pvdJ	pyoverdine biosynthesis protein PvdJ	3.30	1.07E-06
PA2402	peptide synthase	3.26	5.01E-26
PA3783	hypothetical protein	3.23	7.97E-19
PA0543	hypothetical protein	3.14	9.53E-21
PA3076	hypothetical protein	3.13	2.91E-22
PA0098	3-oxoacyl-ACP synthase	3.08	3.05E-20
PA1221	hypothetical protein	3.06	3.75E-23
PA3953	hypothetical protein	3.02	1.69E-17
pcoA	copper resistance protein A	3.00	2.09E-17
fabF2	3-oxoacyl-ACP synthase	2.99	4.13E-14
PA4078	nonribosomal peptide synthetase	2.87	2.18E-18
PA3883	short-chain dehydrogenase	2.84	5.94E-17
PA4093	hypothetical protein	2.76	3.92E-13
PA0474	esterase	2.75	8.41E-12
PA1860	hypothetical protein	2.69	3.50E-14
catA	catechol 1,2-dioxygenase	2.64	5.03E-16

PA0117	short-chain dehydrogenase	2.60	6.09E-12
atuB	citronellol catabolism dehydrogenase	2.47	1.81E-10
pvdA	L-ornithine N5-oxygenase	2.47	2.26E-03
PA3212	ABC transporter ATP-binding protein	2.39	6.89E-10
PA3331	cytochrome P450	2.39	1.54E-10
PA3846	hypothetical protein	2.36	1.33E-09
PA4830	hypothetical protein	2.31	3.18E-05
PA1593	hypothetical protein	2.30	5.45E-07
PA1166	hypothetical protein	2.29	3.57E-10
pchC	pyochelin biosynthetic protein PchC	2.27	1.08E-08
PA4021	transcriptional regulator	2.26	6.49E-10
PA0194	hypothetical protein	2.25	2.24E-09
acoR	transcriptional regulator AcoR	2.25	1.35E-10
PA1594	hypothetical protein	2.24	1.47E-06
PA4009	hypothetical protein	2.19	1.88E-09
PA5222	hypothetical protein	2.11	2.75E-06
PA2557	AMP-binding protein	2.05	8.91E-10
PA0118	hypothetical protein	2.02	4.19E-05
PA2636	hypothetical protein	2.00	6.30E-06
Signal transduction mechanisms			
femR	sigma factor regulator FemR	7.66	8.31E-47
eraS	sensor kinase EraS	6.84	8.10E-47
PA2094	transmembrane sensor	6.30	2.35E-38
PA2833	hypothetical protein	6.22	1.49E-23
PA4895	transmembrane sensor	5.30	8.93E-35
eraR	response regulator EraR	4.96	1.72E-30
PA2881	two-component response regulator	4.93	1.35E-31
PA1945	transcriptional regulator	4.92	3.03E-41
PA2480	two-component sensor	4.84	1.52E-45
PA2133	hypothetical protein	4.66	5.84E-21
PA1438	two-component sensor	4.20	1.24E-31
PA0150	transmembrane sensor	4.17	1.72E-26
stp1	serine/threonine phosphoprotein phosphatase Stp1	4.13	1.23E-26
PA2523	two-component response regulator	3.84	1.64E-20
PA2479	two-component response regulator	3.84	1.50E-19
bfiS	protein BfiS	3.64	1.94E-31
stk1	serine-threonine kinase Stk1	3.61	1.62E-21
ercS	sensor histidine kinase	3.61	9.88E-27
PA2072	hypothetical protein	3.54	3.83E-20
PA1646	chemotaxis transducer	3.53	5.03E-26
PA3959	hypothetical protein	3.51	1.06E-25

PA1665	hypothetical protein	3.39	3.56E-20
PA1433	hypothetical protein	3.31	3.98E-24
PA2788	chemotaxis transducer	3.29	8.30E-25
PA4806	transcriptional regulator	3.26	2.08E-17
ercS'	sensor histidine kinase	3.25	3.27E-25
PA4886	two-component sensor	3.25	2.86E-20
pprA	two-component sensor PprA	3.23	1.24E-23
PA0757	two-component sensor	3.23	3.28E-24
PA1616	hypothetical protein	3.23	8.40E-14
PA2524	two-component sensor	3.20	1.19E-17
copS	two-component sensor CopS	3.11	4.37E-20
PA2005	transcriptional regulator	3.00	4.00E-22
PA4290	chemotaxis transducer	2.98	5.97E-22
PA4982	two-component sensor	2.96	4.63E-17
kdpD	two-component sensor KdpD	2.89	3.16E-08
tpbA	protein tyrosine phosphatase TpbA	2.84	2.72E-14
PA1396	two-component sensor	2.83	2.27E-15
PA3191	two-component sensor	2.78	1.99E-17
PA4781	cyclic di-GMP phosphodiesterase	2.73	5.26E-15
ptrB	repressor PtrB	2.73	7.96E-11
PA0172	hypothetical protein	2.67	2.31E-14
wspC	biofilm formation methyltransferase WspC	2.66	1.45E-17
hisJ	histidine ABC transporter substrate-binding protein HisJ	2.65	3.14E-13
PA0267	hypothetical protein	2.63	3.35E-17
pfeS	two-component sensor histidine kinase PfeS	2.60	2.18E-12
PA1243	sensor/response regulator hybrid protein	2.59	1.14E-15
PA1854	hypothetical protein	2.56	4.57E-13
PA2882	two-component sensor	2.51	3.76E-14
PA2561	methyl-accepting chemotaxis protein CtpH	2.49	6.07E-14
PA4036	two-component sensor	2.47	1.12E-16
PA4955	hypothetical protein	2.38	5.23E-14
PA1260	amino acid ABC transporter substrate-binding protein	2.27	3.11E-07
PA4112	sensor/response regulator hybrid protein	2.27	6.06E-13
PA2867	chemotaxis transducer	2.26	2.33E-13
pfeR	two-component response regulator PfeR	2.25	1.30E-09
mucC	positive regulator for alginate biosynthesis MucC	2.23	1.61E-07
PA3077	two-component response regulator	2.21	2.63E-09
bfiR	protein BfiR	2.21	2.89E-10
PA3462	sensor/response regulator hybrid protein	2.19	2.48E-12

kdpE	two-component response regulator KdpE	2.18	2.33E-08
PA1851	hypothetical protein	2.16	2.72E-09
PA2200	hypothetical protein	2.16	1.19E-08
PA5442	hypothetical protein	2.14	1.31E-12
PA1157	two-component response regulator	2.14	4.69E-06
PA2654	chemotaxis transducer	2.10	7.08E-05
pelD	pellicle/biofilm biosynthesis protein PelD	2.10	1.35E-08
PA3204	two-component response regulator	2.10	7.37E-06
PA2652	methyl-accepting chemotaxis protein	2.10	2.34E-10
PA4074	transcriptional regulator	2.05	7.83E-09
PA3206	two-component sensor	2.04	1.43E-09
chpC	chemotaxis protein	2.03	4.53E-08
Transcription			
PA1884	transcriptional regulator	5.93	6.65E-35
PA2383	transcriptional regulator	5.68	1.20E-39
PA1351	ECF subfamily sigma-70 factor	5.47	2.39E-43
PA1399	transcriptional regulator	5.24	9.36E-46
PA2469	transcriptional regulator	5.19	1.34E-42
PA2681	transcriptional regulator	5.06	5.54E-36
PA2489	transcriptional regulator	4.95	3.11E-31
PA0739	transcriptional regulator	4.87	1.48E-37
PA2497	transcriptional regulator	4.53	1.13E-34
PA1264	transcriptional regulator	4.49	8.55E-36
PA2096	transcriptional regulator	4.43	8.02E-28
PA3381	transcriptional regulator	4.41	1.25E-33
PA5431	transcriptional regulator	4.33	3.53E-33
PA3420	transcriptional regulator	4.24	4.44E-40
PA1653	transcriptional regulator	4.23	1.84E-24
PA2838	transcriptional regulator	4.23	2.05E-33
PA2488	transcriptional regulator	4.19	1.92E-29
PA2848	transcriptional regulator	4.18	5.80E-32
PA1261	transcriptional regulator	4.14	5.18E-26
PA1850	transcriptional regulator	4.13	6.48E-30
PA1300	ECF subfamily sigma-70 factor	4.12	1.83E-24
PA5116	transcriptional regulator	4.07	1.11E-24
PA0279	transcriptional regulator	3.98	2.68E-31
PA1050	hypothetical protein	3.98	1.39E-33
PA2930	transcriptional regulator	3.97	2.24E-32
cynR	DNA-binding transcriptional regulator CynR	3.94	4.06E-24
PA1223	transcriptional regulator	3.92	4.27E-28
PA4203	transcriptional regulator	3.91	1.68E-27

PA3776	transcriptional regulator	3.91	2.22E-25
PA1826	transcriptional regulator	3.90	1.97E-28
PA2121	transcriptional regulator	3.81	1.37E-19
PA3410	ECF subfamily sigma-70 factor	3.70	1.45E-22
PA0149	ECF subfamily sigma-70 factor	3.69	1.80E-23
PA3220	transcriptional regulator	3.67	7.05E-28
PA1285	transcriptional regulator	3.66	1.93E-20
catR	transcriptional regulator CatR	3.65	9.32E-25
PA2665	anaerobic nitric oxide reductase transcriptional regulator	3.56	3.51E-30
PA0512	heme d1 biosynthesis protein NirH	3.54	2.13E-21
PA1864	transcriptional regulator	3.52	5.43E-18
PA2840	ATP-dependent RNA helicase	3.44	3.22E-26
PA1467	hypothetical protein	3.37	7.49E-18
iciA	chromosome replication initiation inhibitor protein	3.36	4.95E-23
PA1879	hypothetical protein	3.33	1.51E-11
PA3565	transcriptional regulator	3.31	1.70E-24
PA2267	transcriptional regulator	3.31	7.08E-19
PA2050	RNA polymerase sigma factor	3.25	5.09E-13
PA0056	transcriptional regulator	3.22	3.41E-24
PA2376	transcriptional regulator	3.18	2.58E-14
chpD	transcriptional regulator	3.16	1.47E-23
soxR	redox-sensitive transcriptional activator SoxR	3.16	5.06E-16
PA1125	NAD-dependent protein deacylase	3.15	4.47E-21
PA2447	transcriptional regulator	3.15	1.94E-17
PA1182	transcriptional regulator	3.12	1.06E-17
PA3782	transcriptional regulator	3.11	2.14E-22
trpI	HTH-type transcriptional regulator TrpI	3.08	3.54E-21
PA4989	transcriptional regulator	3.08	1.49E-21
PA2704	transcriptional regulator	3.08	4.00E-19
PA0791	transcriptional regulator	3.06	9.03E-19
PA0816	transcriptional regulator	3.05	9.88E-17
PA1866	hypothetical protein	3.05	7.36E-19
PA3921	transcriptional regulator	3.04	2.20E-20
PA1403	transcriptional regulator	2.99	9.51E-14
PA0513	heme d1 biosynthesis protein NirG	2.99	1.79E-11
PA2879	transcriptional regulator	2.99	2.92E-13
PA2093	RNA polymerase sigma factor	2.95	1.03E-11
PA0864	transcriptional regulator	2.94	2.03E-18
PA0701	transcriptional regulator	2.92	1.18E-19
PA1226	transcriptional regulator	2.91	7.62E-17

PA3433	transcriptional regulator	2.90	5.46E-20
PA0479	transcriptional regulator	2.89	3.08E-14
PA1627	transcriptional regulator	2.89	1.93E-15
PA0475	transcriptional regulator	2.88	1.78E-13
PA2010	transcriptional regulator	2.85	1.51E-16
PA4902	transcriptional regulator	2.84	6.88E-14
PA0236	transcriptional regulator	2.83	3.65E-18
femI	ECF sigma factor FemI	2.81	4.12E-11
PA5342	transcriptional regulator	2.81	3.44E-17
foxI	ECF sigma factor FoxI	2.80	3.33E-13
PA5032	transcriptional regulator	2.80	5.25E-17
PA1570	transcriptional regulator	2.77	3.32E-12
PA1153	hypothetical protein	2.77	1.21E-10
PA2484	hypothetical protein	2.77	1.97E-12
PA3321	transcriptional regulator	2.76	2.39E-17
PA4157	transcriptional regulator	2.73	1.21E-17
PA2196	transcriptional regulator	2.70	4.06E-10
PA1067	transcriptional regulator	2.69	2.11E-13
PA1229	transcriptional regulator	2.69	1.21E-13
cifR	CifR protein	2.67	1.16E-14
PA2056	transcriptional regulator	2.67	9.23E-15
PA1380	transcriptional regulator	2.67	4.51E-15
PA1859	transcriptional regulator	2.66	5.68E-14
PA3466	ATP-dependent RNA helicase	2.65	5.85E-11
rbsR	ribose operon repressor RbsR	2.64	1.93E-15
PA1413	transcriptional regulator	2.62	1.18E-13
PA0121	hypothetical protein	2.62	1.42E-16
PA2115	transcriptional regulator	2.62	2.35E-14
PA1142	transcriptional regulator	2.61	1.29E-08
PA0477	transcriptional regulator	2.60	8.59E-16
mmsR	transcriptional regulator MmsR	2.59	1.99E-13
PA1263	hypothetical protein	2.59	5.27E-15
PA3269	transcriptional regulator	2.57	4.84E-13
PA2547	transcriptional regulator	2.57	4.42E-12
PA1359	transcriptional regulator	2.55	7.46E-10
PA0828	transcriptional regulator	2.54	2.81E-09
PA2417	transcriptional regulator	2.54	1.78E-13
PA5382	transcriptional regulator	2.53	9.45E-14
PA5085	transcriptional regulator	2.50	8.06E-15
PA1312	transcriptional regulator	2.50	2.51E-11
PA3845	transcriptional regulator	2.46	7.26E-12

PA1026	hypothetical protein	2.45	2.75E-10
PA4174	transcriptional regulator	2.44	3.67E-12
PA1961	transcriptional regulator	2.41	3.50E-10
PA2921	transcriptional regulator	2.41	1.52E-10
PA2534	transcriptional regulator	2.40	6.87E-10
PA3260	transcriptional regulator	2.38	1.12E-07
PA0515	heme d1 biosynthesis protein NirD	2.37	5.23E-10
PA2449	transcriptional regulator	2.37	1.54E-10
PA1328	transcriptional regulator	2.36	3.57E-12
PA2123	transcriptional regulator	2.34	6.10E-10
PA4831	transcriptional regulator	2.34	6.60E-11
glcC	DNA-binding transcriptional regulator GlcC	2.33	8.02E-12
PA2281	transcriptional regulator	2.32	2.81E-07
PA4145	transcriptional regulator	2.28	4.50E-11
aguR	transcriptional regulator AguR	2.27	2.03E-08
PA4987	transcriptional regulator	2.24	2.41E-09
pcaQ	transcriptional regulator PcaQ	2.23	4.22E-11
PA2766	transcriptional regulator	2.23	2.54E-08
PA0253	transcriptional regulator	2.22	6.99E-10
pruR	proline utilization regulator	2.20	1.84E-08
arsR	ArsR family transcriptional regulator	2.19	2.64E-06
PA2076	transcriptional regulator	2.19	2.19E-06
PA4341	transcriptional regulator	2.18	5.56E-10
ampR	transcriptional regulator AmpR	2.16	1.50E-10
PA2270	transcriptional regulator	2.16	6.35E-07
PA1141	transcriptional regulator	2.15	4.13E-10
ptxS	transcriptional regulator PtxS	2.12	1.66E-06
PA5218	transcriptional regulator	2.11	3.34E-10
PA0877	transcriptional regulator	2.08	1.05E-08
PA1978	glycerol metabolism activator	2.06	7.44E-05
nirL	heme d1 biosynthesis protein NirL	2.06	4.79E-07
PA0181	transcriptional regulator	2.06	1.27E-08
PA2556	transcriptional regulator	2.06	5.17E-09
PA1138	transcriptional regulator	2.06	2.11E-09
ptxR	HTH-type transcriptional regulator PtxR	2.04	6.35E-07
PA0797	transcriptional regulator	2.02	3.90E-07
PA1128	transcriptional regulator	2.02	1.64E-05
Translation, ribosomal structure and biogenesis			
PA0814	hypothetical protein	6.99	6.33E-47
PA2499	deaminase	6.32	1.28E-40
ansA	L-asparaginase I	5.26	1.51E-24

PA2179	hypothetical protein	4.14	1.96E-23
PA5470	peptide chain release factor-like protein	3.43	3.97E-17
ligT	2'-5' RNA ligase	3.24	1.85E-17
aph	aminoglycoside 3-N-acetyltransferase	3.11	2.66E-20
PA4342	amidase	3.06	2.31E-20
PA4724	glutamyl-Q tRNA(Asp) synthetase	3.01	2.35E-20
PA3270	hypothetical protein	2.94	2.84E-19
PA4627	16S rRNA methyltransferase	2.89	2.28E-18
tyrS	tyrosine--tRNA ligase	2.80	3.37E-15
PA0704	amidase	2.57	8.25E-12
fmt	methionyl-tRNA formyltransferase	2.57	7.51E-15
selB	selenocysteine-specific elongation factor	2.48	1.45E-14
PA5433	hypothetical protein	2.45	1.71E-13
PA0017	Ribosomal RNA small subunit methyltransferase B	2.42	1.12E-13
PA0054	RNA 2'-phosphotransferase-like protein	2.34	9.18E-10
PA2043	hypothetical protein	2.31	4.97E-10
PA4617	hypothetical protein	2.28	1.62E-12
PA4163	amidase	2.28	1.28E-13
PA0868	peptidyl-tRNA hydrolase	2.19	2.36E-09

Table S3. List of genes downregulated in PANT by at least 2-fold with a false discovery rate (Padj-value) <0.01 during exposure to hexadecane-water interface for 24 h versus the control

Gene	Description	Fold Change	Padj-value
Amino acid transport and metabolism			
arcB	ornithine carbamoyltransferase	-292.66	1.84E-62
glnK	nitrogen regulatory protein P-II 2	-131.24	3.17E-76
arcD	arginine/ornithine antiporter	-124.31	7.41E-56
arcA	arginine deiminase	-111.40	1.48E-78
arcC	carbamate kinase	-68.39	2.00E-42
serA	D-3-phosphoglycerate dehydrogenase	-43.83	1.03E-36
iscS	cysteine desulfurase	-34.16	1.35E-45
phhA	phenylalanine 4-monooxygenase	-27.28	1.08E-137
glnA	glutamine synthetase	-25.23	3.89E-42
ilvH	acetolactate synthase small subunit	-23.26	8.43E-21
cysE	O-acetylserine synthase	-22.67	1.31E-69
serC	3-phosphoserine/phosphohydroxythreonine aminotransferase	-19.60	1.24E-21
braC	branched-chain amino acid ABC transporter substrate-binding protein BraC	-18.95	2.05E-73
hisE	phosphoribosyl-ATP pyrophosphatase	-18.49	5.69E-38
PA5547	hypothetical protein	-17.30	1.07E-32
spuB	glutamine synthetase	-17.16	5.09E-50
PA0604	ABC transporter	-16.70	5.72E-25
leuA	2-isopropylmalate synthase	-15.27	1.02E-35
spuD	putrescine ABC transporter substrate-binding protein SpuD	-15.26	9.77E-43
argB	acetylglutamate kinase	-14.78	2.85E-84
pheA	bifunctional chorismate mutase/prephenate dehydratase	-14.31	3.56E-26
hisG	ATP phosphoribosyltransferase	-13.94	4.93E-20
ilvE	branched-chain amino acid aminotransferase	-12.04	1.15E-30
hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase	-10.85	1.47E-26
dadA	D-amino acid dehydrogenase small subunit	-9.81	3.72E-84
PA0605	ABC transporter permease	-9.76	8.41E-12
PA4913	ABC transporter	-9.46	1.70E-15
PA1750	phospho-2-dehydro-3-deoxyheptonate aldolase	-9.34	4.07E-11
braF	ABC transporter ATP-binding protein	-9.22	2.62E-19
trpG	anthranilate synthase component II	-9.09	1.84E-20
trpE	anthranilate synthase component I	-8.99	4.35E-20

PA1089	hypothetical protein	-8.68	4.39E-11
speD	S-adenosylmethionine decarboxylase	-7.79	2.40E-10
PA0006	D-glycero-beta-D-manno-heptose-1,7-bisphosphate 7-phosphatase	-7.71	2.57E-11
PA5152	ABC transporter ATP-binding protein	-7.61	6.66E-14
cysM	cysteine synthase B	-7.60	1.41E-16
spuH	polyamine transporter PotI	-7.39	2.79E-12
gcvH1	glycine cleavage system protein H	-7.33	1.77E-21
metE	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	-7.29	1.53E-57
PA0606	ABC transporter permease	-7.05	3.74E-16
PA3602	hypothetical protein	-7.01	1.22E-38
argG	argininosuccinate synthase	-6.91	2.19E-17
spuI	glutamine synthetase	-6.83	4.94E-51
cysK	cysteine synthase A	-6.83	4.48E-32
aruE	succinylglutamate desuccinylase	-6.43	2.36E-53
PA5378	hypothetical protein	-6.29	4.08E-15
aruB	N-succinylarginine dihydrolase	-6.28	5.41E-44
glyA3	serine hydroxymethyltransferase	-6.28	7.71E-24
PA5370	major facilitator superfamily transporter	-6.24	2.71E-14
spuE	spermidine ABC transporter substrate-binding protein SpuE	-6.13	6.48E-13
PA0602	ABC transporter	-6.10	6.07E-11
PA4796	hypothetical protein	-6.09	1.69E-57
putA	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	-5.82	3.47E-64
PA2776	hypothetical protein	-5.80	1.77E-21
PA5376	ABC transporter ATP-binding protein	-5.78	4.06E-31
gloA1	lactoylglutathione lyase	-5.73	2.15E-36
aroQ1	3-dehydroquinate dehydratase	-5.64	1.49E-10
PA3255	hypothetical protein	-5.60	1.26E-16
gloA3	lactoylglutathione lyase	-5.59	9.97E-28
lysC	aspartokinase	-5.58	2.47E-22
PA1810	ABC transporter	-5.53	2.52E-13
PA5283	transcriptional regulator	-5.51	4.77E-20
asd	aspartate-semialdehyde dehydrogenase	-5.50	1.33E-22
aroP1	aromatic amino acid transporter AroP	-5.45	3.90E-07
metH	B12-dependent methionine synthase	-5.43	3.50E-17
PA4500	ABC transporter	-5.41	1.76E-10
PA0323	ABC transporter	-5.33	3.51E-09
PA0484	hypothetical protein	-5.15	6.74E-08
PA2609	hypothetical protein	-5.04	4.36E-25
gdhB	NAD-specific glutamate dehydrogenase	-5.01	2.25E-43

hisC2	histidinol-phosphate aminotransferase	-4.94	4.33E-26
braG	ABC transporter ATP-binding protein	-4.89	1.46E-21
pepP	aminopeptidase	-4.88	2.22E-37
PA4912	branched-chain amino acid ABC transporter	-4.86	9.34E-11
hisF1	imidazole glycerol phosphate synthase subunit HisF	-4.82	9.81E-22
PA4715	aminotransferase	-4.81	8.61E-27
aspA	aspartate ammonia-lyase	-4.80	1.02E-15
PA0789	amino acid permease	-4.77	1.40E-16
dapD	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	-4.76	6.18E-18
ltaA	low specificity l-threonine aldolase	-4.74	7.86E-36
potD	polyamine ABC transporter substrate-binding protein PotD	-4.73	1.35E-05
spuG	polyamine transporter PotH	-4.72	9.17E-09
aotQ	arginine/ornithine ABC transporter permease AotQ	-4.59	1.45E-05
PA5249	hypothetical protein	-4.50	3.97E-24
metF	5,10-methylenetetrahydrofolate reductase	-4.40	1.29E-18
speE	polyamine aminopropyltransferase	-4.29	1.32E-08
aroB	3-dehydroquinate synthase	-4.21	2.71E-32
braE	branched-chain amino acid ABC transporter permease BraE	-4.20	2.43E-17
PA4757	leucine export protein LeuE	-4.16	2.58E-16
speC	ornithine decarboxylase	-4.02	7.88E-06
PA1811	solute-binding protein	-3.94	4.49E-10
speA	arginine decarboxylase	-3.91	1.89E-27
hisC1	histidinol-phosphate aminotransferase	-3.85	2.65E-09
PA5095	ABC transporter permease	-3.75	3.97E-15
thrC	threonine synthase	-3.72	3.07E-15
PA2828	aminotransferase	-3.63	2.69E-07
PA5377	ABC transporter permease	-3.54	3.92E-16
PA0266	5-aminovalerate aminotransferase DavT	-3.53	3.47E-22
kynA	tryptophan 2,3-dioxygenase	-3.49	7.34E-15
PA2040	glutamine synthetase	-3.45	3.34E-15
gdhA	glutamate dehydrogenase	-3.45	6.42E-19
PA2831	hypothetical protein	-3.43	5.64E-15
PA4910	ABC transporter ATP-binding protein	-3.40	1.29E-08
PA3890	ABC transporter permease	-3.39	4.26E-12
PA3389	ring-cleaving dioxygenase	-3.38	1.51E-04
trpD	anthranilate phosphoribosyltransferase	-3.38	7.10E-09
PA5317	dipeptide ABC transporter substrate-binding protein	-3.31	5.08E-14
PA0603	ABC transporter ATP-binding protein	-3.30	1.30E-11
hisI	phosphoribosyl-AMP cyclohydrolase	-3.27	3.64E-13

PA3766	aromatic amino acid transporter	-3.20	3.43E-06
PA1491	transporter	-3.07	3.36E-05
PA4909	ABC transporter ATP-binding protein	-3.04	1.97E-12
prlC	oligopeptidase A	-3.02	2.50E-19
phhC	aromatic amino acid aminotransferase	-3.01	6.76E-15
aruC	acetylornithine aminotransferase	-2.99	2.97E-16
PA2041	amino acid permease	-2.94	2.03E-04
PA3798	aminotransferase	-2.94	8.96E-12
lysP	lysine-specific permease	-2.93	2.56E-09
leuD	isopropylmalate isomerase small subunit	-2.90	3.87E-16
PA2114	major facilitator superfamily transporter	-2.88	6.65E-12
hisM	histidine ABC transporter permease HisM	-2.84	1.51E-04
PA2042	serine/threonine transporter SstT	-2.82	1.48E-07
PA2393	dipeptidase	-2.81	1.38E-07
braB	branched-chain amino acid transporter	-2.73	4.99E-09
PA2592	spermidine/putrescine-binding protein	-2.73	5.94E-04
PA1009	hypothetical protein	-2.72	1.64E-06
PA0325	ABC transporter permease	-2.70	3.45E-10
PA1916	amino acid permease	-2.68	1.79E-08
thrH	phosphoserine phosphatase	-2.64	7.36E-03
PA4858	hypothetical protein	-2.62	8.31E-06
PA5326	hypothetical protein	-2.56	4.16E-08
PA4502	ABC transporter	-2.55	1.23E-10
PA5137	hypothetical protein	-2.54	3.40E-10
pvdN	pyoverdine biosynthesis protein PvdN	-2.48	1.57E-08
phnW	2-aminoethylphosphonate--pyruvate transaminase	-2.47	9.56E-10
PA3253	ABC transporter permease	-2.46	9.79E-05
ldcA	lysine-specific pyridoxal 5'-phosphate-dependent carboxylase LdcA	-2.45	3.21E-13
PA3236	glycine betaine-binding protein	-2.41	2.70E-07
trpB	tryptophan synthase subunit beta	-2.39	2.42E-12
PA3261	hypothetical protein	-2.39	2.91E-07
aroK	shikimate kinase	-2.38	2.32E-10
aotM	arginine/ornithine ABC transporter permease AotM	-2.37	1.06E-06
PA0313	L-cysteine ABC transporter protein YecS	-2.34	1.23E-09
pepA	leucyl aminopeptidase	-2.34	5.65E-10
gltB	glutamate synthase subunit alpha	-2.31	2.24E-13
leuC	3-isopropylmalate dehydratase large subunit	-2.30	5.02E-10
hisB	imidazoleglycerol-phosphate dehydratase	-2.22	1.07E-08
PA5074	ABC transporter ATP-binding protein	-2.20	5.89E-04
PA5509	hypothetical protein	-2.20	2.26E-08
gcvH2	glycine cleavage system protein H	-2.20	8.61E-04

PA1256	amino acid ABC transporter ATP binding protein	-2.20	1.73E-05
spuF	polyamine transporter PotG	-2.19	4.72E-06
PA2897	transcriptional regulator	-2.18	7.11E-10
pchB	isochorismate-pyruvate lyase	-2.15	1.92E-06
PA3641	amino acid permease	-2.14	1.32E-05
PA4548	D-amino acid oxidase	-2.13	2.47E-06
PA5396	hypothetical protein	-2.08	9.36E-05
pchP	phosphorylcholine phosphatase	-2.06	5.01E-06
PA4023	transporter	-2.03	1.31E-08
PA4960	phosphoserine phosphatase	-2.03	4.78E-09
trpF	N-(5'-phosphoribosyl)anthranilate isomerase	-2.02	3.57E-06
Carbohydrate transport and metabolism			
ppsA	phosphoenolpyruvate synthase	-20.39	1.65E-28
glmM	phosphoglucosamine mutase	-17.34	4.81E-16
PA4425	phosphoheptose isomerase	-14.77	8.79E-12
eno	enolase	-12.87	5.12E-62
PA5167	C4-dicarboxylate-binding protein	-12.24	9.79E-18
tpiA	triosephosphate isomerase	-11.86	4.35E-23
rmd	oxidoreductase Rmd	-8.44	4.12E-12
fda	fructose-1,6-bisphosphate aldolase	-7.61	7.00E-27
PA4466	phosphoryl carrier protein	-7.40	4.99E-29
gapA	glyceraldehyde 3-phosphate dehydrogenase	-7.04	2.47E-32
fbp	fructose-1,6-bisphosphatase	-6.93	3.66E-16
PA1517	hypothetical protein	-6.78	7.97E-13
PA3295	HIT family protein	-6.27	6.02E-09
PA5168	dicarboxylate transporter	-5.87	1.31E-10
rfaD	ADP-L-glycero-D-mannoheptose-6-epimerase	-5.78	3.37E-26
pykA	pyruvate kinase	-5.55	6.53E-46
rbsB	ribose ABC transporter substrate-binding protein	-5.19	2.30E-40
PA4616	C4-dicarboxylate-binding protein	-4.91	2.13E-08
pgi	glucose-6-phosphate isomerase	-4.78	1.07E-25
glpR	glycerol-3-phosphate regulon repressor	-4.41	1.54E-20
wzm	LPS efflux transporter membrane protein	-4.35	2.12E-09
tal	transaldolase B	-4.31	4.47E-20
rpe	ribulose-phosphate 3-epimerase	-4.19	1.45E-17
PA1683	methylthioribulose-1-phosphate dehydratase	-4.00	1.13E-10
glmR	GlmR transcriptional regulator	-3.73	4.38E-11
PA3001	glyceraldehyde-3-phosphate dehydrogenase	-3.29	3.67E-13
PA1490	transcriptional regulator	-3.20	1.97E-09
PA2678	ABC transporter permease	-3.13	2.91E-05
ilvD	dihydroxy-acid dehydratase	-2.92	1.04E-17

PA5160	drug efflux transporter	-2.80	3.09E-09
PA3188	sugar ABC transporter permease	-2.70	9.79E-05
zwf	glucose-6-phosphate 1-dehydrogenase	-2.62	5.39E-11
tktA	transketolase	-2.57	5.60E-12
PA1293	hypothetical protein	-2.54	4.51E-07
PA3430	aldolase	-2.51	6.65E-12
glpF	glycerol uptake facilitator protein	-2.51	1.20E-07
PA4834	hypothetical protein	-2.49	2.64E-09
PA1831	hypothetical protein	-2.24	2.88E-10
prpB	2-methylisocitrate lyase	-2.09	2.60E-08
PA0458	major facilitator superfamily transporter	-2.06	1.03E-08
Cell cycle control, cell division, chromosome partitioning			
ftsZ	cell division protein FtsZ	-139.60	1.37E-97
fleN	flagellar synthesis regulator FleN	-22.86	1.09E-65
ftsE	cell division protein FtsE	-16.29	1.38E-31
ftsL	cell division protein FtsL	-16.01	6.84E-24
minD	cell division inhibitor MinD	-15.01	1.26E-18
ftsA	cell division protein FtsA	-11.34	1.15E-75
minE	cell division topological specificity factor MinE	-7.58	9.48E-11
PA1366	hypothetical protein	-5.26	3.93E-10
PA1192	tRNA 2-thiocytidine biosynthesis protein TtcA	-5.11	8.53E-10
PA3634	cell division protein FtsB	-3.92	8.28E-10
ftsW	cell division protein FtsW	-3.88	6.27E-15
zipA	cell division protein ZipA	-3.54	1.70E-21
PA3201	intracellular septation protein A	-3.50	1.10E-12
soj	chromosome partitioning protein Soj	-3.46	1.78E-10
ftsK	DNA translocase FtsK	-3.25	2.42E-11
PA5028	hypothetical protein	-2.73	1.69E-09
rodA	rod shape-determining protein	-2.62	3.25E-10
PA4686	hypothetical protein	-2.39	5.80E-10
PA2972	hypothetical protein	-2.23	8.48E-06
gidA	tRNA uridine 5-carboxymethylaminomethyl modification protein GidA	-2.14	2.90E-08
Cell motility			
fliD	B-type flagellar hook-associated protein	-25.96	1.79E-29
cheZ	protein phosphatase CheZ	-24.80	5.34E-26
flgB	flagellar basal-body rod protein FlgB	-21.37	6.37E-28
flgG	flagellar basal body rod protein FlgG	-17.71	4.63E-45
flgC	flagellar basal body rod protein FlgC	-15.03	8.95E-18
flgD	flagellar basal body rod modification protein	-13.61	5.98E-18
flgL	flagellar hook-associated protein FlgL	-12.22	5.33E-33
pilB	type 4 fimbrial biogenesis protein PilB	-11.63	2.54E-22

pilN	type 4 fimbrial biogenesis protein PilN	-11.37	1.20E-12
PA1093	hypothetical protein	-10.17	1.20E-10
flgF	flagellar basal body rod protein FlgF	-10.07	8.24E-21
pilW	type 4 fimbrial biogenesis protein PilW	-9.97	1.35E-16
fimU	type 4 fimbrial biogenesis protein FimU	-9.83	5.27E-12
fliM	flagellar motor switch protein FliM	-8.88	1.70E-25
fliQ	flagellar biosynthesis protein FliQ	-6.87	1.82E-15
fliC	B-type flagellin	-6.67	1.92E-14
PA1464	purine-binding chemotaxis protein	-6.58	1.27E-35
pilV	type 4 fimbrial biogenesis protein PilV	-6.31	8.35E-07
flgE	flagellar hook protein FlgE	-6.07	9.69E-22
lppL	lipopeptide LppL	-5.89	1.38E-12
pilT	twitching motility protein PilT	-5.79	3.04E-17
pilX	type 4 fimbrial biogenesis protein PilX	-5.74	1.05E-17
PA1442	flagellar basal body protein FliL	-5.64	4.72E-20
flhA	flagellar biosynthesis protein FlhA	-5.63	1.29E-17
flgK	flagellar hook-associated protein FlgK	-5.55	3.69E-45
pilE	type 4 fimbrial biogenesis protein PilE	-4.87	8.02E-09
fliG	flagellar motor switch protein FliG	-4.67	1.33E-14
pilI	twitching motility protein PilI	-4.47	4.71E-13
PA5233	flagellar basal body protein FliL	-4.43	2.95E-19
flgH	flagellar basal body L-ring protein	-4.29	1.47E-29
pilP	type 4 fimbrial biogenesis protein PilP	-4.14	2.23E-06
PA4039	hypothetical protein	-3.91	4.24E-10
pilZ	type 4 fimbrial biogenesis protein PilZ	-3.80	1.58E-09
flgI	flagellar basal body P-ring protein	-3.74	2.83E-20
cupC3	usher CupC3	-3.10	6.83E-05
fliR	flagellar biosynthesis protein FliR	-2.24	3.11E-06
motA	flagellar motor protein MotA	-2.14	1.69E-07
Cell wall/membrane/envelope biogenesis			
pilK	methyltransferase PilK	-2.10	1.24E-05
oprH	PhoP/Q and low Mg2+ inducible outer membrane protein H1	-2116.31	3.90E-115
oprF	outer membrane porin F	-438.20	5.04E-197
oprL	peptidoglycan associated lipoprotein OprL	-158.49	5.05E-82
mscL	large-conductance mechanosensitive channel	-50.41	2.84E-56
lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	-48.55	3.34E-41
oprG	outer membrane protein OprG	-46.03	1.82E-80
prc	tail-specific protease	-34.65	1.31E-40
lpxA	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase	-32.43	2.13E-44

lspA	lipoprotein signal peptidase	-21.73	2.35E-41
rmlC	dTDP-4-dehydrorhamnose 3,5-epimerase	-20.86	3.49E-34
PA3647	hypothetical protein	-19.25	7.50E-41
tolA	translocation protein TolA	-18.22	1.19E-30
PA4420	S-adenosyl-methyltransferase MraW	-16.88	1.20E-32
lytB	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	-15.41	6.59E-18
mraY	phospho-N-acetylmuramoyl-pentapeptide-transferase	-13.31	8.26E-33
gidB	16S rRNA methyltransferase GidB	-13.07	5.91E-17
rmlA	glucose-1-phosphate thymidylyltransferase	-12.44	7.29E-21
ftsQ	cell division protein FtsQ	-11.69	1.36E-78
cmpX	hypothetical protein	-11.25	1.93E-25
opr86	outer membrane protein Opr86	-10.95	2.95E-14
PA5546	hypothetical protein	-9.74	4.36E-37
wapR	alpha-1,3-rhamnosyltransferase WapR	-9.62	2.47E-17
ftsI	penicillin-binding protein 3	-9.59	4.16E-58
PA2800	hypothetical protein	-9.57	1.33E-19
wbpM	nucleotide sugar epimerase/dehydratase WbpM	-8.62	7.81E-13
PA1198	hypothetical protein	-8.48	1.40E-13
PA0938	hypothetical protein	-8.40	5.20E-14
PA4457	arabinose-5-phosphate isomerase KdsD	-8.11	6.25E-16
gmd	GDP-mannose 4,6-dehydratase	-8.00	5.52E-15
dacC	D-ala-D-ala-carboxypeptidase	-7.93	1.84E-59
lepA	elongation factor 4	-7.79	2.24E-16
PA0664	hypothetical protein	-7.15	1.30E-09
wbpZ	glycosyltransferase WbpZ	-6.46	1.11E-09
PA0011	lipid A biosynthesis lauroyl acyltransferase	-6.29	3.80E-09
migA	alpha-1,6-rhamnosyltransferase MigA	-6.22	1.95E-15
PA5551	hypothetical protein	-6.18	1.61E-30
lolA	outer-membrane lipoprotein carrier protein	-6.06	7.98E-22
PA0045	hypothetical protein	-5.86	8.28E-11
lptF	outer membrane porin F	-5.82	3.08E-39
murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	-5.34	8.08E-23
murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	-5.30	4.12E-45
murB	UDP-N-acetylenolpyruvoylglucosamine reductase	-5.02	8.20E-15
PA4394	hypothetical protein	-4.97	2.37E-26
waaL	O-antigen ligase WaaL	-4.90	1.56E-05
PA0667	hypothetical protein	-4.88	3.25E-07
ddlB	D-alanine--D-alanine ligase	-4.77	1.06E-25
rmlB	dTDP-D-glucose 4,6-dehydratase	-4.74	1.54E-14
mltB1	murein hydrolase B	-4.72	1.34E-12
mltD	membrane-bound lytic murein transglycosylase D	-4.71	1.48E-11

PA2988	hypothetical protein	-4.37	9.54E-09
murC	UDP-N-acetylmuramate--L-alanine ligase	-4.36	2.43E-30
algD	GDP-mannose 6-dehydrogenase AlgD	-4.27	3.41E-06
mexA	multidrug resistance protein MexA	-4.23	8.63E-24
PA1391	glycosyl transferase family protein	-4.14	1.25E-08
waaG	UDP-glucose:(heptosyl) LPS alpha 1,3-glucosyltransferase WaaG	-4.01	7.88E-17
betT1	choline transporter BetT	-3.81	8.95E-13
PA5251	hypothetical protein	-3.64	1.17E-06
PA5291	choline transporter	-3.58	8.34E-19
plcH	hemolytic phospholipase C	-3.52	9.86E-07
ostA	organic solvent tolerance protein OstA	-3.44	1.97E-09
PA1389	glycosyl transferase family protein	-3.39	1.99E-05
PA1388	hypothetical protein	-3.32	3.70E-05
glmU	bifunctional glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridyltransferase	-3.27	1.95E-12
blc	outer membrane lipoprotein Blc	-3.19	4.36E-11
pslA	biofilm formation protein PslA	-3.07	1.90E-15
dgkA	diacylglycerol kinase	-3.05	1.67E-06
PA1014	glycosyl transferase family protein	-2.95	3.52E-05
alg8	glycosyltransferase alg8	-2.86	7.01E-05
PA5003	hypothetical protein	-2.76	2.74E-14
ponA	penicillin-binding protein 1A	-2.75	9.09E-19
PA2291	glucose-sensitive porin	-2.74	5.31E-04
PA3353	hypothetical protein	-2.50	2.36E-06
PA3468	hypothetical protein	-2.45	1.20E-07
sltB1	soluble lytic transglycosylase B	-2.43	1.86E-08
kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	-2.40	3.32E-07
murF	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	-2.38	1.29E-15
mrcB	penicillin-binding protein 1B	-2.37	3.02E-07
lgt	prolipoprotein diacylglyceryl transferase	-2.36	5.62E-09
PA1011	hypothetical protein	-2.31	5.13E-07
PA3623	hypothetical protein	-2.29	6.31E-12
PA3472	hypothetical protein	-2.28	1.10E-06
PA4735	hypothetical protein	-2.22	1.10E-10
wzt	ABC transporter	-2.21	8.51E-10
PA4374	resistance-nodulation-cell division (RND) efflux membrane fusion protein	-2.17	3.73E-05
dapA	4-hydroxy-tetrahydrodipicolinate synthase	-2.16	5.78E-05
PA5232	hypothetical protein	-2.07	5.98E-06
wbpX	glycosyltransferase WbpX	-2.06	2.58E-07

lpxD	UDP-3-O-acylglucosamine N-acyltransferase	-2.00	2.24E-06
Coenzyme transport and metabolism			
ilvC	ketol-acid reductoisomerase	-76.59	3.21E-44
sahH	adenosylhomocysteinase	-59.77	2.25E-93
spuC	aminotransferase	-48.12	1.26E-30
bioB	biotin synthase	-24.96	2.03E-37
PA4615	oxidoreductase	-22.30	2.89E-33
ilvI	acetolactate synthase 3 catalytic subunit	-21.93	1.40E-26
phhB	pterin-4-alpha-carbinolamine dehydratase	-17.97	2.56E-83
folE2	GTP cyclohydrolase I	-17.91	3.61E-54
hemB	delta-aminolevulinic acid dehydratase	-15.18	1.91E-19
lis	lipoyl synthase	-14.23	1.50E-49
PA1772	ribonuclease activity regulator protein RraA	-13.69	1.06E-50
cysD	sulfate adenylyltransferase subunit 2	-11.90	2.73E-15
hemN	oxygen-independent coproporphyrinogen-III oxidase	-11.02	1.98E-22
pncB1	nicotinate phosphoribosyltransferase	-8.72	2.50E-19
folP	dihydropteroate synthase	-8.10	9.79E-19
lipB	lipoate-protein ligase B	-7.47	7.61E-22
folE1	GTP cyclohydrolase I	-7.45	2.38E-13
PA0862	hypothetical protein	-7.36	1.07E-30
metK	S-adenosylmethionine synthetase	-6.72	8.63E-22
rimK	ribosomal protein S6 modification protein	-6.59	2.66E-20
ribA	GTP cyclohydrolase II	-6.41	4.80E-20
ribE	6,7-dimethyl-8-ribityllumazine synthase	-6.28	9.39E-21
pdxY	pyridoxamine kinase	-6.03	8.63E-11
PA0655	2-nonaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	-4.86	8.21E-24
pncB2	nicotinate phosphoribosyltransferase	-4.68	4.58E-16
PA0132	beta alanine--pyruvate transaminase	-4.63	1.02E-12
PA4805	hypothetical protein	-4.54	2.43E-11
bioA	adenosylmethionine--8-amino-7-oxononanoate aminotransferase BioA	-4.54	1.33E-21
thiG	thiazole synthase	-4.40	2.13E-18
hemL	glutamate-1-semialdehyde aminotransferase	-4.21	1.04E-24
PA4675	TonB-dependent receptor	-4.17	6.09E-23
nadB	L-aspartate oxidase	-3.93	3.16E-30
PA3518	hypothetical protein	-3.83	3.34E-07
PA2993	hypothetical protein	-3.59	6.13E-20
PA5237	3-octaprenyl-4-hydroxybenzoate carboxy-lyase	-3.46	2.01E-17
nadC	nicotinate-nucleotide pyrophosphorylase	-3.23	1.14E-14
coaE	dephospho-CoA kinase	-3.18	7.68E-06
nadA	quinolinate synthetase	-3.08	4.29E-20

hemF	coproporphyrinogen III oxidase	-2.84	6.89E-13
ispB	octaprenyl-diphosphate synthase	-2.74	1.07E-10
ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	-2.40	6.49E-08
hemE	uroporphyrinogen decarboxylase	-2.37	1.06E-04
ribF	bifunctional riboflavin kinase/FMN adenylyltransferase	-2.36	8.59E-06
PA5257	hypothetical protein	-2.34	5.35E-14
nadE	NAD synthetase	-2.15	4.78E-04
panD	aspartate alpha-decarboxylase	-2.08	1.13E-03
PA0389	hypothetical protein	-2.07	3.55E-04
Defense mechanisms			
ampC	beta-lactamase	-15.79	2.34E-53
mexB	multidrug resistance protein MexB	-8.35	1.34E-19
PA5230	ABC transporter permease	-7.33	2.86E-14
msbA	transporter MsbA	-6.20	3.78E-19
PA2812	ABC transporter ATP-binding protein	-4.53	2.43E-07
PA0749	hypothetical protein	-4.25	5.54E-06
PA4375	multidrug efflux protein	-4.15	4.83E-08
PA5514	beta-lactamase	-4.12	2.31E-12
ampD	N-acetyl-anhydromuranmyl-L-alanine amidase	-3.46	2.18E-12
PA5542	hypothetical protein	-3.13	2.60E-11
PA4037	ABC transporter ATP-binding protein	-2.34	1.00E-06
PA2811	ABC transporter permease	-2.23	1.14E-04
PA2018	multidrug efflux protein	-2.10	4.69E-08
mexF	resistance-nodulation-cell division (RND) multidrug efflux transporter MexF	-2.04	1.90E-08
PA0158	resistance-nodulation-cell division (RND) efflux transporter	-2.01	3.87E-10
Energy production and conversion			
sucC	succinyl-CoA ligase subunit beta	-208.78	9.80E-72
sucD	succinyl-CoA ligase subunit alpha	-171.75	1.66E-119
lpdG	2-oxoglutarate dehydrogenase complex dihydrolipoyl dehydrogenase	-166.79	7.15E-79
atpD	ATP synthase subunit beta	-140.46	1.60E-96
atpH	ATP synthase subunit delta	-125.68	1.64E-87
atpG	ATP synthase subunit gamma	-118.29	4.28E-46
atpF	ATP synthase subunit B	-117.77	3.61E-48
atpA	ATP synthase subunit alpha	-113.89	1.59E-51
sdhA	succinate dehydrogenase flavoprotein subunit	-112.42	2.96E-81
sdhB	succinate dehydrogenase iron-sulfur subunit	-84.70	3.10E-57
nuoI	NADH-quinone oxidoreductase subunit I	-68.71	1.35E-55
icd	isocitrate dehydrogenase	-59.62	3.80E-63

sucA	2-oxoglutarate dehydrogenase subunit E1	-52.61	3.66E-56
etfB	electron transfer flavoprotein subunit beta	-49.88	3.51E-136
gltA	citrate synthase	-47.87	9.78E-45
sdhC	succinate dehydrogenase subunit C	-45.04	3.77E-47
sdhD	succinate dehydrogenase subunit D	-43.63	5.70E-38
PA5046	malic enzyme	-41.51	2.79E-91
iscU	scaffold protein	-40.84	3.16E-36
nuoE	NADH-quinone oxidoreductase subunit E	-36.44	2.30E-53
ccoO2	cbb3-type cytochrome C oxidase subunit II	-34.29	2.28E-20
PA4429	cytochrome C1	-30.10	1.63E-36
nuoB	NADH-quinone oxidoreductase subunit B	-21.84	3.75E-34
PA4431	iron-sulfur protein	-20.96	5.37E-22
PA4430	cytochrome b	-20.92	8.24E-26
fdxA	ferredoxin I	-20.02	8.61E-42
azu	azurin	-18.38	1.41E-72
nuoJ	NADH-quinone oxidoreductase subunit J	-18.10	1.81E-24
idh	isocitrate dehydrogenase	-17.99	8.83E-38
ccoP2	cytochrome C oxidase cbb3-type subunit CcoP	-17.19	5.34E-60
PA5435	pyruvate carboxylase subunit B	-15.71	4.39E-39
nuoK	NADH-quinone oxidoreductase subunit K	-15.52	9.64E-24
atpC	ATP synthase subunit epsilon	-15.47	4.16E-22
atpB	ATP synthase subunit A	-14.99	2.77E-15
ccoO1	cbb3-type cytochrome C oxidase subunit II	-13.41	2.96E-24
aceE	pyruvate dehydrogenase subunit E1	-13.39	1.66E-86
ccoP1	cytochrome C oxidase cbb3-type subunit CcoP	-13.35	4.79E-20
PA1551	ferredoxin	-12.78	5.00E-18
nqrD	Na(+)-translocating NADH-quinone reductase subunit D	-12.43	5.43E-11
PA0918	cytochrome b561	-12.38	4.52E-18
PA5312	aldehyde dehydrogenase	-12.33	1.17E-56
nqrF	Na(+)-translocating NADH-quinone reductase subunit F	-11.74	6.24E-83
acnB	aconitate hydratase B	-11.63	9.46E-104
etfA	electron transfer flavoprotein subunit alpha	-11.61	6.21E-90
pckA	phosphoenolpyruvate carboxykinase	-11.57	1.60E-17
PA0317	hypothetical protein	-10.58	3.19E-24
nqrC	Na(+)-translocating NADH-quinone reductase subunit C	-10.36	6.14E-48
ppa	inorganic pyrophosphatase	-10.23	1.13E-15
nuoD	NADH:-quinone oxidoreductase subunit C/D	-10.21	5.34E-35
sth	soluble pyridine nucleotide transhydrogenase	-9.76	1.51E-12
PA2953	electron transfer flavoprotein-ubiquinone oxidoreductase	-9.09	8.27E-39

nqrE	Na(+)-translocating NADH-quinone reductase subunit E	-8.74	1.63E-15
nuoH	NADH-quinone oxidoreductase subunit H	-8.46	3.52E-39
aceA	isocitrate lyase	-8.38	6.69E-19
rubA2	rubredoxin	-8.34	9.34E-14
sucB	2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase	-7.86	5.94E-52
nqrB	Na(+)-translocating NADH-quinone reductase subunit B	-7.75	3.67E-40
betB	betaine aldehyde dehydrogenase	-7.25	5.29E-18
coxB	cytochrome C oxidase subunit II	-6.84	9.06E-13
nuoM	NADH-quinone oxidoreductase subunit M	-6.39	4.41E-41
cyoA	cytochrome o ubiquinol oxidase subunit II	-6.21	4.43E-09
PA0541	hypothetical protein	-5.92	2.83E-29
fpr	ferredoxin-NADP reductase	-5.90	3.44E-17
cyoC	cytochrome o ubiquinol oxidase subunit III	-5.78	6.69E-07
fdnH	nitrate-inducible formate dehydrogenase subunit beta	-5.72	1.58E-43
PA4571	cytochrome C	-5.63	1.89E-40
gltP	glutamate/aspartate:proton symporter	-5.18	6.64E-22
adhC	alcohol dehydrogenase	-5.10	8.96E-39
coxA	cytochrome C oxidase subunit I	-4.89	3.29E-10
coIII	cytochrome C oxidase subunit III	-4.85	9.82E-09
nuoA	NADH-quinone oxidoreductase subunit A	-4.80	3.91E-07
glcB	malate synthase G	-4.79	1.17E-33
cyoB	cytochrome o ubiquinol oxidase subunit I	-4.77	1.18E-07
PA4348	hypothetical protein	-4.74	5.76E-16
fdx2	(2Fe-2S) ferredoxin	-4.70	1.71E-11
PA5491	cytochrome	-4.19	2.44E-14
PA3471	NAD-dependent malic enzyme	-3.91	1.91E-23
PA5190	nitroreductase	-3.91	1.58E-17
glpK	glycerol kinase	-3.90	5.27E-20
nuoN	NADH-quinone oxidoreductase subunit N	-3.85	1.66E-26
PA5445	coenzyme A transferase	-3.76	2.66E-26
gabD	glutarate-semialdehyde dehydrogenase DavD	-3.73	1.10E-22
PA1751	hypothetical protein	-3.72	4.04E-09
gor	glutathione reductase	-3.57	3.67E-15
PA3954	hypothetical protein	-3.51	3.06E-13
atpI	ATP synthase subunit I	-3.42	8.59E-05
dctA	C4-dicarboxylate transport protein	-3.38	2.73E-21
bkdA1	2-oxoisovalerate dehydrogenase subunit alpha	-3.28	2.73E-25
PA3795	oxidoreductase	-3.28	1.72E-15
nuoF	NADH dehydrogenase I subunit F	-3.22	6.08E-22

bkdA2	2-oxoisovalerate dehydrogenase subunit beta	-3.12	6.09E-14
prpC	methylcitrate synthase	-3.09	1.67E-15
aceF	dihydrolipoamide acetyltransferase	-3.05	3.98E-17
PA2956	hypothetical protein	-2.99	4.93E-14
PA5325	hypothetical protein	-2.96	9.13E-05
PA4434	oxidoreductase	-2.80	2.84E-09
cioB	cyanide insensitive terminal oxidase	-2.75	1.37E-13
PA4022	aldehyde dehydrogenase	-2.73	3.01E-08
nqrA	Na(+)-translocating NADH-quinone reductase subunit A	-2.66	1.30E-13
cc4	cytochrome C4	-2.65	1.18E-05
nuoG	NADH-quinone oxidoreductase subunit G	-2.63	2.57E-20
acnA	aconitate hydratase	-2.52	1.36E-09
ndh	NADH dehydrogenase	-2.47	1.42E-10
cioA	cyanide insensitive terminal oxidase	-2.45	7.05E-08
fdnI	nitrate-inducible formate dehydrogenase subunit gamma	-2.41	7.47E-13
PA4333	fumarase	-2.39	3.16E-12
PA0953	thioredoxin	-2.35	5.01E-03
rubA1	rubredoxin	-2.28	2.00E-04
narH	respiratory nitrate reductase subunit beta	-2.27	4.03E-06
PA0366	coniferyl aldehyde dehydrogenase	-2.21	4.71E-05
ackA	acetate kinase	-2.17	1.74E-06
cycB	cytochrome C5	-2.11	1.15E-08
nuoL	NADH-quinone oxidoreductase subunit L	-2.10	2.56E-08
Hypothetical, unclassified, unknown			
PA4738	hypothetical protein	-1033.66	4.90E-80
PA5482	hypothetical protein	-940.57	2.43E-65
pmpR	transcriptional regulator PmpR	-78.91	9.60E-37
iscA	iron-binding protein IscA	-73.02	1.44E-54
pasP	hypothetical protein	-56.82	1.62E-121
PA0974	hypothetical protein	-38.84	4.04E-38
PA4421	cell division protein MraZ	-38.31	6.01E-28
PA1847	Fe/S biogenesis protein NfuA	-30.94	5.20E-95
PA2950	reductase	-27.07	3.71E-26
PA3819	hypothetical protein	-20.62	5.06E-67
PA0320	hypothetical protein	-19.58	3.85E-25
PA4460	hypothetical protein	-19.35	1.84E-16
PA3808	hypothetical protein	-17.08	2.95E-25
PA4104	hypothetical protein	-15.81	1.28E-69
PA0665	iron-sulfur cluster insertion protein ErpA	-15.71	4.29E-26
PA2659	hypothetical protein	-15.70	4.48E-43

PA1371	hypothetical protein	-14.97	3.24E-23
PA0329	hypothetical protein	-14.82	7.21E-19
PA5446	hypothetical protein	-13.56	2.81E-17
PA5001	hypothetical protein	-13.31	5.39E-32
PA5286	hypothetical protein	-12.20	4.58E-34
PA5229	hypothetical protein	-12.04	2.48E-29
PA4611	hypothetical protein	-11.48	4.34E-29
PA5333	hypothetical protein	-11.44	9.79E-19
PA0586	hypothetical protein	-11.41	1.91E-13
PA5055	hypothetical protein	-11.23	1.00E-51
PA5227	hypothetical protein	-10.94	1.66E-57
PA4766	hypothetical protein	-10.93	7.49E-15
PA1769	phosphoenolpyruvate synthase regulatory protein	-10.66	8.60E-20
PA5178	hypothetical protein	-10.18	1.55E-46
PA4395	nucleotide-binding protein	-9.89	1.27E-60
PA1533	nucleoid-associated protein	-9.67	2.95E-30
PA2630	hypothetical protein	-9.03	8.58E-20
PA4106	hypothetical protein	-9.01	7.86E-30
PA2621	ATP-dependent Clp protease adapter protein Clp	-8.92	8.46E-15
PA2705	hypothetical protein	-8.90	5.52E-16
PA4605	hypothetical protein	-8.60	1.99E-09
PA2992	hypothetical protein	-8.10	4.06E-14
nirS	nitrite reductase	-7.53	2.17E-16
PA0937	hypothetical protein	-7.37	7.50E-10
PA1034	hypothetical protein	-7.36	3.29E-07
PA3046	hypothetical protein	-7.29	1.00E-08
PA1035	hypothetical protein	-7.10	4.29E-14
PA1574	hypothetical protein	-7.07	1.04E-17
PA3756	hypothetical protein	-6.38	1.09E-11
PA3979	hypothetical protein	-6.25	1.14E-13
PA3040	hypothetical protein	-6.21	1.33E-39
PA3826	hypothetical protein	-5.89	6.69E-11
PA4746	hypothetical protein	-5.87	2.03E-06
PA0563	hypothetical protein	-5.77	2.95E-14
PA4842	hypothetical protein	-5.65	2.53E-29
PA0084	hypothetical protein	-5.61	9.51E-26
PA3998	hypothetical protein	-5.44	3.86E-13
PA4459	hypothetical protein	-5.37	2.79E-16
PA4530	zinc-binding protein	-5.22	7.45E-10
PA1659	hypothetical protein	-5.07	2.52E-06
PA3696	hypothetical protein	-5.03	2.50E-17

PA4701	hypothetical protein	-4.87	8.70E-21
PA0392	hypothetical protein	-4.82	1.84E-13
PA0013	hypothetical protein	-4.81	3.06E-07
PA0529	hypothetical protein	-4.81	2.84E-18
PA0038	hypothetical protein	-4.72	4.18E-20
PA5423	hypothetical protein	-4.71	1.47E-21
PA1842	hypothetical protein	-4.68	2.06E-10
PA0020	hypothetical protein	-4.61	4.16E-22
PA4384	hypothetical protein	-4.50	2.81E-18
PA1516	hypothetical protein	-4.46	4.44E-12
PA3440	hypothetical protein	-4.42	1.26E-12
PA2706	hypothetical protein	-4.25	3.55E-19
PA3732	hypothetical protein	-4.24	4.32E-09
PA3697	hypothetical protein	-4.24	5.33E-15
PA4532	hypothetical protein	-4.22	6.33E-10
PA1075	hypothetical protein	-4.13	1.78E-07
PA3012	hypothetical protein	-4.12	2.90E-05
PA0046	hypothetical protein	-4.00	2.18E-11
PA1684	acireductone dioxygenase	-3.94	2.59E-07
PA1667	hypothetical protein	-3.92	5.96E-08
PA4940	hypothetical protein	-3.92	1.91E-07
PA4441	hypothetical protein	-3.85	4.18E-31
PA1658	hypothetical protein	-3.79	3.43E-07
PA5424	hypothetical protein	-3.67	8.20E-15
PA3237	hypothetical protein	-3.65	6.41E-07
PA4515	hydroxylase	-3.64	3.72E-07
PA3801	hypothetical protein	-3.62	1.13E-22
PA0661	hypothetical protein	-3.62	2.43E-04
PA0284	hypothetical protein	-3.61	6.83E-07
PA0270	hypothetical protein	-3.51	5.28E-12
PA4564	hypothetical protein	-3.51	1.73E-06
PA1657	hypothetical protein	-3.46	2.37E-04
PA0948	hypothetical protein	-3.42	6.48E-11
PA0578	hypothetical protein	-3.39	7.43E-11
PA4005	hypothetical protein	-3.37	1.32E-09
PA0587	hypothetical protein	-3.23	2.68E-05
PA3800	outer membrane protein assembly factor BamB	-3.19	9.51E-20
PA2754	hypothetical protein	-3.19	1.31E-14
PA0951	hypothetical protein	-3.19	3.73E-06
PA0537	hypothetical protein	-3.16	2.73E-14
PA2980	hypothetical protein	-3.12	1.94E-05

PA5460	hypothetical protein	-3.10	3.66E-05
PA2428	hypothetical protein	-3.09	9.86E-10
PA3566	hypothetical protein	-3.07	2.85E-10
PA4445	hypothetical protein	-3.03	6.45E-08
PA0856	hypothetical protein	-3.03	3.94E-06
PA3539	hypothetical protein	-3.02	1.60E-07
PA3413	hypothetical protein	-2.99	1.78E-09
PA0083	hypothetical protein	-2.98	3.54E-10
PA1841	hypothetical protein	-2.97	1.23E-08
PA1550	hypothetical protein	-2.91	1.99E-11
PA5305	hypothetical protein	-2.90	1.88E-08
PA5444	hypothetical protein	-2.88	2.37E-08
icp	inhibitor of cysteine peptidase	-2.87	1.31E-10
pcaC	4-carboxymuconolactone decarboxylase	-2.85	9.26E-07
PA3216	hypothetical protein	-2.83	1.41E-06
PA1508	hypothetical protein	-2.82	7.95E-03
PA1668	hypothetical protein	-2.80	1.99E-06
PA5244	hypothetical protein	-2.76	1.25E-06
PA4105	hypothetical protein	-2.75	1.19E-18
PA0457.1	hypothetical protein	-2.75	2.41E-08
PA0540	hypothetical protein	-2.67	5.82E-05
PA5279	hypothetical protein	-2.66	2.63E-13
PA0319	hypothetical protein	-2.65	2.66E-08
PA2017	hypothetical protein	-2.65	7.98E-11
PA1295	hypothetical protein	-2.62	2.29E-05
PA3674	hypothetical protein	-2.60	3.76E-11
PA0269	hypothetical protein	-2.59	2.13E-08
PA4004	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	-2.59	3.87E-08
PA3041	hypothetical protein	-2.58	2.56E-10
PA2184	hypothetical protein	-2.56	2.71E-04
PA2954	hypothetical protein	-2.54	9.55E-06
PA4798	hypothetical protein	-2.53	1.22E-13
PA0398	hypothetical protein	-2.48	1.48E-06
PA3726	hypothetical protein	-2.46	3.42E-05
PA1392	hypothetical protein	-2.45	7.76E-03
PA4486	hypothetical protein	-2.35	5.73E-08
PA4495	hypothetical protein	-2.33	2.18E-08
PA2864	hypothetical protein	-2.28	6.71E-04
PA2722	hypothetical protein	-2.27	7.34E-05
PA1031	DNA recombination protein RmuC	-2.25	3.53E-08
PA0271	hypothetical protein	-2.24	4.83E-05

PA4090	hypothetical protein	-2.23	1.32E-03
PA0131	beta-alanine degradation protein BauB	-2.20	3.81E-06
PA3951	hypothetical protein	-2.19	1.90E-08
PA4698	hypothetical protein	-2.16	4.01E-05
PA2685	hypothetical protein	-2.13	1.02E-05
PA0567	hypothetical protein	-2.13	2.59E-03
PA1661	hypothetical protein	-2.12	2.55E-03
PA1675	hypothetical protein	-2.12	5.20E-06
PA1792	UDP-2,3-diacylglucosamine hydrolase	-2.07	7.93E-07
PA1042	hypothetical protein	-2.06	1.03E-03
PA0915	hypothetical protein	-2.06	5.17E-04
PA1299	hypothetical protein	-2.06	3.09E-04
PA0565	hypothetical protein	-2.05	2.90E-04
PA0709	hypothetical protein	-2.04	5.57E-03
ssrA		-3369.42	3.52E-169
oprI	outer membrane lipoprotein OprI	-928.55	2.16E-119
rnpB	RNA component of RNaseP, RnpB	-812.66	1.20E-263
crcZ	CrcZ	-796.86	1.20E-63
PA4272.1	P27	-538.00	1.25E-142
PA5481	hypothetical protein	-222.66	4.52E-49
PA3369	hypothetical protein	-135.67	1.12E-35
mvaT	transcriptional regulator MvaT	-125.92	1.26E-113
PA4107	hypothetical protein	-111.02	4.20E-213
PA4270.1	P26	-102.71	4.49E-39
PA4578	hypothetical protein	-95.61	2.91E-118
PA4793	hypothetical protein	-84.66	2.08E-113
PA4406.1		-71.11	6.00E-56
PA4881	hypothetical protein	-70.76	1.77E-28
PA2883	hypothetical protein	-70.12	2.58E-65
phrS	PhrS	-61.84	3.11E-43
atpE	ATP synthase subunit C	-49.19	6.40E-39
PA1414	hypothetical protein	-38.15	3.29E-110
PA3370	hypothetical protein	-34.56	5.77E-23
PA0315	hypothetical protein	-34.01	9.17E-48
PA5494	hypothetical protein	-31.44	6.68E-116
PA0805	hypothetical protein	-31.39	1.06E-50
PA2667	hypothetical protein	-28.89	1.38E-41
PA1076	hypothetical protein	-27.71	4.41E-66
PA0943	hypothetical protein	-25.83	2.71E-28
PA0039	hypothetical protein	-25.62	5.04E-38
PA1761	hypothetical protein	-25.42	3.99E-25

PA5061	hypothetical protein	-25.27	2.09E-70
PA1942	hypothetical protein	-23.02	3.04E-13
PA4623	hypothetical protein	-20.51	4.39E-17
PA4690.5	16S ribosomal RNA	-20.10	1.39E-31
PA5369.5	16S ribosomal RNA	-20.05	5.18E-32
PA1747	hypothetical protein	-19.90	1.73E-29
PA4280.5	16S ribosomal RNA	-19.80	1.02E-31
PA0668.1	16S ribosomal RNA	-19.62	4.19E-32
PA4277.1	tRNA-Thr	-19.14	2.42E-15
PA2805	hypothetical protein	-18.65	2.53E-38
PA5108	hypothetical protein	-18.09	1.95E-40
PA1592	hypothetical protein	-17.66	3.53E-35
kdpF	potassium-transporting ATPase subunit F	-17.40	4.68E-26
pagL	lipid A 3-O-deacylase	-17.21	1.85E-70
PA3691	hypothetical protein	-17.20	5.72E-80
PA2485	hypothetical protein	-15.68	7.81E-13
PA5461	hypothetical protein	-15.57	9.06E-129
PA3031	hypothetical protein	-15.27	1.88E-27
GeneID:880268	unknown	-15.19	5.53E-32
PA4575	hypothetical protein	-15.13	6.81E-37
prtN	transcriptional regulator PrtN	-14.98	4.31E-17
PA1579	hypothetical protein	-13.80	6.33E-26
PA5316.1		-13.75	6.22E-54
PA4607	hypothetical protein	-13.39	2.83E-20
PA0976.1	tRNA-Lys	-13.23	4.77E-07
PA2759	hypothetical protein	-12.88	2.66E-09
PA1804.1	tRNA-Asp	-12.80	5.65E-13
PA4280.2	23S ribosomal RNA	-12.59	5.10E-17
PA0951a	hypothetical protein	-12.56	8.39E-12
oprD	porin D	-12.20	1.47E-12
PA2760	hypothetical protein	-12.05	1.29E-17
PA4690.2	23S ribosomal RNA	-12.00	1.66E-16
PA5369.2	23S ribosomal RNA	-11.84	3.29E-16
PA0668.4	23S ribosomal RNA	-11.83	3.77E-16
PA3574a	copper chaperone CopZ	-11.30	1.04E-21
PA5269	hypothetical protein	-11.29	2.55E-40
PA5347	hypothetical protein	-11.04	1.59E-20
PA4277.3	tRNA-Tyr	-10.98	4.78E-17
PA0621	hypothetical protein	-10.50	7.01E-28
PA1096	hypothetical protein	-10.32	2.03E-11
nrdJb	hypothetical protein	-9.92	5.66E-11

PA1746	hypothetical protein	-9.88	1.86E-20
PA1934	hypothetical protein	-9.57	1.28E-17
PA2560	hypothetical protein	-9.51	2.07E-21
crfX	hypothetical protein	-9.50	1.65E-12
PA5285	hypothetical protein	-9.25	2.22E-22
PA2790	hypothetical protein	-9.22	6.66E-21
PA0940	hypothetical protein	-8.97	7.53E-09
GeneID:878009	unknown	-8.95	1.50E-35
PA4276.1	tRNA-Trp	-8.94	6.90E-08
PA1343	hypothetical protein	-8.70	4.80E-22
PA2453	hypothetical protein	-8.62	5.82E-42
PA3010	hypothetical protein	-8.39	5.14E-14
PA0922	hypothetical protein	-8.37	5.13E-10
PA5526	hypothetical protein	-8.28	4.29E-20
PA4737	hypothetical protein	-8.24	8.44E-14
PA1030	hypothetical protein	-8.22	3.10E-15
PA0261	hypothetical protein	-8.14	1.86E-16
pilY2	type 4 fimbrial biogenesis protein PilY2	-8.12	7.73E-10
PA3662	hypothetical protein	-8.06	1.51E-26
PA0032a	DOPA 4,5-dioxygenase	-8.03	9.71E-28
PA0251	hypothetical protein	-8.02	2.28E-09
PA1190	hypothetical protein	-7.90	4.87E-17
PA1013.1	tRNA-Ser	-7.85	7.77E-17
PA3698	hypothetical protein	-7.73	1.72E-11
PA1206	hypothetical protein	-7.65	1.38E-17
PA0769	hypothetical protein	-7.60	4.36E-25
PA4933	hypothetical protein	-7.52	4.81E-52
PA0012	hypothetical protein	-7.45	1.22E-07
PA4736	hypothetical protein	-7.40	1.03E-20
PA5306	hypothetical protein	-7.36	1.67E-21
PA4972	hypothetical protein	-7.32	1.76E-13
PA0900	hypothetical protein	-7.23	6.93E-38
PA2166	hypothetical protein	-6.92	9.33E-07
PA1767	hypothetical protein	-6.84	2.45E-09
PA3371	hypothetical protein	-6.51	5.70E-09
PA0836.1	P5	-6.50	1.35E-12
PA4377	hypothetical protein	-6.48	6.39E-13
PA0573	hypothetical protein	-6.31	5.08E-05
PA1755	hypothetical protein	-6.28	7.08E-10
PA0905.1	tRNA-Ser	-6.27	7.06E-08
PA2756	hypothetical protein	-6.24	3.57E-09

amiL	AmiL	-6.12	1.20E-06
PA3908	hypothetical protein	-6.10	4.16E-11
PA2793	hypothetical protein	-6.10	1.20E-07
PA2755a	hypothetical protein	-6.05	1.32E-10
PA4531	hypothetical protein	-6.04	1.85E-09
PA3611	hypothetical protein	-5.98	3.32E-11
PA0258	hypothetical protein	-5.86	4.50E-11
PA5527	hypothetical protein	-5.85	1.70E-10
PA4437	hypothetical protein	-5.75	5.48E-08
PA4533	hypothetical protein	-5.73	9.03E-16
PA0736a	hypothetical protein	-5.65	3.99E-21
PA0260	hypothetical protein	-5.63	5.24E-18
PA5566	hypothetical protein	-5.61	1.74E-06
PA1112a	hypothetical protein	-5.45	1.42E-08
PA0955	hypothetical protein	-5.43	1.27E-13
PA3229	hypothetical protein	-5.38	2.84E-09
PA4754	hypothetical protein	-5.37	7.29E-16
PA2568	hypothetical protein	-5.37	4.49E-06
PA3902	hypothetical protein	-5.34	2.12E-09
PA2901	hypothetical protein	-5.30	2.76E-15
PA4685	hypothetical protein	-5.27	1.74E-11
PA0388	hypothetical protein	-5.27	1.65E-25
PA4103	hypothetical protein	-5.26	9.63E-39
amrZ	alginate and motility regulator Z	-5.25	8.57E-14
PA1324	hypothetical protein	-5.23	3.22E-26
PA3033	hypothetical protein	-5.19	5.83E-12
PA1797a	hypothetical protein	-5.13	5.47E-09
PA5397	hypothetical protein	-5.12	2.88E-08
PA2433	hypothetical protein	-5.10	1.04E-20
GeneID:878959	unknown	-5.03	1.75E-25
PA4697	hypothetical protein	-4.96	3.29E-06
PA3278	hypothetical protein	-4.93	1.08E-17
PA5062	hypothetical protein	-4.91	3.34E-13
PA3224	hypothetical protein	-4.87	5.47E-13
PA5405	hypothetical protein	-4.85	1.15E-08
PA1112.1		-4.84	7.71E-04
PA0256	hypothetical protein	-4.84	5.39E-12
PA4537	hypothetical protein	-4.80	2.00E-06
PA2791	hypothetical protein	-4.78	1.72E-06
PA0952	hypothetical protein	-4.73	1.52E-05
PA1244	hypothetical protein	-4.69	1.21E-07

PA3793	hypothetical protein	-4.67	3.41E-12
PA0910	hypothetical protein	-4.66	1.03E-11
PA2736.1	tRNA-Pro	-4.65	1.89E-03
PA4608	hypothetical protein	-4.60	5.37E-21
PA3794	hypothetical protein	-4.57	1.55E-06
PA2581	hypothetical protein	-4.56	5.32E-06
PA3824.1	tRNA-Leu	-4.54	1.30E-04
PA0624	hypothetical protein	-4.49	5.90E-15
PA4639	hypothetical protein	-4.46	2.82E-14
PA0100	hypothetical protein	-4.39	2.71E-08
PA0554	hypothetical protein	-4.37	1.55E-19
PA5271	hypothetical protein	-4.31	1.93E-20
PA2570.1	tRNA-Leu	-4.31	1.63E-04
PA2486	hypothetical protein	-4.29	6.62E-06
PA4278	hypothetical protein	-4.26	4.12E-07
PA0911	hypothetical protein	-4.25	2.90E-04
PA0429	hypothetical protein	-4.24	1.34E-18
PA3740	hypothetical protein	-4.22	1.97E-11
PA4874	hypothetical protein	-4.21	7.64E-21
PA2792	hypothetical protein	-4.20	1.48E-05
prfB	peptide chain release factor 1	-4.19	6.80E-18
PA2799	hypothetical protein	-4.19	1.84E-11
PA4690	hypothetical protein	-4.18	6.35E-05
PA0921	hypothetical protein	-4.05	1.11E-06
PA4683	hypothetical protein	-4.00	2.23E-05
PA4141	hypothetical protein	-4.00	2.03E-09
PA4690a	paraquat-inducible protein A	-3.93	5.31E-04
PA1492	hypothetical protein	-3.92	5.21E-07
PA0713	hypothetical protein	-3.88	2.11E-05
PA5191	hypothetical protein	-3.87	9.69E-05
PA4277.2	tRNA-Gly	-3.83	1.52E-04
PA4390	hypothetical protein	-3.81	4.40E-05
PA2364	hypothetical protein	-3.77	1.53E-10
PA0989	hypothetical protein	-3.76	1.43E-08
PA4313a	hypothetical protein	-3.70	2.93E-14
PA4690.4	tRNA-Ile	-3.70	2.41E-04
PA0905.2	tRNA-Arg	-3.70	1.02E-04
PA1369	hypothetical protein	-3.68	3.16E-04
PA5404	hypothetical protein	-3.67	2.05E-09
PA4802.1	tRNA-Sec	-3.66	7.45E-08
PA0887.1	P7	-3.64	2.45E-04

PA3057	hypothetical protein	-3.63	2.10E-05
PA1509	hypothetical protein	-3.62	3.90E-06
PA0926	hypothetical protein	-3.62	3.48E-10
PA4937.1	tRNA-Leu	-3.60	3.82E-04
PA2565	hypothetical protein	-3.58	2.69E-03
PA0007	hypothetical protein	-3.57	3.47E-17
PA4682	hypothetical protein	-3.56	1.73E-05
PA2820	hypothetical protein	-3.56	4.23E-18
PA2763	hypothetical protein	-3.53	2.94E-04
PA0532	hypothetical protein	-3.50	1.10E-06
PA0060	hypothetical protein	-3.49	3.65E-08
PA2205	hypothetical protein	-3.44	1.87E-08
PA0553	hypothetical protein	-3.44	1.21E-15
PA4469	hypothetical protein	-3.43	1.23E-03
PA2569	hypothetical protein	-3.38	3.06E-04
PA2264	hypothetical protein	-3.34	2.22E-16
PA2753	hypothetical protein	-3.33	2.19E-13
PA5402	hypothetical protein	-3.32	2.72E-06
PA2381	hypothetical protein	-3.30	4.21E-11
PA3572	hypothetical protein	-3.29	2.35E-09
PA4581.1	tRNA-Arg	-3.27	8.16E-08
PA5369.4	tRNA-Ile	-3.24	1.74E-03
PA1308	hypothetical protein	-3.19	6.48E-12
GeneID:879706	unknown	-3.18	9.85E-14
PA2559a	hypothetical protein	-3.18	6.49E-05
PA1383	hypothetical protein	-3.15	4.86E-05
PA3367	hypothetical protein	-3.13	5.25E-07
PA3015	hypothetical protein	-3.11	1.64E-10
PA0135	hypothetical protein	-3.11	3.30E-03
PA2670	hypothetical protein	-3.06	8.18E-05
PA4535	hypothetical protein	-3.05	3.41E-15
PA0442	hypothetical protein	-3.05	6.32E-03
PA3139.1	tRNA-Asn	-3.03	4.36E-03
PA5226	hypothetical protein	-3.02	2.82E-10
PA3362	transporter protein AmiS	-3.01	5.89E-04
ssrS	6S RNA	-2.98	1.11E-15
lecB	fucose-binding lectin PA-IIL	-2.97	3.52E-04
PA0668.2	tRNA-Ile	-2.95	3.08E-03
plcB	phospholipase C	-2.95	7.32E-11
PA3966	hypothetical protein	-2.92	3.99E-03
PA0874	hypothetical protein	-2.91	3.83E-03

PA1038	hypothetical protein	-2.91	2.74E-08
PA0894	hypothetical protein	-2.88	8.85E-08
PA4669.1	tRNA-Gln	-2.85	2.35E-03
PA2761	hypothetical protein	-2.85	5.84E-03
PA0050	hypothetical protein	-2.84	2.28E-06
PA4280.4	tRNA-Ile	-2.82	8.20E-03
PA4108a	hypothetical protein	-2.82	7.90E-07
ffs	4.5S ribosomal RNA	-2.81	7.23E-03
PA3519	hypothetical protein	-2.81	8.39E-05
PA4327	hypothetical protein	-2.78	2.37E-11
PA1387	hypothetical protein	-2.77	6.30E-05
alkB2	alkane-1 monooxygenase	-2.76	1.08E-07
PA3018	hypothetical protein	-2.71	1.85E-09
PA0306a	transcriptional regulator	-2.71	1.55E-07
PA5414	hypothetical protein	-2.71	1.98E-11
PA0714	hypothetical protein	-2.70	6.95E-03
PA3451	hypothetical protein	-2.67	5.70E-03
PA3009	hypothetical protein	-2.67	1.23E-04
PA3716	hypothetical protein	-2.66	1.78E-12
PA4961	hypothetical protein	-2.65	8.44E-15
PA2763a	hypothetical protein	-2.65	6.35E-04
PA0160	hypothetical protein	-2.64	3.77E-03
PA2429	hypothetical protein	-2.64	8.74E-06
PA1370	hypothetical protein	-2.60	2.63E-03
PA1305	hypothetical protein	-2.59	5.58E-10
GeneID:882377	unknown	-2.58	4.95E-03
PA5340	hypothetical protein	-2.57	3.95E-14
PA2775	hypothetical protein	-2.56	1.80E-03
PA2501	hypothetical protein	-2.53	3.86E-07
PA0343	hypothetical protein	-2.52	1.72E-11
PA1106	hypothetical protein	-2.49	5.05E-06
PA1728	hypothetical protein	-2.49	1.17E-03
PA0234	hypothetical protein	-2.47	9.49E-05
PA4782	hypothetical protein	-2.47	2.24E-09
PA4523	hypothetical protein	-2.47	3.03E-11
opdC	histidine porin OpdC	-2.46	1.62E-11
PA2669	hypothetical protein	-2.44	9.40E-03
PA2779	hypothetical protein	-2.43	8.25E-05
PA1641	hypothetical protein	-2.43	2.46E-05
PA4317	hypothetical protein	-2.42	1.03E-04
PA3733a	hypothetical protein	-2.41	8.18E-04

PA5252a	hypothetical protein	-2.40	1.91E-06
PA0505	hypothetical protein	-2.40	1.19E-04
PA0365	hypothetical protein	-2.40	2.75E-03
PA0122	hypothetical protein	-2.38	3.67E-09
PA2559	hypothetical protein	-2.37	2.66E-08
GeneID:881406	unknown	-2.37	7.24E-08
PA1643a	aldehyde-activating protein	-2.32	2.72E-05
PA4681	hypothetical protein	-2.31	2.89E-05
PA1606	hypothetical protein	-2.31	9.41E-04
PA0776	hypothetical protein	-2.29	1.58E-03
PA0845	neutral ceramidase	-2.29	3.13E-06
PA1530	hypothetical protein	-2.28	7.85E-05
PA5533	hypothetical protein	-2.28	5.68E-05
opdP	glycine-glutamate dipeptide porin OpdP	-2.27	9.81E-09
PA4603	hypothetical protein	-2.27	3.59E-07
PA3440a	type III effector protein	-2.26	3.05E-05
PA4596	transcriptional regulator	-2.23	1.75E-03
PA1837a	hypothetical protein	-2.22	1.00E-03
PA1852	hypothetical protein	-2.21	7.34E-06
PA3661	hypothetical protein	-2.21	6.17E-03
algP	alginate regulatory protein AlgP	-2.19	5.58E-07
PA1763	hypothetical protein	-2.16	1.51E-03
PA0109	hypothetical protein	-2.13	8.35E-04
GeneID:883111	unknown	-2.12	1.28E-07
PA1833a	alpha/beta hydrolase	-2.11	8.16E-04
PA4703	hypothetical protein	-2.11	3.11E-03
PA3496	hypothetical protein	-2.11	8.71E-07
opdH	cis-aconitate porin OpdH	-2.08	8.65E-05
PA3488	hypothetical protein	-2.08	2.80E-03
PA0099	hypothetical protein	-2.06	2.16E-03
PA0042	hypothetical protein	-2.06	1.23E-03
PA5520	hypothetical protein	-2.06	9.84E-04
PA1167	hypothetical protein	-2.05	4.79E-06
yfiR	hypothetical protein	-2.03	8.58E-06
PA2754a	hypothetical protein	-2.01	5.84E-03
General function prediction only			
PA4739	hypothetical protein	-1052.39	1.58E-73
hfq	RNA-binding protein Hfq	-88.62	4.01E-68
PA2971	hypothetical protein	-46.39	8.50E-32
fabG	3-oxoacyl-[acyl-carrier-protein] reductase FabG	-44.73	4.17E-70
PA4465	hypothetical protein	-33.70	4.15E-36

hpd	4-hydroxyphenylpyruvate dioxygenase	-28.49	4.40E-97
PA1749	hypothetical protein	-19.28	1.93E-23
PA1372	hypothetical protein	-16.52	5.48E-29
PA4461	ABC transporter ATP-binding protein	-16.21	4.23E-20
PA2604	hypothetical protein	-15.09	6.26E-38
PA3806	23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN	-15.08	5.73E-18
PA3978	hypothetical protein	-14.54	7.30E-28
PA0729	hypothetical protein	-14.53	3.24E-22
PA4426	hypothetical protein	-14.22	9.39E-18
PA2119	alcohol dehydrogenase	-12.70	4.94E-35
PA3615	hypothetical protein	-12.05	9.84E-38
PA1440	hypothetical protein	-12.02	2.62E-22
putP	sodium/proline symporter PutP	-11.82	4.18E-57
PA4794	hypothetical protein	-11.44	9.28E-97
PA3799	GTPase Der	-11.13	2.10E-16
PA4115	hypothetical protein	-10.66	1.98E-68
mliC	lysozyme inhibitor	-10.57	3.14E-18
sspB	ClpXP protease specificity-enhancing factor	-10.46	2.05E-09
PA3753	hypothetical protein	-10.45	5.09E-50
PA0968	hypothetical protein	-9.87	3.37E-13
PA5492	ribosome biogenesis GTP-binding protein YsxC	-9.48	4.35E-20
PA4674	hypothetical protein	-9.08	2.18E-15
PA5545	hypothetical protein	-8.87	7.03E-13
PA5488	hypothetical protein	-8.52	1.19E-40
PA0066	hypothetical protein	-8.44	1.67E-36
obg	GTPase ObgE	-8.08	1.34E-46
PA1788	hypothetical protein	-7.72	1.47E-10
PA2707	hypothetical protein	-7.50	5.49E-51
fdnG	formate dehydrogenase-O major subunit	-7.15	9.38E-69
PA0619	bacteriophage protein	-7.05	2.88E-19
PA0622	bacteriophage protein	-6.95	1.72E-27
pfpI	protease PfpI	-6.80	2.11E-23
PA0623	bacteriophage protein	-6.41	7.96E-13
PA4833	hypothetical protein	-6.40	5.01E-31
PA1807	ABC transporter ATP-binding protein	-6.32	1.93E-16
PA0618	bacteriophage protein	-6.22	2.19E-17
PA1307	hypothetical protein	-6.21	7.46E-39
PA0959	hypothetical protein	-6.04	6.56E-10
PA1012	hypothetical protein	-5.97	1.99E-16
PA2575	hypothetical protein	-5.90	4.29E-41
PA0617	bacteriophage protein	-5.76	1.64E-08

PA3836	hypothetical protein	-5.73	6.82E-32
PA1808	ABC transporter permease	-5.61	1.97E-09
amiE	acylamide amidohydrolase	-5.53	3.97E-18
PA5177	hydrolase	-5.46	3.45E-22
PA3827	hypothetical protein	-5.46	2.06E-23
PA0068	hypothetical protein	-5.37	7.99E-14
PA1762	hypothetical protein	-5.35	7.70E-06
PA4595	ABC transporter ATP-binding protein	-5.31	4.55E-46
PA2631	acetyltransferase	-5.15	5.63E-26
PA0976	7-cyano-7-deazaguanine synthase	-5.12	1.35E-07
PA0608	phosphoglycolate phosphatase	-5.11	1.53E-21
PA3849	nucleoid-associated protein NdpA	-4.96	2.60E-21
PA2566	hypothetical protein	-4.93	2.93E-08
PA3828	hypothetical protein	-4.89	2.06E-09
PA1007	hypothetical protein	-4.89	2.11E-06
PA0124	hypothetical protein	-4.88	1.05E-08
PA0065	5'-nucleotidase	-4.86	1.35E-24
PA4943	GTP-binding protein	-4.86	6.74E-33
PA0620	bacteriophage protein	-4.75	5.71E-08
PA4534	hypothetical protein	-4.75	3.38E-14
pstC	phosphate ABC transporter permease	-4.69	5.75E-22
PA5567	tRNA modification GTPase TrmE	-4.57	4.49E-33
surE	5'-nucleotidase SurE	-4.56	4.72E-15
cat	chloramphenicol acetyltransferase	-4.46	1.12E-05
PA3752	hypothetical protein	-4.46	2.19E-09
PA2536	phosphatidate cytidylyltransferase	-4.39	9.58E-08
PA0935	nucleoside triphosphate pyrophosphohydrolase	-4.38	4.46E-07
PA1643	tRNA 2-selenouridine synthase	-4.30	8.17E-22
PA0115	hypothetical protein	-4.29	1.52E-17
PA0628	hypothetical protein	-4.27	3.74E-08
cbrA	two-component sensor CbrA	-4.23	1.15E-24
PA2884	hypothetical protein	-4.17	9.73E-08
PA4657	hypothetical protein	-4.13	2.93E-20
PA3982	metalloprotease	-4.12	6.10E-13
PA0988	hypothetical protein	-4.12	1.51E-06
PA1829	hypothetical protein	-4.10	5.87E-26
PA0596	hypothetical protein	-4.08	1.53E-20
phzA1	phenazine biosynthesis protein	-4.07	1.21E-03
PA4562	hypothetical protein	-4.07	2.42E-08
senC	cytochrome c oxidase assembly protein SenC	-4.04	6.59E-10
PA1518	5-hydroxyisourate hydrolase	-4.04	5.79E-06

PA5362	hypothetical protein	-4.04	1.81E-14
PA5088	hypothetical protein	-3.98	4.20E-06
PA5521	short-chain dehydrogenase	-3.89	3.72E-11
adhA	alcohol dehydrogenase	-3.89	3.68E-10
PA4882	hypothetical protein	-3.89	2.19E-14
PA3310	hypothetical protein	-3.88	9.30E-08
PA2974	hydrolase	-3.84	1.88E-09
gbcA	protein GbcA	-3.79	6.61E-13
qor	oxygen-dependent quinone oxidoreductase	-3.72	2.43E-23
eco	ecotin	-3.68	6.60E-06
PA0483	acetyltransferase	-3.58	1.91E-10
PA2762	hypothetical protein	-3.53	4.75E-04
spuA	glutamine amidotransferase	-3.53	2.28E-11
PA0627	hypothetical protein	-3.48	4.83E-03
PA0360	hypothetical protein	-3.46	5.07E-21
comL	competence protein ComL	-3.37	1.50E-12
PA1964	ABC-F family ATPase	-3.34	1.06E-11
PA1415	hypothetical protein	-3.31	2.10E-23
PA1135	molecular chaperone Hsp31/glyoxalase	-3.29	9.37E-08
aspP	adenosine diphosphate sugar pyrophosphatase	-3.22	4.38E-20
PA2963	hypothetical protein	-3.17	9.79E-07
PA5540	hypothetical protein	-3.16	2.85E-06
wrbA	NAD(P)H dehydrogenase	-3.12	1.45E-07
PA2564	trans-aconitate 2-methyltransferase	-3.08	1.38E-11
PA4038	hypothetical protein	-2.96	3.84E-09
PA4667	hypothetical protein	-2.88	1.12E-13
PA4714	hypothetical protein	-2.87	1.59E-06
PA0371	hypothetical protein	-2.72	4.78E-14
PA1605	hypothetical protein	-2.71	5.66E-05
pta	phosphate acetyltransferase	-2.67	2.01E-09
PA3747	hypothetical protein	-2.67	1.29E-04
PA4604	hypothetical protein	-2.67	6.76E-11
PA2580	hypothetical protein	-2.67	4.23E-03
PA0485	hypothetical protein	-2.62	1.13E-07
PA1390	glycosyl transferase family protein	-2.43	3.36E-03
PA5314	hypothetical protein	-2.40	9.82E-05
PA1428	hypothetical protein	-2.39	2.42E-06
era	GTPase Era	-2.34	1.99E-06
PA5080	prolyl aminopeptidase	-2.34	2.92E-08
PA4968	hypothetical protein	-2.34	2.86E-06
mqoB	malate:quinone oxidoreductase	-2.33	2.92E-09

PA1575	hypothetical protein	-2.32	3.02E-06
PA3234	acetate permease	-2.27	3.46E-08
PA3616	recombination regulator RecX	-2.25	1.12E-03
PA3663	hypothetical protein	-2.25	2.90E-05
PA4689	hypothetical protein	-2.24	1.73E-13
PA1542	hypothetical protein	-2.23	6.08E-03
PA3079	hypothetical protein	-2.20	5.41E-05
PA4692	sulfite oxidase subunit YedY	-2.17	7.21E-05
PA4438	hypothetical protein	-2.17	3.01E-05
PA4539	hypothetical protein	-2.12	1.47E-08
PA4517	hypothetical protein	-2.12	4.26E-08
PA4584	hypothetical protein	-2.06	1.05E-03
PA4379	hypothetical protein	-2.05	8.08E-04
PA5544	hypothetical protein	-2.02	1.01E-08
PA2770	isomerase	-2.01	5.60E-06
Inorganic ion transport and metabolism			
sodB	superoxide dismutase	-135.79	7.83E-157
PA1673	bacteriohemerythrin	-62.16	9.62E-76
PA0962	DNA-binding stress protein	-60.33	2.83E-52
fur	ferric uptake regulation protein	-26.89	2.00E-79
ppk	polyphosphate kinase	-24.79	2.11E-26
bfrB	bacterioferritin	-24.38	4.10E-48
katA	catalase	-18.91	4.62E-24
PA5208	hypothetical protein	-16.74	1.77E-25
pstB	phosphate ABC transporter ATP-binding protein	-15.38	4.97E-22
PA3983	hypothetical protein	-14.73	1.03E-33
PA5505	TonB-dependent receptor	-13.22	3.31E-105
bfrA	bacterioferritin	-12.09	1.95E-10
PA5078	glucan biosynthesis protein G	-11.15	3.14E-28
phoU	phosphate uptake regulatory protein PhoU	-10.98	1.34E-18
kdpA	potassium-transporting ATPase subunit A	-10.16	3.01E-14
PA5250	hypothetical protein	-9.77	6.24E-17
PA5130	hypothetical protein	-8.98	1.07E-11
PA0950	arsenate reductase	-8.40	2.35E-29
PA1538	flavin-containing monooxygenase	-8.22	6.91E-40
cysP	sulfate ABC transporter substrate-binding protein	-8.21	1.79E-15
pstS	phosphate ABC transporter substrate-binding protein	-7.96	7.42E-14
PA4292	phosphate transporter	-7.09	3.64E-18
cysW	sulfate transporter CysW	-6.94	6.60E-32
PA4880	bacterioferritin	-6.85	9.03E-12
mgtE	Mg transporter MgtE	-6.26	1.13E-13

PA1058	monovalent cation/H+ antiporter subunit F	-6.14	3.65E-11
ccpR	cytochrome C551 peroxidase	-6.05	2.31E-17
trkA	potassium transporter inner membrane associated protein	-5.52	3.87E-20
PA0102	carbonic anhydrase	-5.01	4.31E-27
PA5529	sodium/proton antiporter	-4.72	2.86E-17
PA2608	hypothetical protein	-4.64	1.01E-10
PA5530	MFS dicarboxylate transporter	-4.53	3.55E-06
sodM	superoxide dismutase	-3.91	1.59E-05
PA1057	monovalent cation/H+ antiporter subunit E	-3.80	7.17E-13
PA4514	iron transport outer membrane receptor	-3.74	8.70E-06
corA	magnesium/cobalt transporter	-3.71	1.50E-06
PA2563	sulfate transporter	-3.59	7.39E-13
PA0397	cation efflux system protein	-3.53	5.88E-16
PA4156	TonB-dependent receptor	-3.47	2.49E-12
PA1059	monovalent cation/H+ antiporter subunit G	-3.37	9.94E-08
snr1	cytochrome C Snr1	-3.30	6.49E-05
kdpB	potassium-transporting ATPase subunit B	-3.28	1.09E-04
PA5217	iron ABC transporter substrate-binding protein	-3.09	5.23E-13
PA2607	hypothetical protein	-3.02	1.40E-08
katB	catalase	-2.99	2.77E-13
PA3250	hypothetical protein	-2.91	1.70E-09
thiI	thiamine biosynthesis protein ThiI	-2.75	5.03E-10
PA3265	transporter	-2.73	3.44E-04
kefB	glutathione-regulated potassium-efflux system protein KefB	-2.70	2.98E-09
cmaX	transporter	-2.70	1.54E-05
ppx	exopolyphosphatase	-2.65	2.59E-12
sbp	sulfate-binding protein	-2.56	5.59E-12
cysN	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase	-2.55	1.31E-16
PA3931	hypothetical protein	-2.54	3.44E-04
PA4676	carbonic anhydrase	-2.52	2.06E-04
oprP	phosphate-specific outer membrane porin OprP	-2.51	5.97E-08
antA	anthranilate dioxygenase large subunit	-2.50	6.48E-04
fptA	Fe(III)-pyochelin outer membrane receptor	-2.45	3.20E-11
hitA	ferric iron-binding periplasmic protein HitA	-2.45	2.60E-14
PA0689	hypothetical protein	-2.42	7.95E-05
PA3268	TonB-dependent receptor	-2.35	2.28E-11
narK1	nitrite extrusion protein 1	-2.33	2.04E-08
PA1292	3-mercaptopyruvate sulfurtransferase	-2.23	4.04E-08
norB	nitric oxide reductase subunit B	-2.21	1.67E-04

PA0688	alkaline phosphatase L	-2.18	4.45E-05
np20	transcriptional regulator	-2.16	2.17E-07
PA0128	hypothetical protein	-2.07	3.72E-03
PA1541	drug efflux transporter	-2.04	1.50E-03
cysI	sulfite reductase	-2.04	1.70E-07
PA5504	D-methionine ABC transporter	-2.03	1.95E-07
Intracellular trafficking, secretion, and vesicular transport			
secY	preprotein translocase subunit SecY	-125.42	6.09E-58
secB	preprotein translocase subunit SecB	-36.73	1.89E-85
PA3822	preprotein translocase subunit YajC	-34.83	3.10E-33
tolR	translocation protein TolR	-22.79	7.01E-21
secA	preprotein translocase subunit SecA	-21.45	2.79E-40
tolB	translocation protein TolB	-19.88	3.51E-24
tolQ	translocation protein TolQ	-19.86	2.82E-15
secG	preprotein translocase subunit SecG	-17.16	3.39E-23
pilM	type 4 fimbrial biogenesis protein PilM	-16.46	5.99E-19
tatA	twin-arginine translocation protein TatA	-16.13	1.30E-74
PA5568	inner membrane protein translocase subunit YidC	-15.24	1.71E-31
secE	preprotein translocase subunit SecE	-12.52	5.57E-24
pilF	type 4 fimbrial biogenesis protein PilF	-12.18	3.25E-17
secF	preprotein translocase subunit SecF	-12.03	2.60E-47
lepB	signal peptidase I	-9.03	2.51E-15
pilY1	type 4 fimbrial biogenesis protein PilY1	-8.62	3.44E-38
pilQ	type 4 fimbrial biogenesis outer membrane protein PilQ	-8.46	5.30E-15
pilU	twitching motility protein PilU	-8.01	9.52E-17
pilO	type 4 fimbrial biogenesis protein PilO	-7.92	1.18E-10
PA2973	peptidase	-6.50	1.87E-12
pilD	type 4 prepilin peptidase PilD	-6.03	5.74E-19
PA1478	heme exporter protein CcmD	-5.74	1.74E-04
PA4624	hypothetical protein	-4.89	2.73E-08
PA2983	translocation protein TolQ	-4.12	4.13E-09
pscU	translocation protein in type III secretion	-4.04	3.85E-10
flp	type IVb pilin Flp	-3.99	1.74E-03
fliE	flagellar hook-basal body complex protein FliE	-3.85	1.84E-09
cupB1	fimbrial subunit CupB1	-3.83	1.74E-04
cupC1	fimbrial subunit CupC1	-3.75	6.67E-06
PA5284	hypothetical protein	-3.69	2.06E-10
PA2633	hypothetical protein	-3.52	2.63E-14
secD	preprotein translocase subunit SecD	-3.43	9.65E-13
xcpT	type II secretion system protein G	-3.02	2.73E-08
PA5205	multiple drug resistance protein MarC	-2.99	5.63E-07

PA4541	hypothetical protein	-2.91	2.31E-16
fimT	type 4 fimbrial biogenesis protein FimT	-2.88	1.20E-05
PA1382	type II secretion system protein	-2.76	1.43E-04
PA2672	type II secretion system protein	-2.68	1.61E-05
PA0095	hypothetical protein	-2.38	1.19E-10
oprM	outer membrane protein OprM	-2.34	1.64E-13
PA1832	protease	-2.09	6.01E-06
PA3619	hypothetical protein	-2.07	6.24E-06
PA2676	type II secretion system protein	-2.04	1.84E-03
Lipid transport and metabolism			
acpP	acyl carrier protein	-120.66	2.51E-94
PA1830	hypothetical protein	-33.63	2.09E-34
fabA	3-hydroxydecanoyl-ACP dehydratase	-31.28	4.86E-23
gcdH	glutaryl-CoA dehydrogenase	-25.56	1.30E-96
foaB	3-ketoacyl-CoA thiolase	-21.65	2.67E-29
fabZ	3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ	-17.76	3.84E-24
PA1288	hypothetical protein	-17.64	2.88E-74
PA0461	acyltransferase	-16.92	2.52E-23
dhcA	dehydrocarnitine CoA transferase subunit A	-14.38	2.29E-40
gcpE	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin)	-13.79	9.19E-40
liuA	isovaleryl-CoA dehydrogenase	-13.34	1.71E-64
pssA	phosphatidylserine synthase	-11.26	4.39E-31
accA	acetyl-CoA carboxylase carboxyltransferase subunit alpha	-11.03	2.08E-23
PA5436	acetyl-CoA carboxylase subunit alpha	-10.80	3.70E-48
speA	3-ketoacyl-ACP reductase	-10.00	8.33E-20
accC	acetyl-CoA carboxylase biotin carboxylase subunit	-9.73	9.80E-29
fabI	NADH-dependent enoyl-ACP reductase	-8.78	1.61E-53
PA4767	hypothetical protein	-7.57	1.08E-33
PA0506	acyl-CoA dehydrogenase	-7.39	1.90E-29
accD	acetyl-CoA carboxylase carboxyltransferase subunit beta	-7.11	1.79E-14
dhcB	dehydrocarnitine CoA transferase subunit B	-7.08	8.89E-46
PA1748	enoyl-CoA hydratase	-6.71	3.39E-09
faoA	fatty acid oxidation complex subunit alpha	-6.49	2.50E-49
desA	delta-9 fatty acid desaturase DesA	-6.41	1.31E-39
pcs	phosphatidylcholine synthase	-5.30	1.59E-25
PA4435	acyl-CoA dehydrogenase	-4.77	1.11E-18
PA3302	hypothetical protein	-4.43	4.18E-20
PA1821	enoyl-CoA hydratase	-4.34	4.70E-14
PA5519	acyl-CoA thioesterase	-4.32	2.83E-17

PA0449	acyl-CoA thioesterase	-4.12	5.26E-35
rhlA	rhamnosyltransferase subunit A	-3.82	2.61E-06
PA4589	hypothetical protein	-3.73	8.66E-12
PA3741	acyl-CoA thioesterase	-3.69	4.11E-05
lptA	lysophosphatidic acid acyltransferase	-3.57	2.42E-14
tesB	acyl-CoA thioesterase II	-3.50	1.75E-10
PA0358	hypothetical protein	-3.36	7.87E-09
PA4015	hypothetical protein	-3.17	2.85E-06
pqsC	hypothetical protein	-3.11	4.34E-06
PA2550	acyl-CoA dehydrogenase	-3.02	3.62E-10
azoR3	FMN-dependent NADH-azoreductase	-2.84	4.52E-08
PA4636	hypothetical protein	-2.78	6.90E-07
PA5371	acyl-CoA thioesterase	-2.72	2.64E-10
alkB1	alkane-1 monooxygenase	-2.65	4.92E-03
PA3727	hypothetical protein	-2.60	9.46E-10
dxs	1-deoxy-D-xylulose-5-phosphate synthase	-2.59	2.74E-12
uppS	ditrans,polycis-undecaprenyl-diphosphate synthase	-2.57	2.95E-14
PA1737	3-hydroxyacyl-CoA dehydrogenase	-2.51	8.52E-08
PA3972	acyl-CoA dehydrogenase	-2.32	4.43E-05
PA1022	acyl-CoA dehydrogenase	-2.24	3.09E-06
plsX	phosphate acyltransferase	-2.21	1.45E-04
liuB	methylcrotonyl-CoA carboxylase subunit beta	-2.11	2.05E-04
pldA	phospholipase D	-2.08	2.46E-10
pgpA	phosphatidylglycerophosphatase A	-2.01	2.79E-05
Nucleotide transport and metabolism			
purC	phosphoribosylaminoimidazole-succinocarboxamide synthase	-39.92	7.27E-49
ndk	nucleoside diphosphate kinase	-39.33	5.01E-26
prs	ribose-phosphate pyrophosphokinase	-19.72	3.02E-25
purN	phosphoribosylglycinamide formyltransferase	-15.07	1.07E-19
carB	carbamoyl phosphate synthase large subunit	-14.69	1.76E-50
pyrG	CTP synthetase	-11.29	7.67E-21
purU1	formyltetrahydrofolate deformylase	-8.74	5.20E-50
nrdJa	ribonucleoside-diphosphate reductase	-6.90	2.96E-18
cmk	cytidylate kinase	-6.26	2.26E-14
purU2	formyltetrahydrofolate deformylase	-6.18	7.14E-14
PA1514	ureidoglycolate hydrolase	-6.17	5.54E-10
nrdB	ribonucleotide-diphosphate reductase subunit beta	-6.06	1.35E-25
thyA	thymidylate synthase	-5.91	2.02E-25
upp	uracil phosphoribosyltransferase	-5.81	5.45E-08
adk	adenylate kinase	-5.75	9.89E-16
gmk	guanylate kinase	-5.73	4.27E-21

uraA	uracil permease	-5.71	1.43E-24
purM	phosphoribosylformylglycinamidine cyclo-ligase	-5.63	2.66E-09
carA	carbamoyl phosphate synthase small subunit	-4.86	2.18E-11
pyrB	aspartate carbamoyltransferase	-4.43	9.57E-18
PA4645	hypoxanthine-guanine phosphoribosyltransferase	-4.40	2.28E-09
purA	adenylosuccinate synthetase	-4.13	1.04E-25
nrdA	ribonucleotide-diphosphate reductase subunit alpha	-3.93	4.38E-11
purB	adenylosuccinate lyase	-3.65	1.35E-06
PA5081	hypothetical protein	-3.37	2.97E-10
PA3480	deoxycytidine triphosphate deaminase	-3.25	2.27E-06
PA3767	hypothetical protein	-3.22	1.28E-05
PA0990	hypothetical protein	-3.12	1.08E-05
guaA	GMP synthase	-3.06	3.00E-09
purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	-2.85	8.00E-10
pyrH	uridylate kinase	-2.55	2.62E-13
cyaA	adenylate cyclase	-2.47	1.65E-12
purF	amidophosphoribosyltransferase	-2.47	5.09E-07
PA0148	adenosine deaminase	-2.38	7.18E-09
PA3043	deoxyguanosinetriphosphate triphosphohydrolase	-2.14	7.84E-06
PA0656	HIT family protein	-2.04	7.97E-04
apt	adenine phosphoribosyltransferase	-2.02	1.72E-05
Posttranslational modification, protein turnover, chaperones			
groEL	molecular chaperone GroEL	-438.43	3.76E-180
ahpC	alkyl hydroperoxide reductase	-163.61	5.55E-89
lon	Lon protease	-156.49	1.05E-202
groES	co-chaperonin GroES	-116.82	2.18E-203
PA3529	peroxidase	-70.98	8.10E-39
ppiB	peptidyl-prolyl cis-trans isomerase B	-64.71	8.96E-41
hflC	protease subunit HflC	-53.28	2.44E-52
clpX	ATP-dependent protease ATP-binding subunit ClpX	-51.17	1.95E-37
tig	trigger factor	-50.62	5.13E-42
PA2827	methionine sulfoxide reductase B	-48.26	5.36E-59
dnaK	molecular chaperone DnaK	-42.84	6.22E-39
dsbA	thiol:disulfide interchange protein DsbA	-41.35	7.00E-65
hflK	protease subunit HflK	-37.36	6.53E-89
trxA	thioredoxin	-35.11	2.38E-47
clpP	ATP-dependent Clp protease proteolytic subunit	-33.35	1.60E-48
PA3262	FkbP-type peptidyl-prolyl cis-trans isomerase	-32.03	1.99E-33
PA0838	glutathione peroxidase	-31.32	2.71E-90
ccoQ1	cytochrome C oxidase cbb3-type subunit CcoQ	-27.80	1.26E-28

clpA	ATP-binding protease component ClpA	-23.03	4.41E-47
ccoQ2	cytochrome C oxidase cbb3-type subunit CcoQ	-21.23	1.82E-21
ftsH	cell division protein FtsH	-20.51	3.32E-140
PA1095	B-type flagellar protein FliS	-19.58	1.62E-23
mucD	serine protease MucD	-17.26	9.14E-25
ppiD	peptidyl-prolyl cis-trans isomerase D	-17.11	4.74E-25
bcp	bacterioferritin comigratory protein	-15.73	1.91E-27
PA4558	FkbP-type peptidyl-prolyl cis-trans isomerase	-15.04	9.03E-18
slyD	peptidyl-prolyl cis-trans isomerase SlyD	-14.60	1.14E-16
ccoN2	cbb3-type cytochrome C oxidase subunit I	-13.82	2.22E-22
sspA	stringent starvation protein A	-13.77	5.80E-19
clpB	chaperone protein ClpB	-13.28	1.15E-36
PA2826	glutathione peroxidase	-10.62	1.73E-13
ppiA	peptidyl-prolyl cis-trans isomerase A	-9.60	5.22E-13
grx	glutaredoxin	-9.21	5.51E-24
trxB1	thioredoxin reductase	-9.21	2.64E-26
PA3533	hypothetical protein	-8.42	2.89E-54
dsbC	thiol:disulfide interchange protein DsbC	-8.14	1.09E-10
grpE	heat shock protein GrpE	-7.91	4.81E-20
PA0941	hypothetical protein	-7.78	1.55E-08
smpB	SsrA-binding protein	-7.72	1.53E-20
pcm	protein-L-isoaspartate O-methyltransferase	-7.46	1.12E-28
surA	chaperone SurA	-7.32	4.48E-52
PA3326	ATP-dependent Clp protease proteolytic subunit	-6.97	7.11E-11
hscB	co-chaperone HscB	-6.96	2.63E-25
lpxO2	lipopolysaccharide biosynthetic protein LpxO	-6.81	3.77E-10
htpG	chaperone protein HtpG	-6.74	4.93E-18
ccoN1	cbb3-type cytochrome C oxidase subunit I	-6.70	3.81E-12
dsbH	disulfide bond formation protein	-6.46	5.01E-13
PA0779	ATP-dependent protease	-6.40	1.11E-25
PA3350	flagellar basal body P-ring biosynthesis protein FlgA	-6.10	5.17E-13
PA5254	FkbP-type peptidyl-prolyl cis-trans isomerase	-5.92	1.96E-09
PA2618	arginyl-tRNA--protein transferase	-5.78	8.00E-10
PA4576	ATP-dependent protease	-5.77	5.68E-55
PA1006	hypothetical protein	-5.70	2.18E-08
PA0462	hypothetical protein	-5.67	4.52E-17
PA0975	radical activating enzyme	-5.41	1.26E-06
PA2821	glutathione S-transferase	-5.32	9.50E-24
PA2610	hypothetical protein	-4.96	4.78E-10
PA5005	carbamoyl transferase	-4.91	3.91E-22
PA1623	hypothetical protein	-4.68	1.01E-29

PA3450	antioxidant protein	-4.60	4.87E-08
PA1768	hypothetical protein	-4.47	1.18E-05
PA1564	sulfurtransferase TusA	-4.46	1.97E-05
lpxO1	lipopolysaccharide biosynthetic protein LpxO	-4.32	1.02E-08
tpx	2-Cys peroxiredoxin	-4.02	2.50E-16
PA5148	hypothetical protein	-3.74	4.26E-21
PA3338	hypothetical protein	-3.72	2.13E-08
fppA	Flp prepilin peptidase FppA	-3.69	5.14E-07
aat	leucyl/phenylalanyl-tRNA--protein transferase	-3.64	1.59E-14
ccmC	heme exporter protein CcmC	-3.47	4.46E-16
PA0653	hypothetical protein	-3.44	3.98E-04
PA2813	glutathione S-transferase	-3.36	1.12E-14
PA0107	cytochrome C oxidase assembly protein	-3.24	8.49E-08
hslU	ATP-dependent protease ATP-binding subunit HslU	-3.19	7.22E-15
hscA	chaperone protein HscA	-3.14	9.08E-16
PA1191	hypothetical protein	-3.14	6.15E-08
glnD	bifunctional uridylyltransferase/uridylyl-removing protein	-3.14	1.41E-10
PA5196	hypothetical protein	-3.07	3.33E-13
PA0848	alkyl hydroperoxide reductase	-2.99	8.11E-09
ppiC2	peptidyl-prolyl cis-trans isomerase C2	-2.88	9.77E-07
PA1033	glutathione S-transferase	-2.79	7.24E-10
PA1655	glutathione S-transferase	-2.74	6.81E-08
ohr	organic hydroperoxide resistance protein	-2.71	1.82E-07
PA1287	glutathione peroxidase	-2.67	8.20E-08
PA1203	hypothetical protein	-2.42	1.27E-07
PA0457	hypothetical protein	-2.32	1.18E-07
PA4133	cbb3-type cytochrome C oxidase subunit I	-2.32	2.02E-06
ccmH	cytochrome c-type biogenesis protein CcmH	-2.28	5.78E-05
cysT	sulfate transporter CysT	-2.28	3.41E-04
ibpA	heat-shock protein IbpA	-2.26	1.48E-06
hslV	ATP-dependent protease peptidase subunit	-2.23	1.87E-04
ppiC1	peptidyl-prolyl cis-trans isomerase C1	-2.10	2.00E-04
fklB	peptidyl-prolyl cis-trans isomerase FklB	-2.05	1.21E-05
flgJ	peptidoglycan hydrolase FlgJ	-2.02	2.10E-06
Replication, recombination and repair			
hupB	DNA-binding protein HU	-639.88	7.77E-118
himA	integration host factor subunit alpha	-166.99	2.33E-150
recF	DNA replication and repair protein RecF	-55.84	2.39E-65
PA5348	DNA-binding protein	-46.32	4.82E-68
himD	integration host factor subunit beta	-34.29	2.41E-24
dnaN	DNA polymerase III subunit beta	-25.82	1.28E-25

ygdP	RNA pyrophosphohydrolase	-20.84	3.02E-29
topA	DNA topoisomerase I	-19.19	1.07E-19
gyrB	DNA gyrase subunit B	-18.23	1.08E-137
crc	catabolite repression control protein	-17.38	8.21E-21
PA4424	hypothetical protein	-17.18	1.13E-18
PA3940	DNA binding protein	-15.72	6.14E-38
ung	uracil-DNA glycosylase	-14.42	2.49E-19
recA	recombinase A	-11.07	2.33E-92
parE	DNA topoisomerase IV subunit B	-10.18	1.01E-34
dnaB	replicative DNA helicase	-9.55	7.76E-20
rnhB	ribonuclease HII	-9.26	1.30E-39
ruvA	Holliday junction ATP-dependent DNA helicase RuvA	-9.12	7.21E-13
gyrA	DNA gyrase subunit A	-8.91	1.19E-40
dnaE	DNA polymerase III subunit alpha	-7.66	3.99E-30
tag	DNA-3-methyladenine glycosidase I	-7.54	5.81E-08
ogt	methylated-DNA--protein-cysteine methyltransferase	-6.41	3.41E-10
ruvC	crossover junction endodeoxyribonuclease RuvC	-6.24	1.61E-10
nth	endonuclease III	-6.02	1.41E-16
sbcB	exonuclease I	-6.01	3.85E-15
rep	ATP-dependent DNA helicase Rep	-5.83	2.23E-08
uvrB	excinuclease ABC subunit B	-4.80	1.96E-16
PA0947	DNA replication initiation factor	-4.51	1.52E-13
ruvB	Holliday junction ATP-dependent DNA helicase RuvB	-4.40	6.08E-16
PA0257	hypothetical protein	-4.24	7.47E-06
xthA	exonuclease III	-3.96	1.46E-12
PA2613	recombination factor protein RarA	-3.88	2.34E-16
rnhA	ribonuclease HI	-3.85	2.67E-12
rnt	ribonuclease T	-3.84	4.65E-12
PA2221	hypothetical protein	-3.78	4.82E-05
PA0987	hypothetical protein	-3.78	1.05E-05
polA	DNA polymerase I	-3.45	1.74E-15
PA3140	hypothetical protein	-3.39	2.78E-04
PA0979	hypothetical protein	-3.38	5.89E-05
PA4998	hypothetical protein	-3.07	9.56E-10
PA1938	hypothetical protein	-2.85	8.84E-05
PA0978	hypothetical protein	-2.85	1.29E-04
dnaA	chromosome replication initiator DnaA	-2.74	4.54E-18
PA0728	bacteriophage integrase	-2.72	3.16E-03
PA1368	hypothetical protein	-2.66	2.39E-03
PA1937	hypothetical protein	-2.44	2.14E-03
PA3263	recombination associated protein RdgC	-2.33	1.70E-06

recN	DNA repair protein RecN	-2.27	3.53E-09
uvrC	excinuclease ABC subunit C	-2.19	5.15E-07
uvrD	DNA-dependent helicase II	-2.14	1.24E-07
dnaG	DNA primase	-2.08	3.75E-09
parC	DNA topoisomerase IV subunit A	-2.06	6.29E-06
Secondary metabolites biosynthesis, transport and catabolism			
PA1202	hydrolase	-66.48	1.75E-152
PA4454	hypothetical protein	-19.11	2.50E-24
fabB	3-oxoacyl-ACP synthase	-9.52	5.23E-33
PA0957	hypothetical protein	-8.45	3.35E-13
antB	anthranilate dioxygenase small subunit	-5.55	2.66E-10
pcaG	protocatechuate 3,4-dioxygenase subunit alpha	-5.31	5.65E-24
PA5245	glutamine amidotransferase	-5.08	7.28E-19
PA5150	short-chain dehydrogenase	-5.02	8.44E-22
fadD1	long-chain-fatty-acid--CoA ligase	-4.96	2.99E-25
fadD2	long-chain-fatty-acid--CoA ligase	-4.03	1.36E-06
PA3924	long-chain-fatty-acid--CoA ligase	-3.52	9.55E-15
PA5174	beta-ketoacyl synthase	-3.41	9.04E-12
catC	muconolactone delta-isomerase	-3.40	3.75E-07
PA4456	ABC transporter ATP-binding protein	-3.34	1.76E-13
hmgA	homogentisate 1,2-dioxygenase	-3.29	2.10E-28
PA1537	Baeyer-Villiger monooxygenase	-3.15	3.03E-17
PA1835	hypothetical protein	-3.07	1.58E-09
fabF1	3-oxoacyl-ACP synthase	-3.04	2.35E-13
PA3213	hypothetical protein	-3.02	2.61E-08
PA4453	hypothetical protein	-3.02	1.97E-08
PA1828	short-chain dehydrogenase	-2.97	1.62E-13
PA1088	hypothetical protein	-2.80	2.38E-15
PA3334	acyl carrier protein	-2.72	2.59E-04
lasI	acyl-homoserine-lactone synthase	-2.60	3.25E-03
PA5507	hypothetical protein	-2.47	1.22E-05
PA0318	hypothetical protein	-2.47	6.35E-13
PA5026	hypothetical protein	-2.42	2.06E-06
PA2419	hydrolase	-2.22	4.18E-04
Signal transduction mechanisms			
PA3919	hypothetical protein	-89.60	2.82E-80
cheY	chemotaxis protein CheY	-45.35	6.63E-66
PA0588	hypothetical protein	-39.44	8.28E-33
PA3309	hypothetical protein	-38.66	9.11E-90
ptsN	nitrogen regulatory IIA protein	-37.31	4.79E-86
pilG	pilus biosynthesis/twitching motility protein PilG	-33.89	1.62E-30

rsmA	carbon storage regulator	-31.74	2.82E-36
PA3205	hypothetical protein	-28.71	5.99E-27
PA2137	hypothetical protein	-23.32	1.83E-21
PA5153	amino acid ABC transporter substrate-binding protein	-23.19	1.99E-47
PA1789	hypothetical protein	-21.36	5.53E-29
pprB	two-component response regulator PprB	-17.92	8.71E-57
PA0431	hypothetical protein	-16.48	2.17E-56
bfmR	protein BfmR	-14.04	3.08E-101
PA3349	chemotaxis protein	-12.75	2.83E-25
mucA	sigma factor AlgU negative regulator MucA	-12.02	3.97E-38
lexA	LexA repressor	-10.66	1.02E-20
spoT	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	-10.47	8.30E-40
PA0601	two-component response regulator	-10.44	6.27E-17
aotJ	arginine/ornithine ABC transporter substrate-binding protein AotJ	-10.37	1.25E-28
hom	homoserine dehydrogenase	-10.20	1.46E-19
PA2798	two-component response regulator	-10.11	8.18E-14
PA5138	hypothetical protein	-9.55	8.97E-15
relA	GTP pyrophosphokinase	-9.40	7.93E-40
pilJ	twitching motility protein PilJ	-9.06	5.32E-80
PA2797	hypothetical protein	-8.52	1.63E-13
algR	alginate biosynthesis regulatory protein AlgR	-7.68	1.10E-20
dksA	suppressor protein DksA	-7.61	6.66E-15
gacA	response regulator GacA	-7.25	1.85E-08
PA4381	two-component response regulator	-6.85	2.65E-14
PA0250	hypothetical protein	-6.77	3.40E-21
anr	transcriptional regulator Anr	-6.35	1.19E-15
PA3017	hypothetical protein	-6.06	1.10E-32
PA4032	two-component response regulator	-5.98	8.49E-09
PA0314	L-cysteine ABC transporter protein FliY	-5.70	1.31E-23
ntrB	two-component sensor NtrB	-5.48	2.83E-15
PA3981	hypothetical protein	-5.42	7.37E-45
PA3825	hypothetical protein	-5.23	3.20E-10
vfr	cAMP-regulatory protein	-5.05	2.67E-07
ptsP	phosphoenolpyruvate-protein phosphotransferase PtsP	-5.02	3.64E-37
PA2572	two-component response regulator	-4.64	2.70E-08
PA0861	hypothetical protein	-4.61	2.15E-24
PA5139	hypothetical protein	-4.59	1.23E-09
rocS1	two-component sensor	-4.58	4.97E-12
PA5082	ABC transporter	-4.48	1.79E-12

PA4915	chemotaxis transducer	-4.47	4.69E-19
rocR	DNA-binding response regulator RocR	-4.38	1.24E-07
PA2583	sensor/response regulator hybrid protein	-4.37	3.80E-08
rhlI	acyl-homoserine-lactone synthase	-4.34	1.10E-12
PA5270	hypothetical protein	-4.32	7.24E-14
inaA	hypothetical protein	-4.10	6.39E-13
cbpA	cAMP-binding protein A	-4.07	3.87E-06
PA4352	hypothetical protein	-4.02	1.11E-10
PA0179	two-component response regulator	-3.97	7.94E-09
PA5346	hypothetical protein	-3.91	8.93E-30
pheC	cyclohexadienyl dehydratase	-3.89	5.44E-19
typA	regulatory protein TypA	-3.86	1.64E-11
narL	transcriptional regulator NarL	-3.83	8.92E-22
wspA	chemotaxis transducer	-3.81	1.19E-22
PA2822	hypothetical protein	-3.70	2.85E-06
parR	two-component response regulator ParR	-3.70	9.55E-05
fleQ	transcriptional regulator FleQ	-3.69	1.47E-18
amiR	aliphatic amidase regulator	-3.61	1.73E-11
PA5076	ABC transporter	-3.48	2.81E-08
PA1342	ABC transporter	-3.44	9.74E-15
PA2567	hypothetical protein	-3.33	2.91E-14
PA3865	amino acid binding protein	-3.33	1.66E-16
PA4606	hypothetical protein	-3.32	1.80E-21
algZ	alginate biosynthesis protein AlgZ/FimS	-3.23	5.42E-17
PA3345	hypothetical protein	-3.20	5.39E-06
PA5536	hypothetical protein	-3.19	1.32E-07
PA5017	hypothetical protein	-3.17	1.12E-21
dnr	transcriptional regulator Dnr	-3.11	2.53E-11
PA2204	ABC transporter	-3.06	4.77E-08
PA0033	hypothetical protein	-3.01	2.29E-08
PA0575	hypothetical protein	-2.82	5.88E-20
phoQ	two-component sensor PhoQ	-2.80	6.37E-09
PA2571	two-component sensor	-2.72	6.67E-04
PA1753	hypothetical protein	-2.50	1.15E-06
pilS	two-component sensor PilS	-2.33	9.18E-10
ptpA	phosphotyrosine protein phosphatase	-2.31	2.74E-05
PA0758	hypothetical protein	-2.29	8.47E-04
PA4870	hypothetical protein	-2.26	1.33E-05
fleS	two-component sensor	-2.24	6.37E-04
apaH	bis(5'-nucleosyl)-tetraphosphatase	-2.23	4.70E-10
PA3714	two-component response regulator	-2.20	3.61E-04

PA0356	hypothetical protein	-2.17	2.23E-05
PA4195	ABC transporter	-2.16	4.95E-04
PA5027	hypothetical protein	-2.02	4.04E-07
Transcription			
rpoA	DNA-directed RNA polymerase subunit alpha	-407.18	3.61E-92
rpoC	DNA-directed RNA polymerase subunit beta'	-159.76	8.01E-128
capB	major cold shock protein CspA	-151.50	4.20E-51
rpoB	DNA-directed RNA polymerase subunit beta	-113.68	9.32E-72
sigX	RNA polymerase sigma factor SigX	-96.94	1.94E-65
PA0456	cold-shock protein	-80.42	1.43E-42
liuR	liu genes regulator	-79.64	5.62E-83
phoP	two-component response regulator PhoP	-48.38	3.65E-51
nusA	transcription elongation factor NusA	-44.20	1.43E-42
greA	transcription elongation factor GreA	-42.43	7.56E-83
PA5301	transcriptional regulator	-40.70	7.48E-58
algQ	anti-RNA polymerase sigma 70 factor	-34.24	5.05E-29
algU	RNA polymerase sigma factor AlgU	-33.67	4.25E-127
nusG	transcription antitermination protein NusG	-31.65	3.40E-29
rpoN	RNA polymerase factor sigma-54	-29.36	7.36E-44
cspD	cold-shock protein CspD	-27.82	1.12E-51
PA2737	hypothetical protein	-25.74	3.34E-23
rpoS	RNA polymerase sigma factor RpoS	-21.72	7.10E-31
cysB	transcriptional regulator CysB	-18.32	5.13E-25
rho	transcription termination factor Rho	-17.45	8.04E-20
flgM	protein FlgM	-17.30	9.29E-60
lasR	transcriptional regulator LasR	-16.11	8.60E-29
rpoZ	DNA-directed RNA polymerase subunit omega	-15.84	4.69E-36
rpoD	RNA polymerase sigma factor RpoD	-14.57	7.42E-67
psrA	transcriptional regulator PsrA	-13.63	6.33E-34
iscR	HTH-type transcriptional regulator	-10.77	1.75E-22
fliA	flagellar biosynthesis sigma factor FliA	-9.90	4.94E-35
ospR	transcriptional regulator	-9.67	7.04E-22
PA1526	transcriptional regulator	-9.29	3.81E-14
pilH	twitching motility protein PilH	-9.23	2.06E-49
PA0942	transcriptional regulator	-8.28	7.52E-16
mexR	multidrug resistance operon repressor MexR	-8.05	1.10E-13
rpoH	RNA polymerase sigma factor RpoH	-7.69	8.31E-37
prtR	HTH-type transcriptional regulator PrtR	-7.41	1.88E-17
PA2577	transcriptional regulator	-7.35	1.52E-15
rocA1	two-component response regulator RocA1	-7.27	1.06E-10
PA3895	transcriptional regulator	-7.23	3.70E-22

PA3034	transcriptional regulator	-6.99	1.96E-14
PA0225	transcriptional regulator	-6.51	2.99E-12
bexR	bistable expression regulator BexR	-6.30	4.67E-35
PA1607	hypothetical protein	-5.67	4.75E-25
PA0939	hypothetical protein	-5.42	2.20E-03
PA2957	transcriptional regulator	-5.24	1.04E-06
PA4279	pantothenate kinase	-5.14	2.95E-06
PA5324	transcriptional regulator	-5.12	2.23E-31
atuR	atu genes repressor	-5.02	4.36E-19
PA2020	transcriptional regulator	-4.54	4.84E-12
rnr	exoribonuclease R	-4.51	1.99E-33
PA0218	transcriptional regulator	-4.50	1.99E-23
PA1759	transcriptional regulator	-4.49	1.49E-34
nalD	transcriptional regulator	-4.47	7.35E-19
PA0116	hypothetical protein	-4.45	8.60E-16
rhlR	transcriptional regulator RhlR	-4.40	1.03E-08
PA0217	transcriptional regulator	-4.32	2.57E-23
birA	biotin--protein ligase	-4.30	5.40E-07
lrp	leucine-responsive regulatory protein	-4.17	3.20E-08
PA3965	transcriptional regulator	-4.15	8.91E-08
PA0125	hypothetical protein	-4.03	3.29E-05
PA5438	transcriptional regulator	-3.98	2.75E-23
PA5475	hypothetical protein	-3.98	1.29E-11
roxR	DNA-binding response regulator RoxR	-3.95	2.82E-09
PA4354	hypothetical protein	-3.67	2.50E-05
PA4499	transcriptional regulator	-3.64	4.22E-07
PA0528	transcriptional regulator	-3.59	4.85E-18
spoOJ	chromosome partitioning protein	-3.54	8.57E-15
oxyR	transcriptional regulator	-3.45	4.20E-16
PA4451	hypothetical protein	-3.41	2.03E-05
nalC	transcriptional regulator	-3.32	1.58E-10
PA2551	transcriptional regulator	-3.28	4.59E-14
gfnR	glutathione-dependent formaldehyde neutralization regulator GfnR	-3.08	4.02E-12
PA5403	transcriptional regulator	-2.99	1.90E-03
PA4080	response regulator	-2.95	3.46E-04
nusB	transcription antitermination protein NusB	-2.85	5.33E-12
rhl	ATP-dependent RNA helicase RhlB	-2.85	4.99E-12
PA0436	transcriptional regulator	-2.84	2.13E-11
PA3458	transcriptional regulator	-2.84	1.40E-08
PA4769	transcriptional regulator	-2.62	8.68E-12
PA1283	transcriptional regulator	-2.62	4.69E-07

PA4784	transcriptional regulator	-2.58	1.96E-03
PA3711	transcriptional regulator	-2.53	1.22E-09
PA0034	two-component response regulator	-2.48	6.53E-06
pvdS	extracytoplasmic-function sigma-70 factor	-2.46	3.68E-03
PA4878	transcriptional regulator	-2.30	1.37E-05
PA3285	ECF subfamily sigma-70 factor	-2.26	5.86E-07
hutC	histidine utilization repressor HutC	-2.26	6.87E-09
PA0428	ATP-dependent RNA helicase	-2.25	6.90E-05
PA3133	transcriptional regulator	-2.21	4.50E-05
PA2758	transcriptional regulator	-2.21	3.44E-04
exsA	exoenzyme S transcriptional regulator ExsA	-2.16	9.79E-03
PA4659	transcriptional regulator	-2.11	1.62E-08
PA5437	transcriptional regulator	-2.07	1.94E-08
PA4436	transcriptional regulator	-2.06	7.29E-07
mvfR	transcriptional regulator MvfR	-2.04	5.09E-06
Translation, ribosomal structure and biogenesis			
rplX	50S ribosomal protein L24	-1261.65	5.41E-187
rpmJ	50S ribosomal protein L36	-1133.64	9.42E-184
rplJ	50S ribosomal protein L10	-1102.73	1.69E-138
rpmI	50S ribosomal protein L35	-1072.76	0.00E+00
PA4463	hypothetical protein	-1018.58	1.47E-142
rplW	50S ribosomal protein L23	-941.66	8.20E-169
rplN	50S ribosomal protein L14	-901.44	2.32E-103
rplL	50S ribosomal protein L7/L12	-886.00	4.70E-131
rplK	50S ribosomal protein L11	-862.84	7.06E-225
rplE	50S ribosomal protein L5	-831.10	1.18E-90
rpsD	30S ribosomal protein S4	-807.43	2.46E-91
infC	translation initiation factor IF-3	-747.63	4.01E-182
rpsS	30S ribosomal protein S19	-678.36	2.51E-130
rpsN	30S ribosomal protein S14	-574.56	2.21E-105
rpmD	50S ribosomal protein L30	-509.49	3.16E-99
rpsM	30S ribosomal protein S13	-435.43	9.87E-131
rplV	50S ribosomal protein L22	-423.66	5.76E-111
rpsE	30S ribosomal protein S5	-422.98	5.92E-78
rplT	50S ribosomal protein L20	-422.84	4.06E-263
rpsQ	30S ribosomal protein S17	-419.05	1.14E-130
rpsC	30S ribosomal protein S3	-414.82	6.79E-82
rpmC	50S ribosomal protein L29	-413.38	3.67E-103
rpsO	30S ribosomal protein S15	-412.00	5.71E-106
rpsK	30S ribosomal protein S11	-351.41	4.19E-131
rplP	50S ribosomal protein L16	-346.84	6.79E-82

rplO	50S ribosomal protein L15	-341.16	1.18E-73
fusA1	elongation factor G	-313.39	4.85E-91
rplR	50S ribosomal protein L18	-296.05	1.81E-124
rplQ	50S ribosomal protein L17	-278.38	5.25E-95
rplC	50S ribosomal protein L3	-258.49	1.21E-64
rpsL	30S ribosomal protein S12	-248.50	2.84E-57
rpsH	30S ribosomal protein S8	-247.14	8.39E-89
rplU	50S ribosomal protein L21	-241.89	1.07E-107
tufA	elongation factor Tu	-230.11	8.29E-105
rplA	50S ribosomal protein L1	-212.25	3.47E-64
rplB	50S ribosomal protein L2	-209.82	3.47E-61
rplF	50S ribosomal protein L6	-201.02	3.38E-86
tufB	elongation factor Tu	-188.31	1.44E-111
rpsG	30S ribosomal protein S7	-187.23	1.73E-86
rplD	50S ribosomal protein L4	-186.49	5.99E-60
rplS	50S ribosomal protein L19	-171.19	7.45E-95
rpsA	30S ribosomal protein S1	-169.33	3.81E-79
rpsB	30S ribosomal protein S2	-157.89	2.28E-54
PA4671	50S ribosomal protein L25/general stress protein Ctc	-145.76	8.71E-89
rpsR	30S ribosomal protein S18	-132.20	6.04E-53
rplM	50S ribosomal protein L13	-128.33	1.12E-52
rpsJ	30S ribosomal protein S10	-113.82	1.97E-43
rpmB	50S ribosomal protein L28	-111.78	2.81E-85
rpmH	50S ribosomal protein L34	-106.63	8.98E-60
rpmA	50S ribosomal protein L27	-100.10	3.38E-81
rpsF	30S ribosomal protein S6	-84.97	2.84E-159
pnp	polynucleotide phosphorylase	-71.94	1.22E-57
tsf	elongation factor Ts	-70.24	2.51E-68
rpmF	50S ribosomal protein L32	-66.76	1.94E-39
efp	elongation factor P	-53.36	1.64E-82
trmD	tRNA (guanine-N(1)-)-methyltransferase	-50.26	8.08E-38
rnpA	ribonuclease P	-49.54	3.22E-38
rimM	ribosome maturation factor RimM	-48.53	1.90E-48
rplI	50S ribosomal protein L9	-44.48	3.79E-152
rpsI	30S ribosomal protein S9	-43.86	1.38E-44
frr	ribosome recycling factor	-33.44	7.46E-36
rpmG	50S ribosomal protein L33	-29.35	4.94E-34
aspS	aspartate--tRNA ligase	-28.42	2.09E-23
rpsT	30S ribosomal protein S20	-27.82	1.12E-37
rpsU	30S ribosomal protein S21	-23.93	1.64E-44
ileS	isoleucine--tRNA ligase	-19.12	7.55E-44

gatC	aspartyl/glutamyl-tRNA amidotransferase subunit C	-18.58	6.10E-36
hisS	histidine--tRNA ligase	-16.72	1.30E-94
PA4852	hypothetical protein	-16.45	5.00E-30
infB	translation initiation factor IF-2	-16.15	8.69E-151
thrS	threonine--tRNA ligase	-14.11	1.31E-23
PA4753	hypothetical protein	-14.06	4.08E-41
PA4673	GTP-dependent nucleic acid-binding protein EngD	-13.45	5.31E-19
infA	translation initiation factor IF-1	-13.15	1.29E-17
def	peptide deformylase	-12.70	1.06E-30
glnS	glutamine--tRNA ligase	-12.06	6.02E-19
PA3614	hypothetical protein	-10.81	4.56E-38
PA4672	peptidyl-tRNA hydrolase	-10.50	1.76E-26
PA5339	hypothetical protein	-9.99	7.19E-60
tyrZ	tyrosine--tRNA ligase	-9.99	4.60E-12
rmf	ribosome modulation factor	-9.53	1.42E-16
omlA	outer membrane lipoprotein OmlA	-9.46	1.23E-12
gatB	aspartyl/glutamyl-tRNA amidotransferase subunit B	-8.58	5.13E-34
tgt	queuine tRNA-ribosyltransferase	-8.27	1.06E-18
rbfA	ribosome-binding factor A	-8.07	3.97E-39
PA5303	hypothetical protein	-7.74	1.92E-40
gltX	glutamate--tRNA ligase	-7.61	8.00E-39
lysS	lysine--tRNA ligase	-7.41	3.11E-21
prfC	peptide chain release factor 3	-7.22	3.03E-14
truB	tRNA pseudouridine synthase B	-7.09	4.64E-29
glyQ	glycine--tRNA ligase subunit alpha	-6.51	9.29E-09
proS	proline--tRNA ligase	-6.08	3.20E-20
valS	valine--tRNA ligase	-6.05	3.47E-29
serS	serine--tRNA ligase	-5.87	2.95E-17
rpsP	30S ribosomal protein S16	-5.64	1.00E-46
truA	tRNA pseudouridine synthase A	-5.34	1.11E-19
cafA	cytoplasmic axial filament protein	-5.34	9.22E-11
PA1766	hypothetical protein	-5.30	7.73E-15
PA0916	ribosomal protein S12 methylthiotransferase RimO	-4.95	1.01E-06
argS	arginine--tRNA ligase	-4.80	2.28E-18
map	methionine aminopeptidase	-4.60	1.75E-24
ftsJ	cell division protein FtsJ	-4.38	7.64E-18
pheS	phenylalanine--tRNA ligase subunit alpha	-3.95	4.51E-12
rpmE	50S ribosomal protein L31	-3.86	1.78E-14
PA1678	50S ribosomal protein L3 glutamine methyltransferase	-3.69	3.22E-09
PA3601	50S ribosomal protein L31 type B	-3.26	3.60E-06
osmE	OsmE family transcriptional regulator	-3.23	1.31E-17

PA3980	(dimethylallyl)adenosine tRNA methylthiotransferase	-3.16	2.04E-17
leuS	leucine--tRNA ligase	-3.11	2.59E-09
rluD	pseudouridine synthase	-3.01	8.66E-11
PA3945	hypothetical protein	-2.99	3.66E-10
ksgA	ribosomal RNA small subunit methyltransferase A	-2.97	1.79E-14
metG	methionine--tRNA ligase	-2.85	2.50E-07
trmU	tRNA-specific 2-thiouridylase MnmA	-2.69	8.74E-11
PA5127	rRNA methylase	-2.62	7.73E-08
PA1944	hypothetical protein	-2.61	1.03E-03
trmA	tRNA (uracil-5-)-methyltransferase	-2.46	9.02E-13
rph	ribonuclease PH	-2.43	1.64E-12
PA1472	hypothetical protein	-2.42	7.69E-05
rne	ribonuclease E	-2.28	3.22E-05
PA2795	tRNA-dihydrouridine synthase A	-2.26	2.91E-08
PA3199	hypothetical protein	-2.26	1.15E-08
alaS	alanine--tRNA ligase	-2.14	6.63E-05

Table S4. List of genes upregulated in PASL by at least 2-fold with a false discovery rate (Padj-value) <0.01 during exposure to hexadecane-water interface for 24 h versus the control.

Gene	**Description**	**Fold Change**	**Padj-value**
Cell cycle control, cell division, chromosome partitioning			
ftsL	cell division protein FtsL	2.36	1.62E-31
Energy production and conversion			
atpI	ATP synthase subunit I	2.22	1.08E-14
PA4430	cytochrome b	2.05	3.17E-48
Hypothetical, unclassified, unknown			
PA2621	ATP-dependent Clp protease adapter protein Clp	2.64	7.91E-21
PA4690.1	5S ribosomal RNA	2.24	2.05E-09
PA4280.1	5S ribosomal RNA	2.15	1.74E-08
PA4421	cell division protein MraZ	2.04	2.81E-24
General function prediction only			
PA2971	hypothetical protein	2.01	1.24E-26
Intracellular trafficking, secretion, and vesicular transport			
tolR	translocation protein TolR	2.00	1.48E-13
Posttranslational modification, protein turnover, chaperones			
clpP	ATP-dependent Clp protease proteolytic subunit	2.19	8.98E-50
PA0941	hypothetical protein	2.10	9.18E-14
Signal transduction mechanisms			
mucA	sigma factor AlgU negative regulator MucA	2.33	1.89E-72
Transcription			

algU	RNA polymerase sigma factor AlgU	2.85	4.39E-80
PA2737	hypothetical protein	2.18	4.42E-33
nusG	transcription antitermination protein NusG	2.05	1.29E-20
Translation, ribosomal structure and biogenesis			
rpsL	30S ribosomal protein S12	2.09	1.27E-16
rpmF	50S ribosomal protein L32	2.04	8.27E-11
rplD	50S ribosomal protein L4	2.01	6.32E-33

Reference:

[1] M.J. Franklin, D.E. Nivens, J.T. Weadge, P.L. Howell, Biosynthesis of the Pseudomonas aeruginosa extracellular polysaccharides, alginate, Pel, and Psl, Frontiers in microbiology 2 (2011) 167.