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Systems biology defines the biological significance of redox-active proteins during cellulose degradation in an aerobic bacterium

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1 **Summary**

2 Microbial depolymerization of plant cell walls contributes to global carbon balance and is
3 a critical component of renewable energy. The genomes of lignocellulose degrading
4 microorganisms encode diverse classes of carbohydrate modifying enzymes, although
5 currently there is a paucity of knowledge on the role of these proteins *in vivo*. We report
6 the comprehensive analysis of the cellulose degradation system in the saprophytic
7 bacterium *Cellvibrio japonicus*. Gene expression profiling of *C. japonicus* demonstrated
8 that three of the twelve predicted β -1,4 endoglucanases (*cel5A*, *cel5B*, and *cel45A*) and
9 the sole predicted cellobiohydrolase (*cel6A*) showed elevated expression during growth
10 on cellulose. Targeted gene disruptions of all thirteen predicted cellulase genes showed
11 that only *cel5B* and *cel6A* were required for optimal growth on cellulose. Our analysis also
12 identified three additional genes required for cellulose degradation: *lpmo10B* encodes a
13 lytic polysaccharide monooxygenase (LPMO), while *cbp2D* and *cbp2E* encode proteins
14 containing carbohydrate binding modules and predicted cytochrome domains for electron
15 transfer. CjLPMO10B oxidized cellulose and Cbp2D demonstrated spectral properties
16 consistent with redox function. Collectively, this report provides insight into the biological
17 role of LPMOs and redox proteins in cellulose utilization and suggests that *C. japonicus*
18 utilizes a combination of hydrolytic and oxidative cleavage mechanisms to degrade
19 cellulose.

20

21 **Introduction**

22 The biosynthesis and subsequent degradation of plant cell walls (lignocellulose) is a
23 major contributor to the global carbon balance, with over 100 billion tons of lignocellulose
24 being turned over annually (Leschine, 1995). Lignocellulose has also recently emerged
25 as an abundant renewable substrate for the biofuel sector. Currently, the major
26 impediment to commercial production of lignocellulosic biofuels is their high cost, which
27 results, in part, from the inefficiency and expense associated with lignocellulose
28 depolymerization (Lynd *et al.*, 2002). The majority of enzymes in commercial use for
29 depolymerization of lignocellulose are derived from microbes, therefore, an improved
30 understanding of the degradation of lignocellulose by microbes is needed to facilitate
31 improvements in the efficiency of this process (Wilson, 2012).

32

33 Bacteria, in addition to fungi, can depolymerize the composite polysaccharides of plant
34 cell walls. At a biochemical level, one of the best understood lignocellulose-degrading
35 bacterial systems is derived from *Cellvibrio japonicus*, a Gram-negative bacterium that
36 utilizes a system of dispersed extracellular lignocellulases (Yamane *et al.*, 1971). The
37 genomic sequence of *C. japonicus* revealed ~150 genes predicted to encode enzymes
38 that contribute to the deconstruction of the plant cell wall (DeBoy *et al.*, 2008). Although
39 several of the glycoside hydrolases and polysaccharide lyases that degrade the major
40 components of the plant cell wall have been biochemically characterized (Gilbert, 2010),
41 the significance of these enzymes in a biological context remains poorly understood. For
42 example, there is significant biochemical redundancy between many of the major enzyme
43 classes (Gilbert *et al.*, 1987, Gilbert *et al.*, 1988), but it is unclear whether this translates
44 to functional redundancy *in vivo*. Additionally, *in vitro* studies have shown that a cohort of
45 oxygenases, known as lytic polysaccharide monooxygenases (LPMOs) plays an
46 important role in the depolymerization of crystalline polysaccharides (Levasseur *et al.*,

1 2013, Lombard *et al.*, 2014). Previous studies have shown that LPMOs act in synergy
2 with glycoside hydrolases during degradation cellulose and chitin (Vaaje-Kolstad *et al.*,
3 2010, Phillips *et al.*, 2011, Quinlan *et al.*, 2011, Forsberg *et al.*, 2014). However, the
4 significance of these oxidation reactions in a biologically relevant *in vivo* setting remains
5 unexplored.

6
7 In addition to numerous glycoside hydrolases, polysaccharide lyases and two LPMOs
8 (defined henceforth as CjLPMO10A and CjLPMO10B), the genome of *C. japonicus*
9 encodes several proteins that display no sequence similarity to the catalytic modules of
10 carbohydrate modifying enzymes, but contain non-catalytic carbohydrate binding
11 modules (CBMs) that likely target cellulose, implying a role in the degradative process.
12 Intriguingly, some of these carbohydrate-binding proteins (Cbps) also contain modules
13 that link them to redox processes required for LPMO function (Forsberg *et al.*, 2011,
14 Langston *et al.*, 2011). To understand the mechanism by which these enzyme systems
15 degrade a chemically and physically complex substrate requires an integrated approach
16 that combines biochemical and transcriptomic analysis to develop hypotheses that can
17 then be tested through gene inactivation studies. We have employed this type of systems
18 biology strategy to explore the role of the seventeen Cbps and enzymes predicted to
19 comprise the cellulose degrading apparatus of *C. japonicus*. Presented data show that
20 LPMOs have a significant physiological role in the degradation of cellulose, and that two
21 proteins, predicted to have a redox function, play a pivotal role in the utilization of
22 crystalline cellulose.

23 24 **Results**

25 *Growth in insoluble cellulose leads to up-regulation of only a subset of glycoside*
26 *hydrolases.* Comparison of gene expression during exponential phase growth in
27 microcrystalline cellulose (Avicel) containing media identified statistically significant (p-
28 value ≥ 0.05) up-regulation of 941 genes and down regulation of 892 genes compared to
29 glucose grown cells (**Table S1**), including elevated expression of the predicted β -1,4
30 endoglucanase genes *cel5D*, *cel5G*, *cel5H*, and *cel45A* (**Fig. 1A**). In addition, fourteen
31 Cbp genes were up-regulated during exponential phase growth in Avicel, including all six
32 genes of the *cbp2* class. Overall, exponential phase growth in Avicel led to elevated
33 expression of less than 3% of *C. japonicus* genes predicted to encode glycoside
34 hydrolases, as compared to growth in the glucose reference medium, and only four (out
35 of thirteen) genes predicted to encode β -1,4 endoglucanases.

36
37 To identify potential differences in gene expression that are associated with growth on
38 crystalline and amorphous cellulose, we compared the expression profile of exponential
39 and stationary phase cells cultured on Avicel, which is composed of ~40% amorphous
40 (disordered) cellulose and ~60% crystalline cellulose (Thygesen, 2005, Park *et al.*, 2010).
41 Based on previous studies with purified enzymes, the amorphous cellulose would be
42 expected to be depolymerized first by *C. japonicus*, followed by the more recalcitrant
43 crystalline cellulose (Sasaki *et al.*, 1979). Therefore, exponential phase growth would be
44 expected to be associated with depolymerization of amorphous cellulose, whereas
45 stationary phase would be associated with utilization of crystalline cellulose. The
46 exponential to stationary comparison identified up-regulation of 121 genes and the down-

1 regulation of 114 genes (**Table S1**). Genes with elevated expression during stationary
2 phase growth in Avicel included *cel5A* and *cel5B*, which encode β -1,4 endoglucanases
3 (**Fig. 1C**), and *cel6A*, predicted to encode a cellobiohydrolase gene, as well as predicted
4 carbohydrate binding proteins *cbp2D* and *cbp2E*. Therefore, the transition from
5 exponential phase to stationary phase growth in Avicel containing medium led to changes
6 in expression of only a small number of glycoside hydrolases predicted to be involved in
7 cellulose degradation.

8
9 Although the differences in gene expression between exponential phase and stationary
10 phase growth in Avicel could reflect the transition from amorphous to crystalline cellulose,
11 it could also simply reflect changes in growth rate, which has been shown to control
12 expression of cellulose degrading genes in other systems (Raman *et al.*, 2011, Riederer
13 *et al.*, 2011). To differentiate between these two possibilities we carried out comparative
14 expression profiling of exponential and stationary phase cells grown in medium containing
15 glucose. Genes whose expression was controlled by growth rate would be expected to
16 show differential regulation under these two growth conditions. Comparison of gene
17 expression profiles during exponential and stationary phase growth in glucose identified
18 large changes in global gene expression (**Table S1**), including sharp up-regulation of
19 *cbp2B* and *cbp6C*, and more modest activation of *cel5D*, *cel5G*, *cbp2C*, *cbp6A*, *lpmo10B*
20 and *cbp35C* (**Fig. 1B**). Therefore, *C. japonicus* encodes a number of predicted cellulose
21 degrading enzymes whose expression appears to be growth rate controlled. However,
22 the genes subjected to differential transcription during different phases of growth on
23 Avicel did not display elevated expression in cells cultured on glucose (**Fig. S1**).
24 Collectively, these data are consistent with two classes of gene expression during growth
25 in microcrystalline cellulose: a cohort of genes that are regulated by growth rate, and a
26 second class of genes whose expression are responsive to the physical state of cellulose.

27
28 *Gene disruption studies identify genes required for growth on crystalline cellulose.* The
29 transcriptomic data identified candidate genes whose expression was elevated during
30 either exponential or stationary phase growth in Avicel. The function of these genes was
31 evaluated by targeted gene disruption and characterization of growth of the resultant
32 mutants in media containing cellulose as the sole carbon source. Additionally, we
33 disrupted all of the predicted β -1,4 endoglucanases in the *C. japonicus* genome that
34 were constitutively expressed under our growth conditions, as it was formally possible
35 that they may also contribute to cellulose degradation. Disruptions of *cbp2D*, *cbp2E*,
36 *cel5B*, *cel5A* and *cel6A* severely affected growth on filter paper (**Fig. 2**) as a cellulose
37 source (filter paper was chosen for the initial growth analysis due its high degree of
38 crystallinity and ease of measurement of cell density). The *cbp2D*, *cbp2E*, and *cel5B*
39 mutants showed the strongest phenotypes, displaying 3-7-fold decreases in growth rate
40 with respect to wild type in medium containing filter paper (**Table S2**). Additionally, the
41 *cbp2D* and *cbp2E* mutants achieved only ~40% of the cell density of wild type.
42 Disruption of *cel5A* and *cel6A* showed similar growth rates as wild type, but achieved
43 only ~60% of the final density of wild type.

44
45 Mutants that displayed phenotypes in medium containing filter paper were then cultured
46 on Avicel, which yielded somewhat different growth profiles. Growth of *C. japonicus* on

1 Avicel produced a complex growth curve involving a short period of exponential growth
2 (**Fig. S1**), a transient period of growth stasis that lasted approximately six hours, followed
3 by resumption of cell division at a reduced growth rate and entry into stationary phase.
4 The *cbp2D* and *cbp2E* mutants displayed a similar exponential phase growth rate to wild
5 type *C. japonicus* (**Fig. S2**). However, after the transient period of growth stasis, these
6 mutants grew more slowly than wild type, leading to a 50-fold decrease in final cell
7 number. The *cel5B* and *cel6A* mutants did not display detectable phenotypes in Avicel
8 containing medium, despite the strong phenotypes observed in medium containing highly
9 crystalline filter paper. In contrast, the *lpmo10B* mutant showed a 20-fold decrease in final
10 cell number when grown on Avicel, but this mutant did not have a phenotype on filter
11 paper. Overall, our results indicated that most of the genes that were up-regulated during
12 stationary phase growth in Avicel were required for optimum growth on cellulose, though
13 the phenotypes observed were dependent on the cellulose substrate.

14
15 *Biochemical properties of proteins critical for cellulose degradation by C. japonicus.* The
16 data described above showed that *cel5B* and *cel6A* were critical for growth on filter paper,
17 *lpmo10B* was required for optimal growth on Avicel, and *cbp2D* and *cbp2E* were critical
18 for growth on both substrates. Recombinant forms of each of these genes were
19 expressed in *E. coli* and the encoded proteins were purified to electrophoretic
20 homogeneity (except Cbp2D, which was membrane associated when expressed in *E.*
21 *coli*) and their biochemical properties characterized. The data indicated that Cel5B acted
22 as an endoglucanase that displayed a strong preference for soluble substrates such as
23 carboxymethyl cellulose (CMC), barley β -glucan, cellohexaose or disordered forms of
24 cellulose such as phosphoric acid-swollen cellulose (PASC) (**Fig. 3A**), and generated a
25 mixture of cellooligosaccharides as products.

26
27 Purified Cel6A exhibited very limited activity against soluble substrates (carboxymethyl
28 cellulose, CMC; β -glucan and cellohexaose), but showed higher activity against insoluble
29 cellulose. The enzyme was significantly more active than the endoglucanase against
30 PASC, Avicel and filter paper (**Fig. 3A**). This difference of activity is even more obvious
31 on bacterial microcrystalline cellulose (BMCC). BMCC is a highly crystalline form of
32 cellulose in which the dimensions of the microfibrils are very different from the plant form
33 of the polysaccharide, likely explaining the different activities displayed by the two
34 enzymes against this substrate. Against BMCC, Cel6A generated primarily cellobiose
35 consistent with a canonical cellobiohydrolase. Unexpectedly, against cellohexaose,
36 PASC, and to a limited extent Avicel, particularly after prolonged incubation, Cel6A
37 generated a significant amount of cellotriose, indicative of an endo-mode of action (**Fig.**
38 **4**). Overall, the biochemical properties indicate that Cel6A is a cellobiohydrolase capable
39 of degrading crystalline cellulose, consistent with the phenotype of the mutant lacking
40 *cel6A* in medium containing filter paper. The data, however, also suggest that loops
41 forming the “processive” tunnel are capable of opening, explaining the limited endo-
42 activity displayed by Cel6A against substrates, such as PASC, which contain high
43 concentrations of exposed single cellulose chains. Loop breathing has been shown to be
44 a common feature of cellobiohydrolases generally, explaining why these mainly exo-
45 acting enzymes may exhibit a degree of endo activity (Henrissat & Davies, 1997, Mba
46 Medie *et al.*, 2012). The HPLC profiles generated by the substrate depletion experiments

1 carried out on cellohexaose indicated that Cel5B is at least 100 fold more active on this
2 substrate than Cel6A (**Fig. 4A & B**). Ferricyanide assays on barley β -glucan show that
3 the initial rate for Cel5B was 9.71 mM glucose reducing end equivalents/min/ μ M protein.
4 This is approximately 450 fold higher than Cel6A, which has a value of 21.7 μ M glucose
5 reducing end equivalents/min/ μ M protein. Based on qualitative TLC data, Cel5B was
6 >100-fold more active against CMC than Cel6A (data not shown). The strong preference
7 of Cel5B for soluble glycans, compared to insoluble forms of cellulose is entirely
8 consistent with an endo-mode of action demonstrating that the enzyme is a canonical
9 endo- β 1,4-glucanase

10
11 The time course experiments undertaken with Cel5B on PASC showed that after 24 h the
12 main product is cellobiose followed by significant amounts of glucose and cellotriose (**Fig.**
13 **5D**). At the same time point, cellobiose is the main product generated by Cel6A, but,
14 surprisingly, a significant amount of cellotriose was also observed. No synergy occurred
15 between these two enzymes on that substrate. On BMCC, a drastic difference is seen
16 between Cel5B and Cel6A (**Fig. 5C**). Although Cel5B only generated low but similar
17 amounts of glucose, cellobiose and cellotriose (1-40 μ M) even after 24 h, Cel6A produced
18 significantly larger amounts of cellobiose (300 μ M after 24 h) and only very low amounts
19 of cellotriose (30 μ M). Moreover synergy was observed after only 1 h as an increase of
20 50% of the product generated is observed when the enzymes were incubated together,
21 compared to the sum of the products when the cellulases were incubated individually with
22 BMCC. After 24 h synergy was no longer evident. This could be explained by the fact that
23 at the beginning of the reaction, some cellulose chains are accessible to Cel5B, which
24 can thus generate additional initiation sites for Cel6A. After several hours, only the core
25 crystalline substrate remains, which can only be degraded by Cel6A. A similar level of
26 synergy was also observed between Cel5B and Cel6A when using filter paper and Avicel
27 as the substrate (**Fig. 5A & B**).

28
29 To determine the activity of CjLPMO10B, a predicted lytic polysaccharide
30 monooxygenase, a β -glucosidase was used to generate oxidized glucose, which
31 enabled quantification of bond cleavage. The rates determined were comparable for
32 Avicel, BMCC and filter paper at approximately 7-10 μ M oxidized glucose/ μ M
33 protein/hour and 41 μ M oxidized glucose/ μ M protein/hour for PASC (**Fig. 3C**).
34 CjLPMO10B, although inactive against soluble substrates (CMC, β -glucan and
35 cellohexaose), displayed activity against insoluble cellulose (Avicel, filter paper, BMCC
36 and PASC). The soluble products released from these substrates were analyzed by
37 HPAEC. The data indicated that the enzyme displayed similar activity against crystalline
38 cellulose (BMCC, Avicel and filter paper) but had greater activity against PASC (**Fig.**
39 **3B**). The majority of products generated by CjLPMO10B from cellulose were oxidized
40 celooligosaccharides oxidized at the C1 carbon (aldonic acids), but limited amounts of
41 non-oxidized oligosaccharides with a degree of polymerization (DP) of 2 to 6 were also
42 evident. The oxidized products produced from Avicel, filter paper and BMCC were
43 similar, reaching a DP of 6, whereas the largest oxidized celooligosaccharide produced
44 from PASC had a DP of 9 (**Fig. S3**). These data also provide unique insights into the
45 rate of bond cleavage by an LPMO and the oxidized products released by CjLPMO10B
46 (**Fig. 6**). Generally, the oxidized species increased over approximately 24 h, but after

1 this oligosaccharides with a DP of 5 or greater either plateaued or began to diminish,
2 whereas those with a DP of 4 or lower continued to increase. The same pattern was
3 observed for the non-oxidized products, with those with a DP of 5 or lower increasing in
4 concentration throughout the assay, whereas those with a higher DP either plateauing
5 or decreasing after the first 24-36 hours of activity.

6
7 The biochemical studies described here show differences in activities and specificities for
8 Cel5B, Cel6A and CjLPMO10B on different cellulose substrates. The co-regulation of
9 these enzymes during growth in highly crystalline Avicel could indicate that they act in
10 concert to depolymerize this substrate. Different combinations of these enzymes were
11 applied to cellulose to examine any additive or synergistic activities. The data suggest
12 that reactions containing both Cel5B and Cel6A generated approximately 50% more
13 cellulooligosaccharides than the sum of the products when the enzymes were incubated
14 individually with crystalline cellulose (filter paper and BMCC) and Avicel, which contains
15 amorphous and crystalline forms of the polysaccharide. The inclusion of CjLPMO10B with
16 the glycoside hydrolases mediated a further increase in the amount of non-oxidized
17 product (**Fig. 5A & B**), indicating that the oxygenase and hydrolases of the cellulolytic
18 system act synergistically. No synergy was observed against PASC, an amorphous form
19 of cellulose.

20 21 **Discussion**

22 Lignocellulose is a complex co-polymer whose depolymerization requires the concerted
23 action of multiple enzyme activities. Consistent with this are the large number of plant cell
24 wall degrading proteins produced by microbes that utilize this composite structure. The
25 significant biochemical redundancy within these enzyme systems, coupled with the
26 diverse mechanisms by which aerobic organisms cleave glycosidic bonds, limits our
27 understanding of the degradative process *in vivo* through simply characterizing the
28 individual components. By combining biochemical studies with transcriptomics and gene
29 inactivation studies, this report has identified the key *physiologically relevant* components
30 of the cellulose degrading system of a model aerobic soil bacterium.

31
32 Surprisingly, of the twelve predicted cellulases in *C. japonicus*, only *cel5B* and *cel6A* are
33 required for optimal utilization of cellulose, which corresponds to a wild type growth rate
34 of 0.07 hr⁻¹ (**Table S2**). The *cel5B* and *cel6A* mutants growth rate is nearly a third of that
35 of wild type. It is important to note that these growth rate phenotypes are specific to
36 cellulose, as growth rate of these mutants in glucose is the same as wild type, removing
37 the possibility that the mutation is causing a more general growth defect. Additionally, the
38 importance of these two glycoside hydrolases in the growth of *C. japonicus* on cellulose
39 does have some resonance with comparable studies in anaerobic organisms where the
40 endoprocessive endoglucanase, Cel9A, and the “reducing end” cellobiohydrolase,
41 Cel48S, were shown to play an important (and in the case of Cel9A essential) role in the
42 growth of *Clostridium phytofermentans* (Tolonen *et al.*, 2009) and *C. thermocellum* (Olson
43 *et al.*, 2010), respectively, on crystalline cellulose. It should be noted that while *C.*
44 *japonicus* might not fare as poorly in a natural environment, as it is able to degrade and
45 consume the hemicellulose and pectin of the plant cell wall, the analogous mutations of

1 a *Clostridium* sp. mutant would be crippling, as these bacteria are considered a cellulose
2 specialists (Zhang & Lynd, 2005).

3
4 Given the preference of Cel5B for disordered cellulose (**Fig. 3A**), it is surprising that it
5 plays a critical role in the growth of *C. japonicus* on filter paper. This might be due to the
6 high level of expression of *cel5B* in response to crystalline forms of the polysaccharide
7 (**Fig. 1C**), compared to the other endoglucanases. Interestingly, dimensions of the
8 microfibrils in BMCC (a crystalline cellulose) are very different from the plant form of the
9 polysaccharide. Indeed BMCC is composed of reticulated network of fine fibers, the
10 diameter of which (0.1 μm) is about one hundredth that of plant-derived fibers. Moreover
11 $\text{I}\alpha$ cellulose is predominant in BMCC whereas plant cellulose is mainly composed of $\text{I}\beta$
12 cellulose (Atalla & Vanderhart, 1984). These two polymorphs differ mainly in the packing
13 arrangement of their hydrogen-bonded sheets. All together these data likely explain the
14 different activities displayed by the enzyme against this substrate. Additionally, the data
15 from **Fig. 5** indicate a degree of synergy between the Cel5B and Cel6A enzymes, which
16 may reflect an element of the classic model for cellulose degradation in which the endo-
17 acting enzyme Cel5B generates additional initiation sites, non-reducing termini, for the
18 predominantly exo-acting Cel6A. In PASC the dominant activity of Cel5B, and the limited
19 endo-activity of Cel6A, mask any potential synergy between these two enzymes.

20
21 While there have been numerous biochemical studies linking LPMOs with the degradation
22 of crystalline carbohydrates (Vaaje-Kolstad *et al.*, 2010, Forsberg *et al.*, 2011, Vaaje-
23 Kolstad *et al.*, 2012), the biological significance of these enzymes *in vivo* remained
24 unclear. Here we demonstrate that CjLPMO10B plays a critical role in the growth of *C.*
25 *japonicus* on Avicel, which contains both crystalline and amorphous regions, but not on
26 filter paper, which is considerably more crystalline. The mutant phenotypes are consistent
27 with the observation that CjLPMO10B can act in synergy with cellulolytic glycoside
28 hydrolases on Avicel but not filter paper. It is possible that in an *in vivo* setting the
29 biologically significant function of the *C. japonicus* LPMO10s is to target regions of
30 cellulose that are at the crystalline-paracrystalline interface, and that these regions are
31 only utilized by *C. japonicus* at the latter stages of the degradative process. Our
32 transcriptomic data suggests that there are major composition changes in the suites
33 cellulases that *C. japonicus* uses over the course of degradation (**Fig. S1**). Additionally,
34 the transcriptomic results on glucose further indicate that expression of cellulases has a
35 substrate detection component to it, and therefore is more sophisticated than that found
36 in *C. thermocellum* (Raman *et al.*, 2011). Current work in our laboratory is examining the
37 physiologically relevant signals for cellulose degradation, and work in *Neurospora crassa*
38 suggest that the signal may be soluble cellodextrins (Znameroski *et al.*, 2012), though the
39 differences between this fungus and *C. japonicus* must be taken into account. For
40 example, while many bacteria contain only one or two LPMOs, fungi often contain several
41 such enzymes. It is possible that different fungal LPMOs potentiate cellulose
42 depolymerization at distinct stages of the degradative process, and thus contribute to the
43 complete saccharification process. However, it should also be noted that a *Neurospora*
44 LPMO9 was recently shown to cleave xyloglucan (Agger JW, 2014), and thus different
45 fungal LPMOs may have evolved to target distinct glycans within the plant cell wall.

1
2 A significant finding of the expression profiling studies was the identification of two genes
3 of unknown function, *cbp2D* and *cbp2E*, which displayed elevated expression during
4 growth in the presence of Avicel. Disruption of *cbp2D* and *cbp2E* led to dramatic growth
5 phenotypes in media that contained filter paper and Avicel as a sole carbon source. Only
6 disruption of *gspD*, a component of the Type II Secretion System (TTSS) required for
7 extracellular secretion of the cellulose degrading apparatus (Gardner & Keating, 2010)
8 showed a more severe growth defect. Importantly, the *cbp2D* and *cbp2E* mutants did not
9 show phenotypes in media containing soluble CMC (**Fig. S2**). Therefore, these genes
10 play a specific role in the degradation of crystalline and microcrystalline forms of cellulose.
11 Cbp2D and Cbp2E are predicted to be extracellular proteins that contain a cellulose-
12 binding CBM2 domain, as well as a Ycel domain which, in a close structural homolog to
13 Cbp2E, was shown to bind to ubiquinone (Vincent *et al.*, 2010). In addition, Cbp2D is also
14 predicted to contain two cytochrome C domains. Cytochrome C and ubiquinone are
15 required for diverse electron transfer reactions in bacteria (Richter & Ludwig, 2009),
16 including their well-established role in respiration (Kranz *et al.*, 2002), but a role for these
17 “respiratory chain” oxido-reduction molecules in the depolymerization of cellulose has not
18 previously been reported. While biochemical studies could not identify the precise role of
19 these proteins in cellulose degradation, recombinant Cbp2D, although insoluble in *E. coli*,
20 displayed spectral properties entirely consistent with a redox function (**Fig. S4**). We
21 propose, therefore, that Cbp2D/E contribute to cellulose degradation by supplying
22 electrons to the LPMOs, analogous to cellobiose dehydrogenase enzymes in fungal
23 cellulolytic systems (Phillips *et al.*, 2011). However, several issues remain unresolved.
24 First, the nature of the electron donor for Cbp2D/E is unknown. In fungal systems, CDHs
25 transfer electrons to LPMOs using non-oxidized celooligosaccharides as electron donors
26 (Phillips *et al.*, 2011), however bioinformatic examination of the *C. japonicus* genome did
27 not identify genes with convincing sequence similarity to fungal CDHs.

28
29 The effect of Cbp2D and Cbp2E on the utilization of filter paper appears to be independent
30 of C₇LPMO10s. It is possible that the degradation of this highly crystalline form of cellulose
31 requires polysaccharide oxygenases that do not display similarity to the current three
32 families of LPMOs. In this scenario, the primary role of Cbp2D and Cbp2E involves
33 donation of electrons to these currently unknown polysaccharide oxygenases, as well as
34 to LPMO10 enzymes. An alternative hypothesis is that Cbp2D plays a direct role in the
35 cleavage of highly crystalline cellulose such as filter paper. A potential mechanism for this
36 process is through Fenton chemistry mediated by Cbp2D, which contains multiple heme
37 domains where such chemistry may occur. However, the inability of Cbp2D to bind
38 oxygen argues against a direct role for the protein in cellulose oxidation through Fenton
39 reactions. Thus we favor a role for Cbp2D/E in electron shuttling within the cellulose
40 oxidation system.

41
42 In summary, this study illustrates the power of genome-aided biology to elucidate the
43 genetic underpinnings of complex physiological processes. In addition to defining the
44 critical components of a seemingly redundant class of genes, the GH5 glycoside
45 hydrolases, we have identified novel genes, *cbp2D* and *cbp2E*, which play a key role in
46 the depolymerization of cellulose. This use of systems approaches will continue to inform

1 our model of bacterial lignocellulose degradation. Additionally, the genetic tools
2 developed for *C. japonicus* will be invaluable in ecological investigations examining how
3 lignocellulose-degrading bacteria influence the global carbon balance.

4 5 **Experimental Procedures**

6 *Bacterial strain.* *Cellvibrio japonicus* sp. nov. strain Ueda107 was obtained from the
7 National Collections of Industrial, Marine and Food Bacteria and used for transcriptional
8 profiling.

9
10 *C. japonicus growth conditions.* *C. japonicus* strains were grown in MOPS minimal
11 medium (Neidhardt *et al.*, 1974). Glucose (0.5% w:v), soluble cellulose (CMC, 1% w:v),
12 microcrystalline cellulose (Avicel, 0.5%, w:v), and crystalline cellulose (filter paper, 0.5%
13 w:v) were used as sole carbon and energy source. All incubations were performed at 30
14 °C with high aeration (225 rpm). For mutational analysis experiments, cells were grown
15 in 18 mm tubes and growth was measured at OD₆₀₀ in a Spec20D+ (Thermo Scientific)
16 spectrophotometer or via CFU counting, as described previously (Gardner & Keating,
17 2010). All experiments were performed in biological triplicate. When used, antibiotics
18 were present in the medium at the following concentrations: gentamicin, 15 (µg/ml),
19 kanamycin, 50 (µg/ml). All chemicals were purchased from Fisher.

20
21 *Mutant construction.* Mutations in *C. japonicus* were made by vector integration (Gardner
22 & Keating, 2012). Plasmid pK18*mobsacB*, with an internal 500 bp fragment of the gene
23 to be inactivated, was electroporated into S17 λ_{PIR} with selection for kanamycin
24 resistance, and subsequently introduced into *C. japonicus* by conjugation. The mating
25 mixture was cultured at 30 °C for 48hr, then *C. japonicus* transformants were selected for
26 on MOPS-glucose medium containing 50 µg/ml kanamycin and 50 µg/mL valine. Mutant
27 strains were re-streaked to purity and the gene inactivation verified by PCR analysis.

28
29 *RNA isolation and transcriptomic analysis.* Cells grown in cellulosic substrates for
30 transcriptomic analysis were collected and RNA was extracted from the cell pellets as
31 previously described (Gardner & Keating, 2012, Schwalbach *et al.*, 2012). Briefly, *C.*
32 *japonicus* cells for transcriptomic analysis were collected (45 ml) into tubes containing 5
33 ml ice-cold 5% vol/vol unbuffered phenol in ethanol and pelleted by centrifugation
34 (8,000 × g, 4°C, 8 min). The phenol/ethanol was decanted, and the cell pellet flash
35 frozen in dry ice / ethanol and stored at - 80°C. The RNA was extracted from cell pellets
36 and analyzed by agarose gel electrophoresis and Nanodrop (Thermo Scientific).
37 Transcript levels were measured using custom microarrays (Roche NimbleGen) with
38 cDNA prepared using random hexamers and the Invitrogen SuperScript Double-Stranded
39 cDNA Synthesis reagents (Invitrogen). Sample labeling and hybridization followed the
40 manufacturer's instructions. Hybridized arrays were scanned with a NimbleGen MS 200
41 Microarray Scanner and the probe signal intensities were determined using NimbleScan
42 v 2.6 (Roche NimbleGen). The signal intensities were pre-processed by robust multichip
43 averaging (RMA) using ArrayStar (DNASTAR). Gene expression signals were quantile-
44 normalized for all samples, and significant expression changes were assigned to genes
45 exhibiting a ≥ 2-fold change in signal intensity with a 2-way ANOVA model (p-value <
46 0.05). Statistical analysis to find differentially expressed genes was performed using

1 ANOVA with appropriate contrasts in Partek Genomics Suite, version 6.6, 6.13.0516
2 (Partek Inc., St. Louis, MO, USA). Raw data and array information have been submitted
3 to GEO (GSE#XXXXX).

4
5 *Genetic techniques.* Plasmids were introduced into *E. coli* strains by transformation, and
6 into *C. japonicus* by conjugation as described previously (Gardner & Keating, 2010,
7 Gardner & Keating, 2012). A derivative of plasmid pK18*mobsacB* was used for gene
8 disruption in *C. japonicus* (Schafer *et al.*, 1994) and mutants verified by PCR analysis as
9 described previously (Gardner & Keating, 2010).

10
11 *Cloning, expression and purification.* The genes *cel6A*, *cel5B* and *lpmo10B* were
12 amplified by PCR using *C. japonicus* genomic DNA as the template. Both *cel6A* and
13 *cel5B* were cloned into pET21a using the restriction site pairs NdeI/XhoI and NheI/XhoI,
14 respectively, while *lpmo10B* was cloned into pET22b using sewing PCR to place the N-
15 terminal histidine of the mature sequence of the encoded protein, directly following the
16 PelB cleavage site to allow correct protein folding and coordination of the copper in the
17 active site. Both *cbp2D* and *cpb2E* were cloned into pET22b using BamHI/XhoI restriction
18 sites. All the encoded proteins had a C-terminal His₆ tag. Production of Cel6A and Cel5B
19 were carried out in *Escherichia coli* strain Shuffle(DE3), and CjLPMO10B in BL21(DE3).
20 Strains harboring the *cel6A* and *cel5B* genes were grown at 30 °C to an OD of 0.5 at 550
21 nm, cooled to 16 °C, and recombinant gene expression induced using 0.4 mM isopropyl
22 β-D-galactopyranoside (IPTG) and incubation for a further 15 h. To produce CjLPMO10B
23 *E. coli* was cultured for 24 h at 25 °C, cooled to 16 °C, and, followed by addition of 1 mM
24 IPTG and incubation for a further 24 h. Production of Cbp2D was achieved using a pST2
25 plasmid, which encodes the cytochrome C assembly genes required under aerobic
26 growth conditions in *E. coli*. For Cel6A and Cel5B, cell pellets were sonicated, cell debris
27 removed by centrifugation. For CjLPMO10B a periplasmic extraction was carried out as
28 described in (Becker & Hsiung, 1986). The recombinant proteins were purified using
29 immobilized metal ion affinity chromatography using Talon™ (Clontech) by washing with
30 10 mM imidazole and eluting with 100 mM imidazole, as described previously (Charnock
31 *et al.*, 2002).

32
33 *LPMO oxidized product assay.* Assays with CjLPMO10B (1 μM) included 1% final
34 substrate concentration, 1 mM ascorbate, 50 mM sodium phosphate buffer (pH 6.0), and
35 0.1 mg/ml BSA. The reactions were carried out at 37 °C and 180 rpm. Aliquots were
36 taken at regular time intervals, boiled and centrifuged to remove insoluble substrate.
37 Analysis of the total number of oxidized ends in a given reaction was achieved through
38 the addition of 1 unit of β-glucosidase from *T. maritima* (Megazyme), which released
39 glucose-aldonic acid to 40 μl aliquots and incubated at 37 °C for 16 h. The reaction was
40 boiled and any precipitate removed by centrifugation. Reaction products of enzyme
41 assays were analyzed using a CARBOPAC™ PA-1 anion exchange column (Dionex)
42 equipped with a CARBOPAC™ PA-1 guard column. Generally, 40 μl samples were
43 added to 160 μl of filtered water as described by Westereng *et al.* (Westereng *et al.*,
44 2013).

45

1 *Glycoside hydrolase product assay.* Substrate depletion experiments were undertaken
2 using 1 nM Cel5B or 100 nM Cel6A on cellohexaose (0.1% w/v, Megazyme). The
3 reactions were carried out at 37 °C in 50 mM sodium phosphate buffer (pH 6.5)
4 supplemented with 0.1 mg/ml BSA final concentration. Aliquots of 50 µl were taken at
5 regular time intervals up to 24 h, boiled, and 40 µl of each sample was added to 160 µl of
6 filtered water before analysis by HPLC-PAD. The reaction products of Cel5B and Cel6A
7 on PASC (1% w/v) and BMCC (5% w/v) were analyzed over time. The reactions were
8 carried out at 37 °C in 50 mM phosphate buffer (pH 6.5) supplemented by 1 µM of Cel5B
9 or 1 µM of Cel6A and by both enzymes. Aliquots (40 µl) of each reaction at 1 h and 24 h
10 were added to 160 µl of filtered water and analyzed by HPLC-PAD. All experiments were
11 carried out in triplicate.

12
13 The amount of reducing ends produced by purified Cel5B and Cel6A was estimated by
14 the ferricyanide assay following a protocol adapted from Kidby, *et al.* (Kidby & Davidson,
15 1973). The reactions were carried out at 37 °C in 800 µl 50 mM sodium phosphate buffer
16 (pH 6.5). Avicel PH105 (1% w:v), PASC (1% w:v), BMCC (5% w:v) and filter paper (1 X%
17 w:v) were incubated with 5 µM of enzyme. Aliquots of 100 µl were taken from 10 s to 23
18 h and boiled prior to centrifugation. A 40 µl aliquot of the supernatants were added to 200
19 µl of ferricyanide reagent (1.5 g/l ferricyanide, 24 g Na₂CO₃, 1 ml 5 M NaOH, qsp 1l). The
20 samples were incubated at 95 °C for 15 min and cooled to 20 °C before measurement at
21 420 nm. A calibration curve with 0–600 µg/ml glucose was used to calculate the amount
22 of released reducing ends as glucose-reducing end equivalents. All experiments were
23 undertaken in duplicate. For the soluble substrates the reactions were carried out at 37
24 °C in 400 µl 50 mM sodium phosphate buffer (pH 6.5). CMC (1% w:v) and β-glucan from
25 barley (1% w:v, Megazyme, low viscosity) were incubated with 10 nM of Cel5B or 1 µM
26 of Cel6A. The reactions were monitored for 15 min (0, 3, 6, 9, 12, 15) and 25 min (0, 5,
27 10, 15, 20, 25) respectively. Aliquots of 40 µl were directly added to 200 µl ferricyanide
28 reagent. All experiments were undertaken in triplicate.

29
30 *Production of oxidized glucose.* Oxidized glucose was prepared using the method
31 described by Kobayashi, *et al.* (Kobayashi, 1985). Briefly, 3 g of glucose were dissolved
32 in water (2.5 ml), diluted with methanol (5 ml) and warmed to 40°C. An iodine (4.28 g)
33 solution in methanol (60 ml) previously warmed to 40°C was added. At this temperature,
34 a 4% potassium hydroxide solution in methanol was added drop-wise with magnetic
35 stirring until the color of iodine disappeared. The solution was cooled on ice. The
36 precipitated crystalline product was filtered and washed with cold methanol (500 ml)
37 before being dried via vacuum.

38
39 *Purification of Cbp2D.* Purification of soluble protein was attempted in a number of ways.
40 Initially periplasmic extraction was used and after this was unsuccessful sonication of the
41 remaining pellet was tried. Detergents were then used to either solubilize or encourage
42 the protein away from any membrane interactions. Two relatively gentle detergents were
43 first tried, DDM (n-dodecyl-β-D-maltoside) and DM (n-decyl-β-D-maltoside), and then two

1 more relatively aggressive ones, OG (octyl glucoside) and LDAO (lauryldimethylamine-
2 oxide).

3

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16

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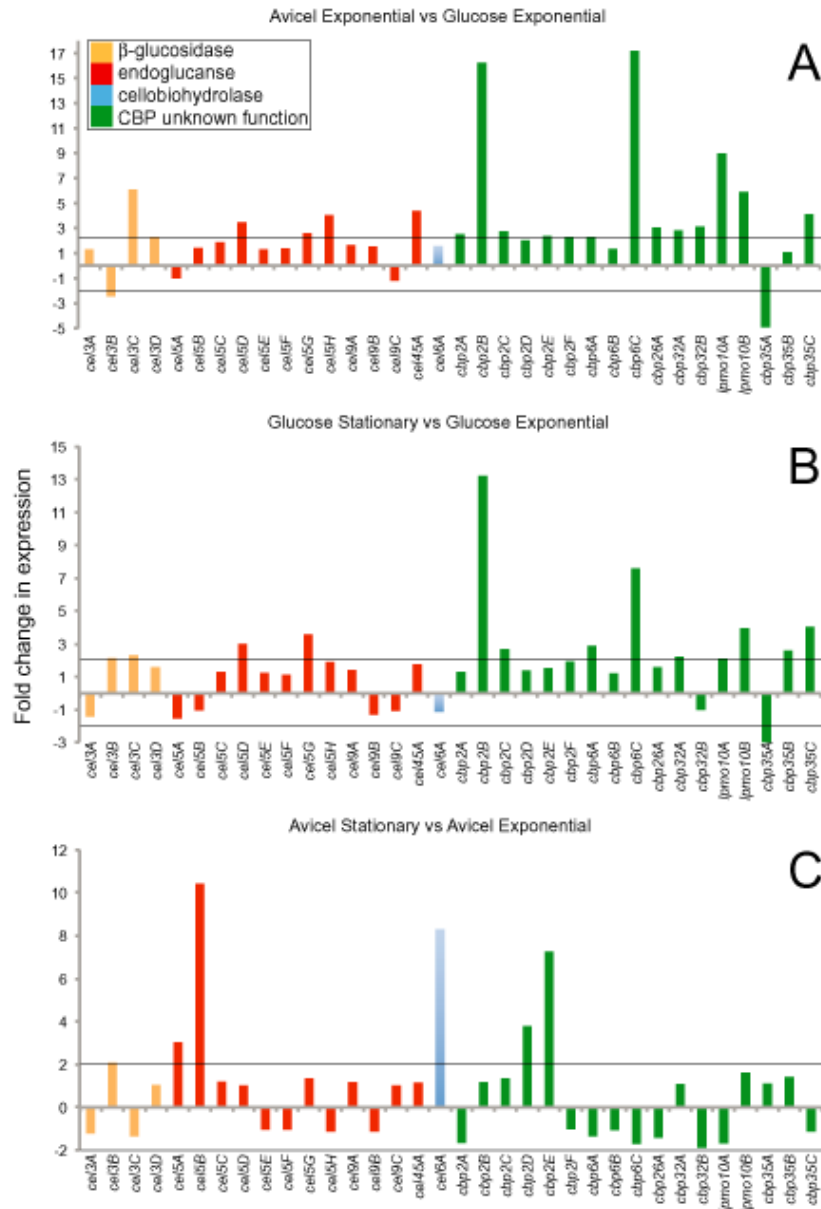
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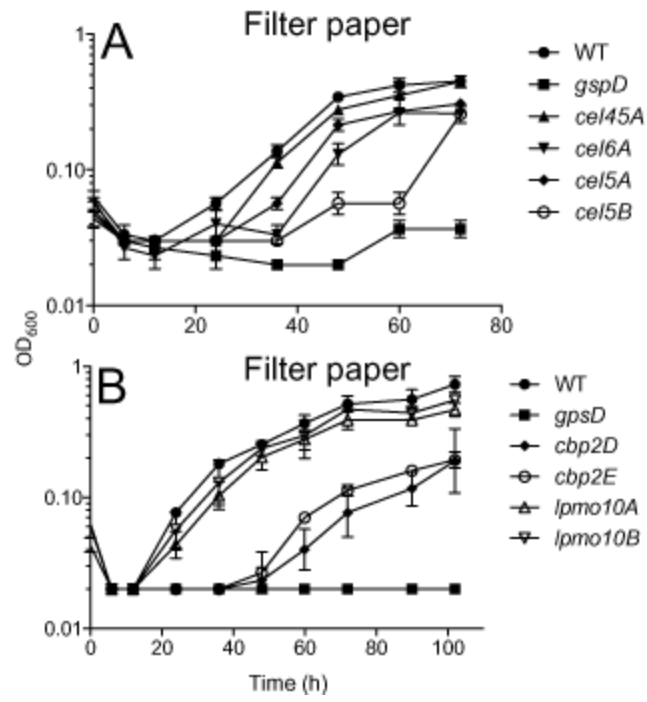
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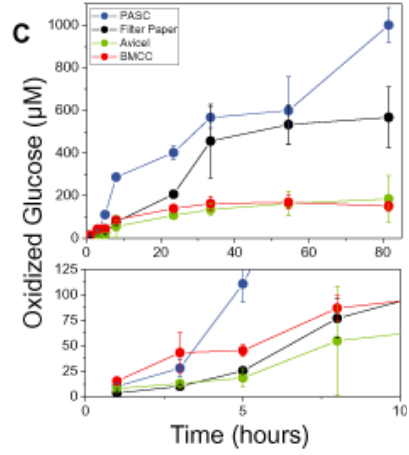
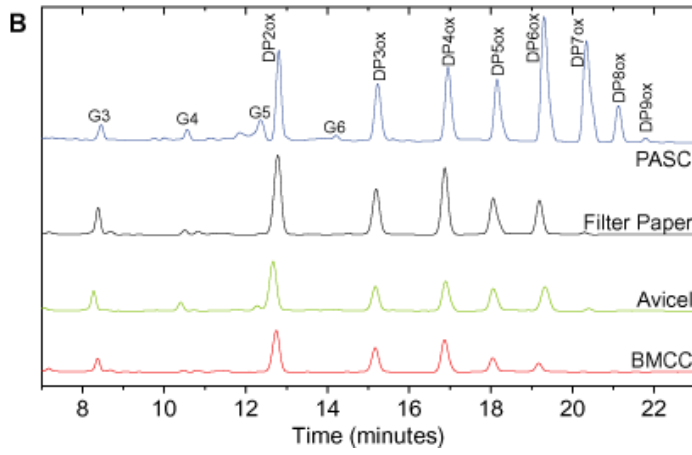
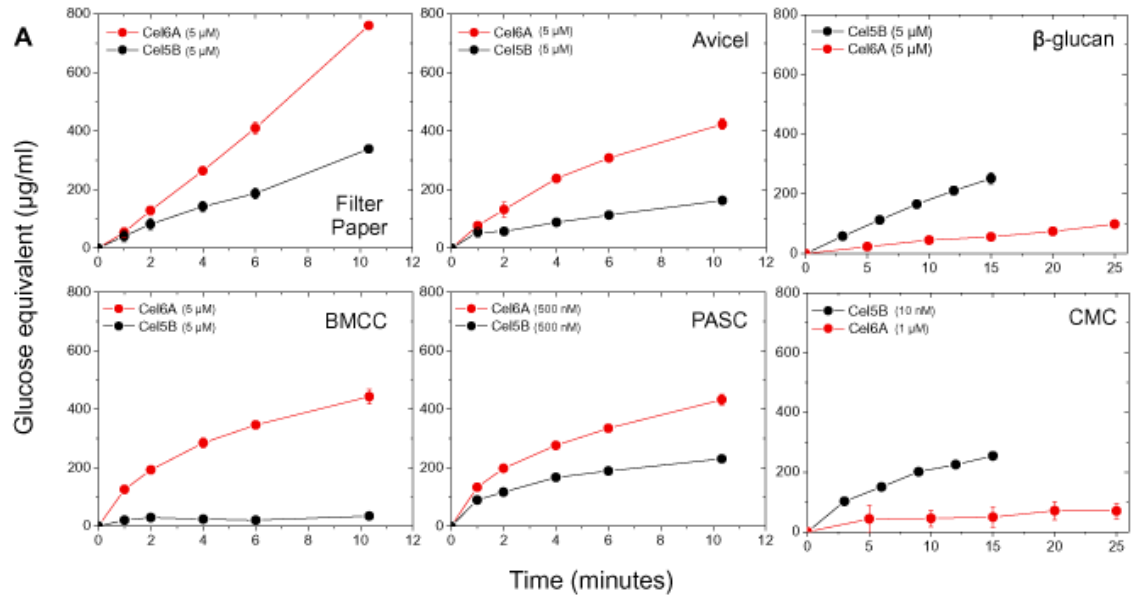
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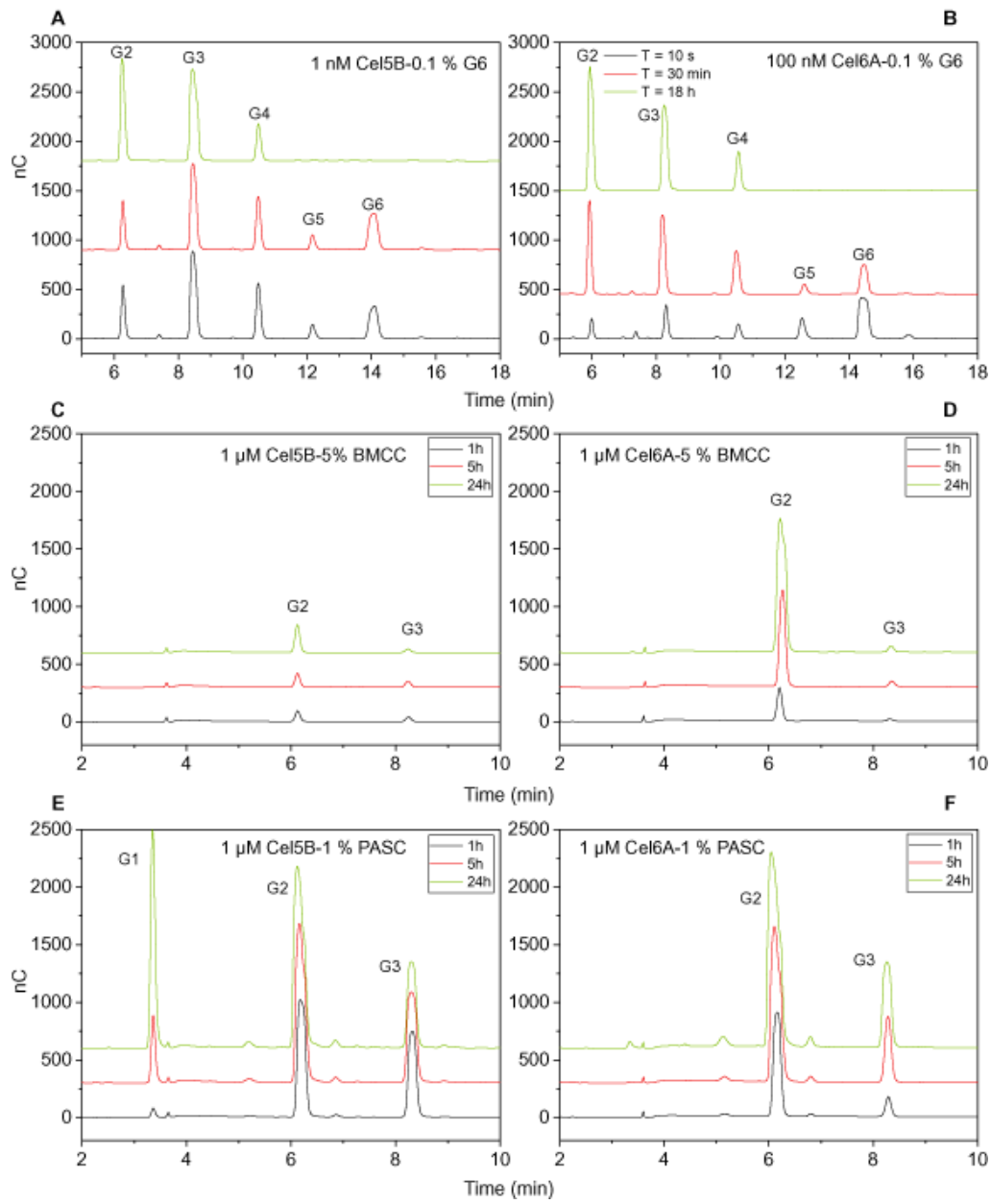
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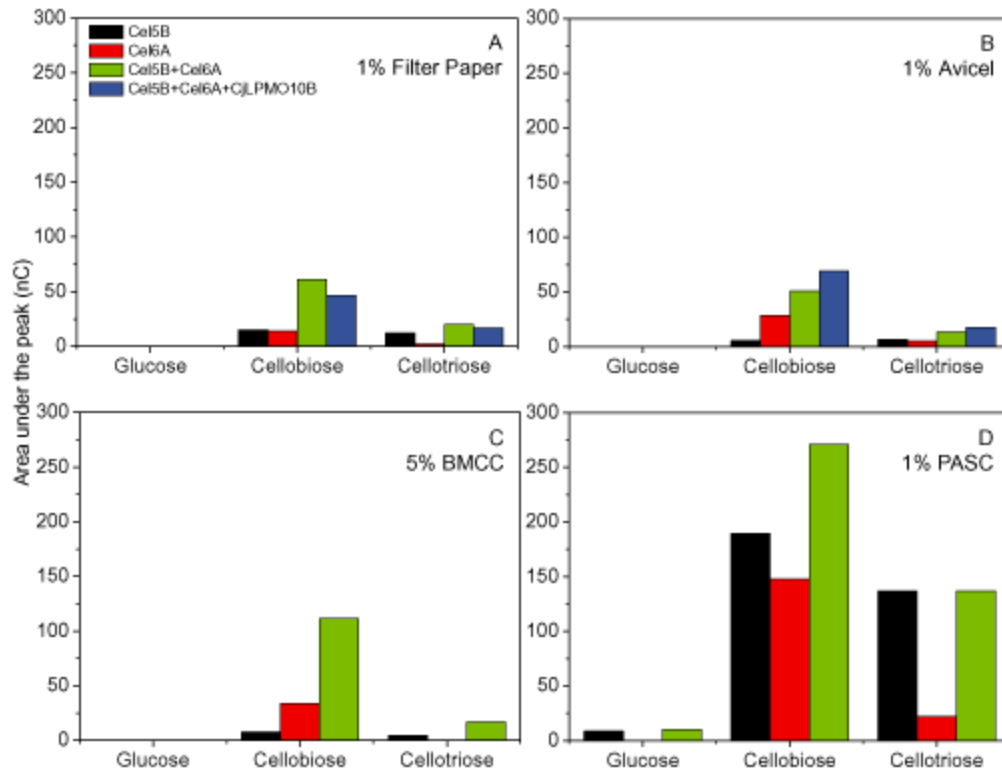


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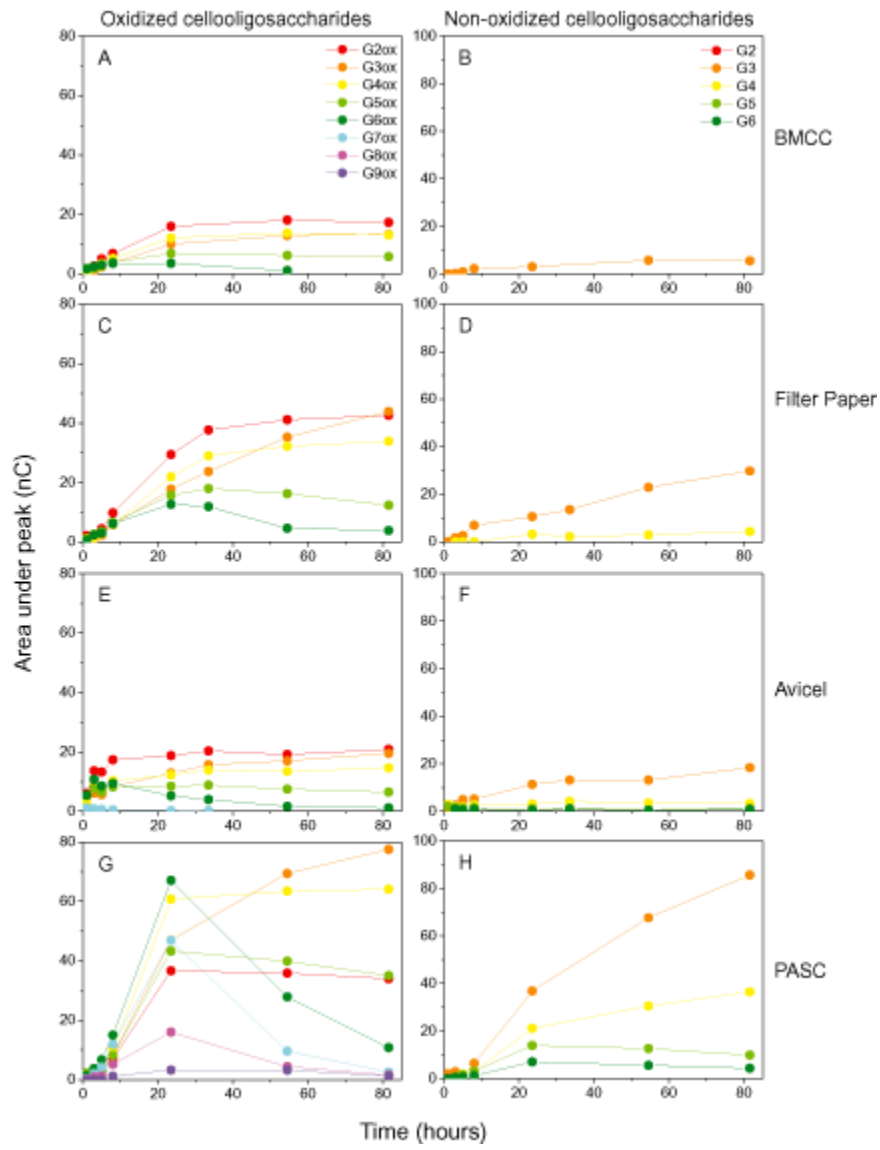
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Fig3

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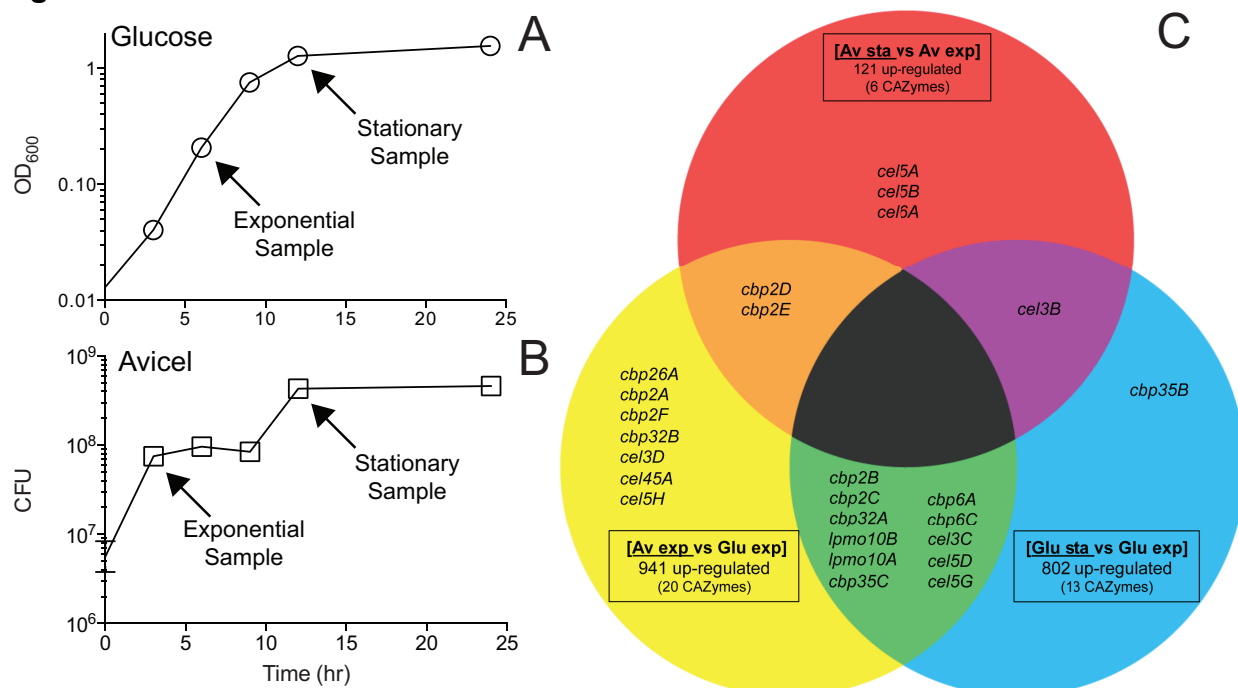
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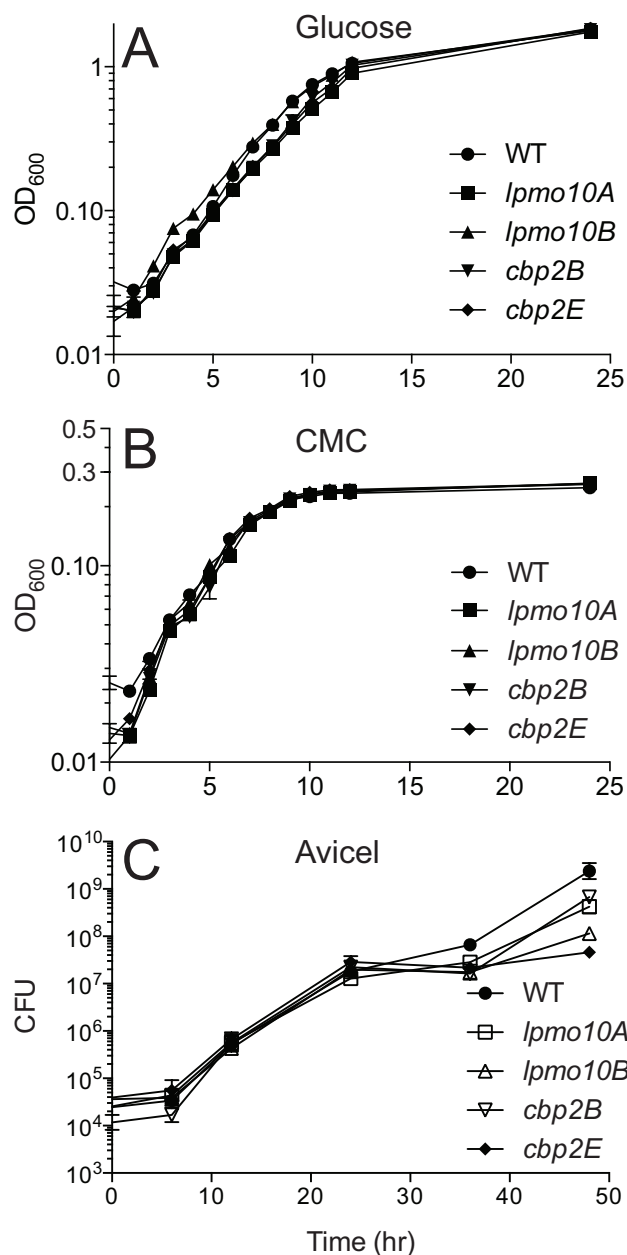


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Fig6

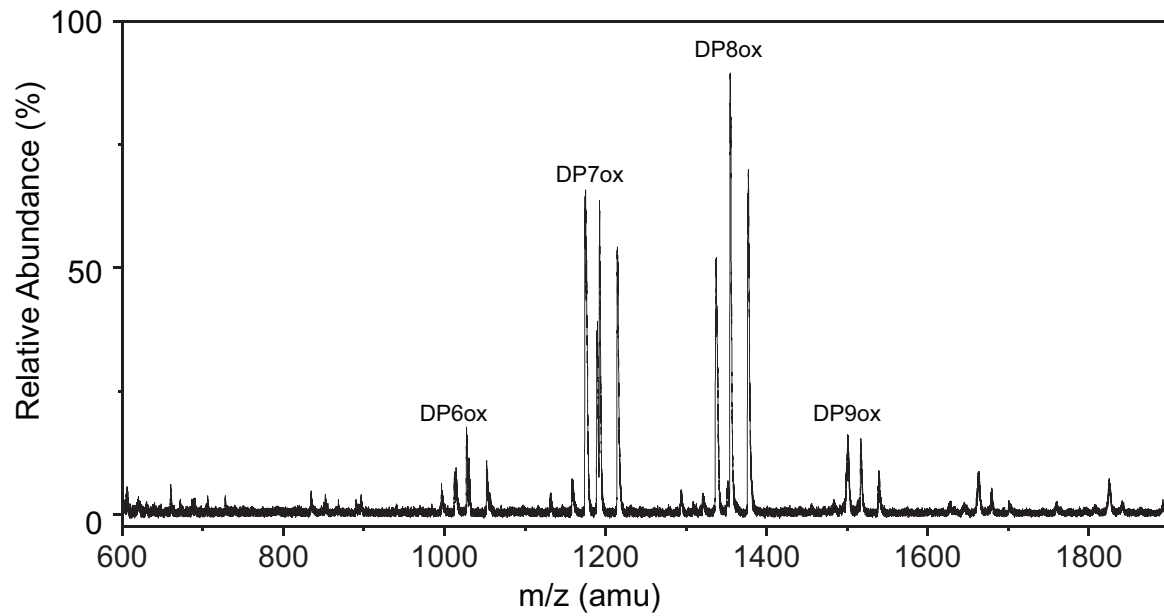
1 **Figure S1**

2
3 **Supplemental Figure S1.** Growth conditions used for expression profiling of *C.*
4 *japonicus*. Wild type *C. japonicus* was cultured in M9 medium with either **A.** glucose
5 (0.5% w:v), or **B.** Avicel (0.5%, w:v) as the sole carbon source. Growth was measured
6 via measurement of optical density (OD) at 600nm for glucose or colony forming units
7 (CFU) for Avicel grown cells. At the indicated arrows, cells were collected for RNA
8 isolation and transcriptomic analysis. All growth experiments were performed in
9 biological triplicate at 30 °C and with high aeration (225 rpm). **C.** Venn Diagram showing
10 cellulase and Cbp gene expression comparisons between glucose (Glu) and Avicel (Av)
11 grown cells during exponential (exp) and stationary (sta) growth phases.
12

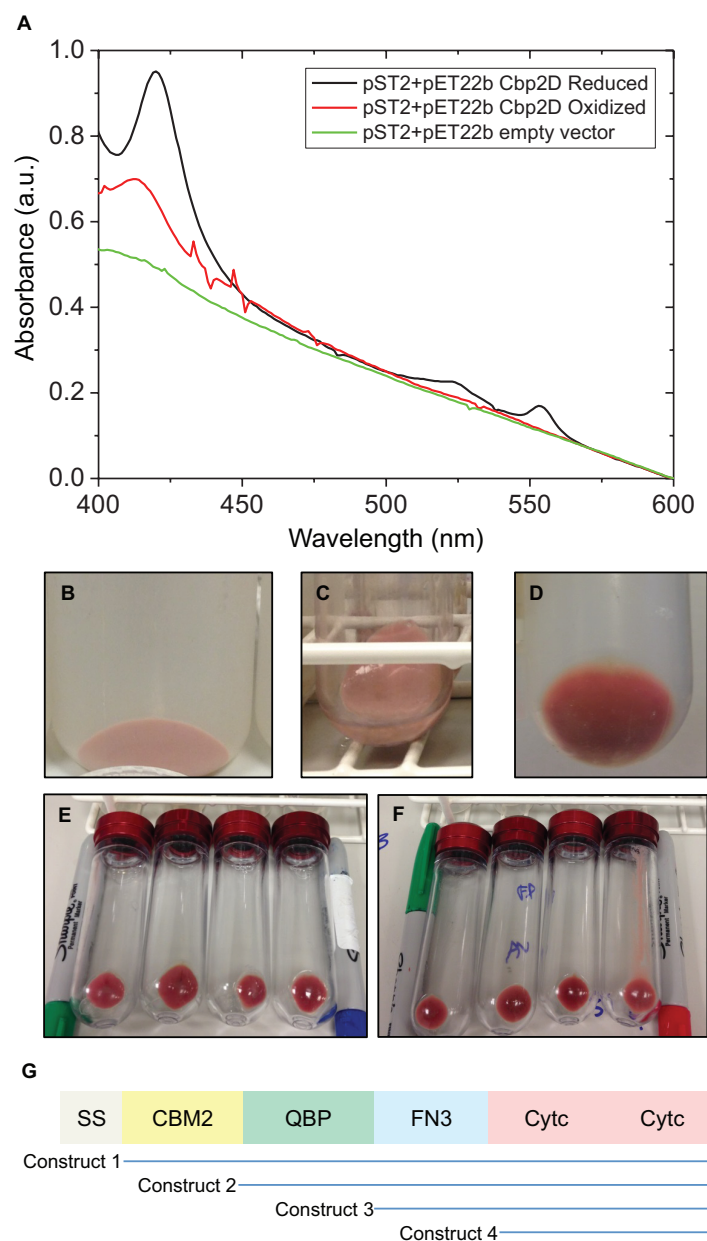
1 **Figure S2**

2
 3 **Supplemental Figure S2.** Growth of *C. japonicus* *cbp* mutants grown on glucose (A),
 4 carboxymethyl cellulose (CMC) (B), or microcrystalline cellulose (Avicel) (C). Wild type
 5 *C. japonicus* and *cbp* mutants were cultured in MOPS medium with (0.5%, w:v.) of the
 6 indicated carbon sources. Growth was measured via viable cell counting (CFU) or
 7 optical density (OD) at 600nm. All growth experiments were performed in biological
 8 triplicate at 30 °C and with high aeration (225 rpm). Error bars represent standard
 9 deviation.

1 **Figure S3**



2
3 **Supplementary Figure S3.** MALDI-TOF analysis of products released during
4 degradation of PASC by *Cj*LPMO10B.
5

1 **Figure S4**

2
3
4 **Supplementary Figure S4.** Characterization of Cbp2D. **A.** Absorbance spectra of the
5 pink Cbp2D membrane pellet with a reductant (sodium dithionite), oxidant (potassium
6 ferricyanide) and membrane pellet with pST2 vector and empty pET22b vector (black,
7 red and green, respectively). Expression of Cbp2D were consistent with the pink
8 coloration of the recombinant cells (**B**). However, purification of soluble Cbp2D was not
9 possible with the pink coloration remaining in the pellets of a periplasmic extraction (**C**),
10 sonication (**D**), 1 % DM or 1 % DDM solubilization (**E**), or a 1 % OG or 1 % LDAO
11 solubilization (**F**). A variety of constructs were attempted, which are shown in (**G**), each
12 producing the same insoluble pink proteins.

1 **Supplemental Table S1.** Log₂-normalized gene expression values for wild type *C.*
 2 *japonicus* during exponential or stationary phase of growth in media containing either
 3 glucose or cellulose (Avicel) as the sole carbon source.

4
 5 **NOTE:** Table S1 presented after Supplemental Table S2 due to length

6
 7 **Supplemental Table S2.** Growth rates and maximum optical densities (OD₆₀₀) of wild
 8 type and mutant *C. japonicus* during growth in media containing glucose or filter paper
 9 as a carbon source.

10

Gene	Glucose ¹		Filter Paper ²	
	Max. Cell Density	Growth rate (hr ⁻¹)	Max. Cell Density	Growth rate (hr ⁻¹)
WT	1.50	0.46	0.45	0.07
<i>cel5A</i>	1.43	0.44	0.31	0.05
<i>cel5B</i>	1.40	0.45	0.26	0.02
<i>cel5C</i>	1.40	0.45	0.49	0.06
<i>cel5D</i>	1.50	0.44	0.43	0.06
<i>cel5E</i>	1.47	0.55	0.45	0.06
<i>cel5F</i>	1.47	0.43	0.44	0.06
<i>cel5G</i>	1.43	0.45	0.42	0.06
<i>cel5H</i>	1.40	0.45	0.44	0.07
<i>cel45A</i>	1.50	0.47	0.45	0.06
<i>cel6A</i>	1.47	0.44	0.26	0.05
<i>cbp2B</i>	1.50	0.41	0.47	0.06
<i>cbp2C</i>	1.43	0.43	0.50	0.06
<i>cbp2D</i>	1.43	0.41	0.19	ND ³
<i>cbp2E</i>	1.47	0.41	0.19	0.01
<i>cbp32B</i>	1.47	0.39	0.44	0.07
<i>lpmo10A</i>	1.40	0.42	0.47	0.06
<i>lpmo10B</i>	1.50	0.44	0.55	0.07
<i>gspD</i>	1.50	0.42	0.04	ND ³

¹ Growth rate measured between 3-6 h of cell culture.

² Growth rate measured between 12-48 h of cell culture.

³ND= no detectable growth rate.

11

Table S1. Gene expression values for wild type *C. japonicus* take at either exponential or stationary phase of growth on either glucose or cellulose (Avicel) as the sole carbon source.

FUNCTION	Symbol	GENE_NAME	Avicel Stationary	Avicel Exponential	Glucose Stationary	Glucose Exponential
chromosomal replication initiation protein	dnaA	CJA_0001	9.8	9.8	9.9	12.2
DNA polymerase III subunit beta	dnaN	CJA_0002	9.6	9.6	9.7	12.0
recombination protein F	recF	CJA_0003	9.5	9.5	9.7	11.7
DNA gyrase, B subunit	gyrB	CJA_0004	9.7	9.6	10.1	12.3
hypothetical protein	-	CJA_0005	10.0	10.1	10.9	10.7
alpha-amylase, putative, amy13G	amy13G	CJA_0006	9.4	9.6	9.2	9.5
carbohydrate binding protein, cbp2A	cbp2A	CJA_0007	9.7	10.4	9.4	9.1
transcriptional regulatory protein	-	CJA_0008	9.3	9.4	9.5	9.1
ABC transporter nitrate-binding protein	nrtA	CJA_0009	9.9	9.9	9.8	9.1
possible nitrate transport system permease protein	-	CJA_0010	10.1	10.0	10.0	8.9
ABC transporter ATP-binding protein	nrtC	CJA_0011	9.7	9.9	9.9	9.2
cyanate hydratase	cynS	CJA_0012	9.9	9.8	9.9	9.6
hypothetical protein	-	CJA_0013	9.1	9.0	9.2	9.1
hypothetical protein	-	CJA_0014	9.1	9.1	9.2	10.3
transglutaminase-like superfamily protein	-	CJA_0015	8.9	8.9	9.0	9.9
Fibronectin type III domain protein	-	CJA_0016	9.8	9.3	9.7	11.2
Rhsfamily protein	-	CJA_0017	9.0	8.8	9.0	10.3
Rhs family protein	-	CJA_0018	9.1	8.9	9.6	10.8
hypothetical protein	-	CJA_0019	9.8	10.7	10.1	11.1
carbohydrate binding protein, putative, cbp35A	cbp35A	CJA_0020	9.3	9.2	9.9	11.5
hypothetical protein	-	CJA_0021	9.6	9.9	9.9	10.4
hypothetical protein	-	CJA_0022	9.3	9.4	9.5	10.3
transcriptional regulator, AsnC family	-	CJA_0023	9.2	9.1	9.2	9.6
2-isopropylmalate synthase	leuA	CJA_0024	9.0	8.9	9.2	11.7
catalase/peroxidase HPI	-	CJA_0025	10.3	10.6	10.9	9.3
hypothetical protein	-	CJA_0026	9.4	9.5	9.9	9.1
putative ABC transporter, permease protein	-	CJA_0027	9.8	9.8	10.1	10.0
putative ABC transporter, ATP-binding protein	-	CJA_0028	10.1	10.0	10.9	10.1
ABC transporter, ATP-binding protein	-	CJA_0029	10.7	10.3	12.0	10.7
efflux ABC transporter, permease protein	-	CJA_0030	10.0	9.7	11.2	10.0
putative ABC transporter, permease protein	-	CJA_0031	9.7	9.7	10.5	9.9
membrane fusion efflux protein	-	CJA_0032	10.0	9.4	11.6	10.9
putative lipoprotein	-	CJA_0033	9.7	10.0	10.7	9.9
hypothetical protein	-	CJA_0034	9.5	9.4	9.6	9.3
MltA-interacting protein MipA superfamily	-	CJA_0035	9.4	10.6	9.3	9.6
hypothetical protein	-	CJA_0036	9.0	9.4	9.1	9.2
response regulator (activator) in two-component regulatory system with RstB	rstA	CJA_0037	9.7	10.6	9.8	9.4

putative two-component regulatory system, sensor kinase protein	-	CJA_0038	9.8	9.9	10.2	9.2
putative TonB dependent receptor	-	CJA_0039	9.0	9.0	9.2	9.4
pectin methylesterase, putative, ce8	-	CJA_0040	9.2	9.4	9.3	9.6
pectin methylesterase, putative, pme8A	pme8A	CJA_0041	9.8	9.8	10.1	9.0
pectate lyase, putative, pel1D	pel1D	CJA_0042	9.3	9.7	9.2	8.8
pectin methylesterase, putative, ce8	-	CJA_0043	9.2	9.2	9.2	8.9
pectate lyase, putative, pel1C	pel1C	CJA_0044	9.2	9.6	9.3	8.9
pectate lyase, putative, pel1F	pel1F	CJA_0045	9.2	9.3	9.2	8.9
putative monovalent cation/H+ antiporter subunit A	-	CJA_0046	9.7	10.0	9.4	9.4
pH adaptation potassium efflux system C transmembrane protein	-	CJA_0047	9.5	9.6	9.6	9.4
putative monovalent cation/H+ antiporter subunit D	-	CJA_0048	9.2	9.3	9.2	9.3
PhaE protein	-	CJA_0049	10.5	10.9	11.1	9.9
putative monovalent cation/H+ antiporter subunit F	-	CJA_0050	11.6	12.2	11.9	10.2
pH adaptation potassium efflux system protein G	-	CJA_0051	10.6	11.9	10.5	9.4
cadmium translocating P-type ATPase	cadA-1	CJA_0052	9.3	9.3	9.1	9.1
pectate lyase, putative, pel1E	pel1E	CJA_0053	11.3	11.7	11.3	9.4
Uvs118	uvs118	CJA_0054	9.8	9.6	10.1	10.5
Uvs117	uvs117	CJA_0055	9.0	8.9	9.0	9.8
glycyl-tRNA synthetase, beta subunit	glyS	CJA_0056	10.5	10.0	10.9	12.7
glycyl-tRNA synthetase subunit alpha	glyQ	CJA_0057	9.8	9.9	9.8	11.8
Uvs112	uvs112	CJA_0058	12.4	11.3	14.6	12.2
hypothetical protein	-	CJA_0059	11.6	12.0	11.3	9.4
Uvs111	uvs111	CJA_0060	12.9	13.3	12.6	10.8
Uvs110	uvs110	CJA_0061	9.9	10.1	10.3	11.3
Gonadoliberin III-related protein	-	CJA_0062	9.8	10.2	9.6	10.4
alpha-L-glutamate ligase homolog	-	CJA_0063	9.6	9.7	9.4	10.4
putative OmpA-like transmembrane domain	-	CJA_0064	10.4	10.2	10.4	9.3
hypothetical protein	-	CJA_0065	9.3	9.4	9.3	8.9
glycosyl transferase, putative, gt4G	gt4G	CJA_0066	11.9	12.1	10.9	10.7
Cyclopropane-fatty-acyl-phospholipid synthase	-	CJA_0067	10.8	10.2	10.6	10.5
hypothetical protein	-	CJA_0068	10.7	10.6	10.3	10.7
peptidyl-prolyl cis-trans isomerase, FKBP-type	-	CJA_0069	12.3	12.6	12.9	11.8
conserved hypothetical protein TIGR00046	-	CJA_0070	11.6	10.8	11.9	11.1
putative lipoprotein	-	CJA_0071	11.5	11.6	13.0	12.1
hypothetical protein	-	CJA_0072	11.2	11.6	10.9	11.4
protein-glutamate methylesterase CheB	cheB	CJA_0073	11.9	12.8	10.5	10.5
type IV pili sensor histidine kinase/response regulator PilL	pilL	CJA_0074	10.6	10.8	10.3	10.8
type IV pili chemotactic methyltransferase PilK	pilK	CJA_0075	11.3	11.2	12.0	11.9
twitching motility protein PilJ	pilJ	CJA_0076	12.6	11.9	13.8	12.6
Protein pill	pill	CJA_0077	10.1	10.0	10.8	11.4

twitching motility protein PilH	pilH	CJA_0078	11.8	11.2	14.4	13.1
hypothetical protein	-	CJA_0079	11.6	11.4	13.7	12.7
twitching motility protein PilG - Pseudomonas aeruginosa	pilG	CJA_0080	11.7	11.1	13.1	12.6
glutathione synthase	gshB	CJA_0081	10.7	10.6	10.8	11.0
TonB family C-terminal domain protein	-	CJA_0082	12.0	11.9	12.0	10.4
Uncharacterized ACR	-	CJA_0083	10.7	10.9	10.8	10.8
conserved hypothetical protein TIGR00250	-	CJA_0084	10.5	10.1	11.1	10.5
Domain of unknown function (DUF1508) family	-	CJA_0085	10.3	10.0	11.6	11.1
twitching motility protein PilU	pilU	CJA_0086	12.1	11.3	13.2	12.0
twitching motility protein	pilT	CJA_0087	11.6	11.8	12.1	11.7
conserved hypothetical protein TIGR00044	-	CJA_0088	10.8	11.1	11.3	11.3
pyrroline-5-carboxylate reductase	proC	CJA_0089	10.4	10.5	10.8	11.4
YGGT family protein	-	CJA_0090	10.9	11.1	11.6	11.5
conserved hypothetical protein TIGR00251	-	CJA_0091	10.8	11.1	11.4	11.0
hypothetical protein	-	CJA_0092	9.8	9.9	9.7	10.0
Tetraacyldisaccharide-1-P 4-kinase	-	CJA_0093	13.8	14.1	13.0	12.6
Excinuclease ATPase subunit	-	CJA_0094	13.3	12.7	13.5	12.8
hypothetical protein	-	CJA_0095	10.2	9.8	10.0	10.4
hypothetical protein	-	CJA_0096	12.3	12.5	11.2	11.2
3-oxoacyl-(acyl carrier protein) synthase I	-	CJA_0097	10.6	10.9	10.0	10.6
acyltransferase	-	CJA_0098	9.7	9.6	9.5	9.6
AMP-ligase	pigH	CJA_0099	12.3	13.3	11.0	10.4
ketosynthase	-	CJA_0100	11.2	12.1	11.1	10.7
acyl carrier protein	acpC	CJA_0101	11.0	11.0	11.5	12.4
ubiquinone/menaquinone biosynthesis methyltransferase UbiE	-	CJA_0102	12.6	12.2	11.2	13.1
hypothetical protein	-	CJA_0103	11.6	10.7	12.3	9.4
FkbO protein	fkbO	CJA_0104	10.1	10.5	9.6	10.0
acyltransferase family protein	-	CJA_0105	10.5	11.1	10.1	9.7
hypothetical protein	-	CJA_0106	11.1	11.7	10.9	10.1
hypothetical protein	-	CJA_0107	11.4	11.9	11.7	12.0
acyl carrier protein	-	CJA_0108	9.5	9.2	10.9	12.1
AMP-binding enzyme family protein	-	CJA_0109	10.0	10.2	9.7	10.8
glycosyl transferase, putative, gt2J	gt2J	CJA_0110	9.5	9.7	9.4	10.0
4-hydroxybenzoyl-CoA thioesterase domain protein	-	CJA_0111	10.6	11.7	10.7	10.7
hypothetical protein	-	CJA_0112	12.0	12.8	12.0	10.2
hypothetical protein	-	CJA_0113	12.0	12.0	11.4	10.2
hypothetical protein	-	CJA_0114	10.0	10.2	10.3	10.1
hypothetical protein	-	CJA_0115	10.3	10.9	10.4	11.3
putative 3-oxoacyl-(acyl-carrier-protein) reductase	-	CJA_0116	10.1	10.2	9.7	11.2
3-oxoacyl-(acyl-carrier-protein) synthase II	fabF-2	CJA_0117	10.6	11.3	10.8	11.5

hypothetical protein	-	CJA_0118	12.2	11.9	13.9	12.9
homoserine O-acetyltransferase	metX	CJA_0119	10.8	10.7	10.9	11.1
methionine biosynthesis protein MetW	metW	CJA_0120	11.1	10.7	11.5	11.7
hypothetical protein	-	CJA_0121	10.6	10.4	10.9	10.9
non-canonical purine NTP pyrophosphatase, rdgB/HAM1 family	rdgB	CJA_0122	9.1	9.2	9.1	9.6
putative oxygen-independent coproporphyrinogen III oxidase	-	CJA_0123	10.7	10.1	10.4	10.4
hypothetical protein	-	CJA_0124	10.2	10.4	11.3	10.0
ATP-dependent DNA helicase RecQ	recQ	CJA_0125	10.8	11.4	11.2	10.7
hypothetical protein	-	CJA_0126	10.2	10.3	10.6	10.3
RHS Repeat family	-	CJA_0127	11.8	10.8	13.9	12.1
Integrase core domain protein	-	CJA_0128	10.0	9.9	11.0	10.9
cytoplasmic membrane protein	-	CJA_0129	12.8	12.6	13.0	11.2
IS66 family element, Orf1 protein	-	CJA_0130	15.3	15.1	14.7	10.9
IS66 family element, Orf2 protein	-	CJA_0131	14.0	12.1	13.7	9.7
IS66 family element, transposase	-	CJA_0132	13.9	12.8	14.1	11.3
Rhs family protein	-	CJA_0133	9.5	9.7	10.2	9.7
Rhs family protein	-	CJA_0134	10.5	10.1	12.2	10.4
hypothetical protein	-	CJA_0135	9.3	9.2	9.6	9.4
phospholipase/carboxylesterase	-	CJA_0136	12.5	11.8	12.4	12.0
Peptidase propeptide and YPEB domain protein	-	CJA_0137	9.7	10.4	10.2	9.8
Peptidase propeptide and YPEB domain protein	-	CJA_0138	9.9	10.7	10.4	9.9
DNA-binding response regulator	-	CJA_0139	10.6	10.6	10.6	10.0
sensor histidine kinase	-	CJA_0140	9.4	9.7	9.3	9.1
ABC transporter, ATP-binding protein	-	CJA_0141	9.7	10.1	9.7	9.3
metallo-beta-lactamase superfamily domain protein	-	CJA_0142	11.1	11.6	11.5	9.8
drug resistance transporter, Bcr/CflA subfamily	-	CJA_0143	10.6	10.7	10.9	9.8
probable partition-related protein	-	CJA_0144	10.3	10.5	11.2	10.1
hypothetical protein	-	CJA_0145	11.1	10.5	11.9	10.7
hypothetical protein	-	CJA_0146	11.3	11.1	13.2	11.9
hypothetical protein	-	CJA_0147	9.3	9.2	10.1	9.5
hypothetical protein	-	CJA_0148	9.7	9.9	10.6	10.0
phosphate regulon sensor protein PhoR	-	CJA_0149	11.0	11.2	11.9	10.0
phosphate regulon transcriptional regulatory protein PhoB	phoB	CJA_0150	9.8	10.0	10.3	10.0
4-hydroxybenzoate polyprenyl transferase	ubiA	CJA_0151	10.5	11.4	10.3	9.9
chorismate--pyruvate lyase	ubiC	CJA_0152	9.9	10.1	10.0	9.6
DNA-binding protein HU	hup	CJA_0153	9.4	9.2	9.5	11.0
proton/glutamate symporter	-	CJA_0154	10.9	10.9	11.1	11.5
hypothetical protein	-	CJA_0155	10.5	10.9	11.2	9.6
imidazoleglycerol-phosphate dehydratase	hisB	CJA_0156	10.2	11.7	10.6	12.4
imidazole glycerol phosphate synthase, glutamine amidotransferase subunit	hisH	CJA_0157	11.8	12.0	11.5	13.0

1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole	hisA	CJA_0158	10.6	11.1	10.1	12.4
imidazole glycerol phosphate synthase subunit HisF	hisF	CJA_0159	11.0	10.8	10.6	11.1
hypothetical protein	-	CJA_0160	9.7	9.3	10.4	11.4
macrophage infectivity potentiator	-	CJA_0161	10.3	9.0	10.7	13.2
anti-RNA polymerase sigma 70 factor	algQ	CJA_0162	11.2	9.9	11.9	12.6
protein-disulfide reductase	dsbH	CJA_0163	11.1	10.6	10.3	11.6
glutamate--cysteine ligase	gshA	CJA_0164	9.6	9.8	9.8	10.3
Flagellar basal body-associated protein FlIL	-	CJA_0165	11.1	10.6	11.1	10.2
hypothetical protein	-	CJA_0166	9.6	10.1	10.1	11.0
transporter, small conductance mechanosensitive ion channel (MscS) family	-	CJA_0167	11.9	11.6	12.5	12.4
gluconate 5-dehydrogenase	-	CJA_0168	10.2	10.0	10.1	9.5
5-keto-4-deoxyurionate isomerase	-	CJA_0169	11.3	11.3	11.2	10.8
unsaturated rhamnogalacturonyl hydrolase, putative, urh105A	urh105A	CJA_0170	10.7	10.9	11.3	9.7
TonB-dependent receptor	-	CJA_0171	9.9	9.8	10.1	9.8
polygalacturonase, putative, pga28A	pga28A	CJA_0172	10.9	11.3	11.1	9.4
hypothetical protein	-	CJA_0173	9.0	8.9	9.1	8.8
dehydratase	-	CJA_0174	10.2	10.7	10.6	9.2
proton-translocating nicotinamide nucleotide transhydrogenase subunit PntA	-	CJA_0175	10.9	11.2	10.7	9.4
NAD(P) transhydrogenase, alpha subunit	pntA	CJA_0176	10.9	10.4	11.2	9.3
proton-translocating nicotinamide nucleotide transhydrogenase subunit PntB	-	CJA_0177	11.5	11.1	10.9	9.4
glyoxylase family protein	-	CJA_0178	9.7	9.7	10.3	9.3
ketodeoxygluconokinase	kdgK	CJA_0179	10.0	10.1	9.9	10.5
D-mannonate oxidoreductase	-	CJA_0180	11.3	11.1	11.3	10.2
pectin methylesterase, putative, pme8C	pme8C	CJA_0181	11.2	11.0	12.0	9.2
putative methyl-accepting chemotaxis protein	-	CJA_0182	10.4	10.2	10.8	9.1
fructose-1,6-bisphosphatase	fbp	CJA_0183	9.9	9.5	9.7	9.3
fructose-bisphosphate aldolase	fbaA	CJA_0184	10.6	10.8	10.3	9.5
triosephosphate isomerase	-	CJA_0185	10.7	11.2	9.9	10.1
hypothetical protein	-	CJA_0186	10.4	10.0	11.3	10.4
putative GGDEF domain protein	-	CJA_0187	11.2	11.3	10.6	9.4
hypothetical protein	-	CJA_0188	9.8	10.8	9.7	9.1
hypothetical protein	-	CJA_0189	11.4	11.7	11.9	9.7
response regulator	-	CJA_0190	10.3	10.0	10.2	9.5
hypothetical protein	-	CJA_0191	11.4	11.4	11.1	11.3
hypothetical protein	-	CJA_0192	10.3	11.1	10.3	11.3
hypothetical protein	-	CJA_0193	9.1	9.1	9.2	10.3
Peptidase family M48 family	-	CJA_0194	11.0	11.7	11.5	11.3
TRAP transporter, DctQ-like membrane protein family	-	CJA_0195	11.5	13.5	10.1	9.8
TRAP transporter, DctM subunit	-	CJA_0196	11.3	11.7	10.8	9.4
acyl-CoA hydrolase	-	CJA_0197	9.5	9.7	9.4	9.0

Cytochrome b561 homolog 2	-	CJA_0198	10.0	10.3	10.0	10.4
ycel-like protein, ycel3	ycel3	CJA_0199	10.6	9.8	13.1	12.1
hypothetical protein	-	CJA_0200	9.1	9.1	9.2	9.8
hypothetical protein	-	CJA_0201	9.8	9.4	9.9	10.0
hypothetical protein	-	CJA_0202	10.7	11.4	10.7	11.4
ribonuclease PH	rph	CJA_0203	9.4	9.4	9.3	11.2
glucan 1,4-beta-glucosidase cel3A	cel3A	CJA_0204	12.1	12.4	11.5	12.0
5,10-methylenetetrahydrofolate reductase	metF	CJA_0205	9.2	9.2	9.1	11.8
S-adenosyl-L-homocysteine hydrolase	ahcY	CJA_0206	10.0	9.8	9.8	12.8
S-adenosylmethionine synthetase	metK	CJA_0207	10.1	10.1	9.6	12.0
transcriptional regulator, ArsR family	-	CJA_0208	11.1	10.9	10.3	10.9
hypothetical protein	-	CJA_0209	11.1	10.4	10.9	12.7
transketolase	tkt	CJA_0210	11.0	10.9	9.9	12.2
phosphoglycerate kinase	pgk	CJA_0211	11.5	10.9	11.2	13.0
pectate lyase, putative, pel3A	pel3A	CJA_0212	11.5	11.8	11.0	9.1
hypothetical protein	-	CJA_0213	12.3	12.2	11.9	9.2
glucan endo-1,3-beta-glucanase, putative, glu81A	glu81A	CJA_0214	9.4	10.0	9.2	8.9
TonB-dependent receptor	-	CJA_0215	9.8	10.3	9.3	8.9
hypothetical protein	-	CJA_0216	10.4	10.7	10.1	9.1
Pass1-related protein	-	CJA_0217	10.4	10.6	10.1	9.1
tryptophan halogenase	-	CJA_0218	10.7	11.2	10.8	9.4
hypothetical protein	-	CJA_0219	11.6	12.4	11.0	9.2
hypothetical protein	-	CJA_0220	11.4	13.1	9.7	9.0
hypothetical protein	-	CJA_0221	10.9	10.3	11.1	9.2
hypothetical protein	-	CJA_0222	9.5	9.9	9.1	8.9
glucan 1,4-beta-glucosidase, putative, cel3C	cel3C	CJA_0223	11.2	11.6	10.2	9.0
beta glucanase, putative, glu16B	glu16B	CJA_0224	10.2	10.4	9.8	8.9
beta glucanase, putative, glu16A	glu16A	CJA_0225	11.1	10.8	10.1	9.1
FAD binding domain protein	-	CJA_0226	10.3	10.2	10.2	9.1
hypothetical protein	-	CJA_0227	11.0	11.3	11.0	9.5
hypothetical protein	-	CJA_0228	9.9	10.0	9.7	9.1
transcriptional regulator, AraC family	-	CJA_0229	11.3	11.4	11.5	11.1
hydrolase, alpha/beta fold family	-	CJA_0230	9.9	10.8	9.6	9.8
Predicted membrane protein	-	CJA_0231	9.8	9.8	9.8	11.4
D-3-phosphoglycerate dehydrogenase	-	CJA_0232	10.5	10.7	9.9	12.4
putative transmembrane efflux protein	-	CJA_0233	10.1	10.3	10.1	9.6
putative lipoprotein	-	CJA_0234	10.8	11.0	10.7	11.9
hypothetical protein	-	CJA_0235	10.8	11.0	10.0	10.6
endo-1, 4-beta mannanase, putative, man26C	man26C	CJA_0236	10.5	10.9	10.4	10.0
PEP-CTERM putative exosortase interaction domain protein	-	CJA_0237	10.6	11.1	10.5	9.8

ribose 5-phosphate isomerase A	rpiA	CJA_0238	9.3	9.4	9.2	10.0
threonine ammonia-lyase, biosynthetic	ilvA	CJA_0239	9.5	9.2	9.2	11.3
Transcriptional regulator	-	CJA_0240	9.7	10.9	9.7	10.3
Na ⁺ /glucose symporter	-	CJA_0241	11.2	12.0	11.1	10.4
hypothetical protein	unk1	CJA_0242	9.2	9.5	9.1	10.2
Unk2	unk2	CJA_0243	10.0	10.3	9.8	10.4
putative 1,4-beta mannosidase man5D	man5D	CJA_0244	9.8	9.7	9.4	9.7
hypothetical protein	-	CJA_0245	8.9	8.9	9.1	8.9
putative alpha-galactosidase, aga27A	aga27A	CJA_0246	9.5	9.6	9.3	9.4
peptidoglycan lytic transglycosylase, putative, plt103B	plt103B	CJA_0247	9.2	9.2	9.3	10.2
Modulator of Rho-dependent transcription termination (ROF) superfamily	-	CJA_0248	10.8	12.2	11.1	10.2
alginate biosynthesis regulatory protein AlgR	algR	CJA_0249	9.6	10.0	9.5	9.7
AlgZ	algZ	CJA_0250	9.7	10.0	9.6	9.6
argininosuccinate lyase	argH	CJA_0251	9.4	9.2	9.5	11.6
hypothetical protein	-	CJA_0252	10.0	9.3	11.7	12.1
Response regulator receiver domain protein	-	CJA_0253	9.2	9.1	9.5	10.1
adenylate cyclase	cyaA	CJA_0254	9.0	9.1	9.0	9.0
ISCja2, transposase	-	CJA_0255	15.3	14.5	15.1	11.5
putative adenylate cyclase	-	CJA_0256	9.5	9.7	9.6	9.2
alpha glucosidase, putative, glc13A	glc13A	CJA_0257	8.8	8.8	8.9	9.1
hypothetical protein	-	CJA_0258	8.8	8.8	8.9	9.1
efflux ABC transporter, permease protein	-	CJA_0259	8.8	8.8	8.8	8.8
ABC transporter, ATP-binding subunit	phnL	CJA_0260	8.8	8.7	8.8	8.8
putative ABC transporter permease	-	CJA_0261	8.8	8.8	8.8	8.9
ABC transporter, ATP-binding protein	-	CJA_0262	8.8	8.8	8.8	8.9
hypothetical protein	-	CJA_0263	8.8	8.8	8.9	9.2
hypothetical protein	-	CJA_0264	8.8	8.8	8.8	8.9
ISCja1, transposase orfA	-	CJA_0265	14.1	13.8	13.7	11.7
ISCja1, transposase orfB	-	CJA_0266	10.0	9.9	10.5	10.0
radical SAM domain protein protein	-	CJA_0267	8.9	8.9	8.9	8.9
hypothetical protein	-	CJA_0268	8.8	8.8	8.8	8.9
adenylate cyclase	-	CJA_0269	8.8	8.8	8.8	8.8
hypothetical protein	-	CJA_0270	9.1	9.0	9.3	9.6
hypothetical protein	-	CJA_0271	9.1	9.0	9.2	9.7
rhamnosyltransferase, putative, gt1B	gt1B	CJA_0272	9.1	9.1	9.2	9.4
peptidase, rhomboid family	-	CJA_0273	8.9	8.8	8.9	8.9
putative toxin secretion ABC transporter, ATP-binding subunit/permease prot	-	CJA_0274	9.4	9.1	9.5	9.1
putative toxin secretion, membrane fusion protein	-	CJA_0275	9.0	9.1	9.0	9.0
carbohydrate binding protein, putative, cbp6B	cbp6B	CJA_0276	9.2	9.3	9.1	8.9
hypothetical protein	-	CJA_0277	9.0	9.1	9.0	9.1

putative sensory box histidine kinase	-	CJA_0278	9.8	9.9	9.8	10.4
hypothetical protein	-	CJA_0279	9.9	10.3	9.3	9.6
transcriptional regulator, LacI family	cebR	CJA_0280	9.0	9.2	9.2	9.7
major facilitator family transporter	-	CJA_0281	10.2	11.0	9.7	9.1
hypothetical protein	-	CJA_0282	8.8	8.8	8.8	8.8
TonB-dependent receptor	-	CJA_0283	9.1	9.1	9.2	10.2
trehalase, putative, tre37A	tre37A	CJA_0284	9.5	10.0	9.5	9.9
hypothetical protein	-	CJA_0285	9.0	8.9	8.9	9.3
CbbY	cbbY	CJA_0286	9.4	9.3	9.3	9.8
beta-hexaminidase, putative, hex20B	hex20B	CJA_0287	11.1	11.2	10.3	9.4
hypothetical protein	-	CJA_0288	9.7	9.5	10.7	10.6
5-formyltetrahydrofolate cyclo-ligase family protein	-	CJA_0289	9.6	9.4	9.3	9.8
hypothetical protein	-	CJA_0290	11.5	11.1	12.3	11.0
Family of unknown function (DUF710) superfamily	-	CJA_0291	9.9	9.6	10.0	11.2
putative conserved hypothetical protein TIGR02449	-	CJA_0292	8.9	8.9	9.0	10.0
yecA family protein	-	CJA_0293	10.4	10.1	10.5	11.6
aminopeptidase P II	pepP	CJA_0294	10.9	11.0	10.7	11.9
2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	ubiF	CJA_0295	10.5	10.8	9.3	10.9
Uncharacterized membrane protein	-	CJA_0296	10.4	10.7	10.5	9.8
hypothetical protein	-	CJA_0297	9.0	8.9	9.0	9.6
cold-shock domain family protein	-	CJA_0298	9.9	9.8	10.8	11.5
hypothetical protein	-	CJA_0299	10.5	11.0	10.5	10.8
acetyltransferase, GNAT family	-	CJA_0300	10.3	11.0	9.8	10.4
hydrolase, NUDIX family	-	CJA_0301	9.7	9.4	9.8	10.5
hypothetical protein	-	CJA_0302	9.5	9.4	9.5	10.1
hypothetical protein	-	CJA_0303	10.7	11.7	10.7	10.5
putative secreted protein	-	CJA_0304	10.6	11.7	10.2	10.6
hypothetical protein	-	CJA_0305	10.8	12.2	9.7	10.0
DbpA RNA binding domain family	-	CJA_0306	12.4	12.5	12.0	11.7
heat shock protein HSP33	hslO	CJA_0307	9.6	9.5	9.5	10.0
hypothetical protein	-	CJA_0308	10.6	10.4	10.3	10.8
heat shock protein 15	hslR	CJA_0309	9.8	9.8	9.9	10.6
HAD-superfamily hydrolase, subfamily IA, variant 3	-	CJA_0310	10.6	10.9	10.5	11.0
ADP-ribose diphosphatase NudE	nudE	CJA_0311	10.3	10.3	10.9	11.1
3'(2'),5'-bisphosphate nucleotidase	cysQ	CJA_0312	11.4	11.7	10.9	10.9
hypothetical protein	-	CJA_0313	9.1	9.0	9.5	9.1
sensory box protein	-	CJA_0314	10.6	10.3	10.3	9.1
hypothetical protein	-	CJA_0315	9.2	9.4	9.1	9.0
molybdate ABC transporter, periplasmic molybdate-binding protein	modA	CJA_0316	10.2	10.2	10.4	10.0
molybdate ABC transporter, permease protein	modB	CJA_0317	10.1	10.4	10.4	9.6

ModC	modC	CJA_0318	9.6	10.4	9.3	9.2
MopB-like protein	modE	CJA_0319	9.5	9.3	9.3	9.4
molybdopterin biosynthetic protein B1	moaB1	CJA_0320	9.3	9.2	9.3	9.6
Molybdenum cofactor biosynthesis protein A	moaA	CJA_0321	10.0	9.9	10.8	10.1
hypothetical protein	-	CJA_0322	8.9	8.8	8.9	8.8
uroporphyrin-III C-methyltransferase	-	CJA_0323	10.9	11.0	14.7	9.0
nitrite reductase [NAD(P)H], large subunit	nirB	CJA_0324	11.0	11.7	14.8	9.1
nitrite reductase [NAD(P)H], small subunit	nirD	CJA_0325	9.5	9.4	11.1	8.8
diguanylate cyclase (GGDEF) domain protein	-	CJA_0326	9.6	9.6	9.5	9.0
cytosine deaminase	-	CJA_0327	11.7	12.5	12.2	9.8
Response regulator receiver domain protein	-	CJA_0328	11.1	12.4	10.3	9.8
putative dual serine/threonine-protein kinase/phosphatase	-	CJA_0329	9.5	9.9	10.0	9.0
nitrate permease	-	CJA_0330	10.2	10.7	13.0	9.0
hypothetical protein	-	CJA_0331	9.2	9.1	9.5	8.8
hypothetical protein	-	CJA_0332	9.8	9.9	9.3	9.1
IS5 family transposase, orfA	-	CJA_0333	10.0	10.2	10.5	10.6
IS3 family transposase, orfA	-	CJA_0334	9.4	9.4	9.6	10.1
IS3 family transposase, orfB	-	CJA_0335	10.8	10.7	10.7	10.1
IS66 family element, transposase	-	CJA_0336	10.4	10.4	12.3	10.1
IS66 family element, Orf2 protein	-	CJA_0337	13.4	12.1	13.7	9.7
IS66 family element, Orf1 protein	-	CJA_0338	10.7	10.3	11.1	9.2
hypothetical protein	-	CJA_0339	9.1	9.0	9.1	9.0
hypothetical protein	-	CJA_0340	8.9	8.9	9.0	9.0
Rhs family protein	-	CJA_0341	9.9	9.6	10.8	9.5
hypothetical protein	-	CJA_0342	9.0	8.9	9.2	9.1
RHS Repeat family	-	CJA_0343	9.0	9.0	9.1	8.9
gluconolactonase precursor	-	CJA_0344	10.0	10.4	10.3	9.7
D-serine deaminase	dsd	CJA_0345	10.0	10.4	9.9	9.3
gluconate permease	-	CJA_0346	9.8	10.3	9.6	9.2
transcriptional regulator, RpiR family	-	CJA_0347	9.7	9.7	10.1	9.5
N-acyl-D-amino acid deacylase family protein	ndeD	CJA_0348	9.5	9.8	9.3	9.5
Endoribonuclease L-PSP superfamily	-	CJA_0349	11.7	11.7	12.1	10.1
N-acetyl-beta-hexosaminidase, putative, hex20A	hex20A	CJA_0350	9.4	9.5	9.7	9.1
hypothetical protein	-	CJA_0351	8.9	9.0	9.0	8.8
transcriptional regulator, AraC family domain protein	-	CJA_0352	9.8	9.6	10.3	8.9
TonB-dependent receptor	-	CJA_0353	10.1	10.3	10.2	9.8
tryptophan halogenase	-	CJA_0354	10.1	9.9	10.9	9.6
Pass1-related protein	-	CJA_0355	9.7	9.6	10.7	9.3
tryptophan halogenase	-	CJA_0356	9.5	9.4	9.9	9.3
glucosyltransferase MdoH	gt2K	CJA_0357	10.8	10.6	10.3	9.6

glucan biosynthesis protein D	mdoD	CJA_0358	10.1	10.2	10.2	10.4
MmoS	mmoS	CJA_0359	10.3	10.5	10.1	9.6
thioredoxin	trx	CJA_0360	12.3	11.4	13.0	13.3
transcription termination factor Rho	rho	CJA_0361	10.2	10.3	10.0	12.6
3-octaprenyl-4-hydroxybenzoate carboxy-lyase	ubiD	CJA_0362	10.5	10.5	10.1	10.8
hypothetical protein	-	CJA_0363	11.7	12.3	12.0	10.4
serine acetyltransferase	-	CJA_0364	10.5	10.9	10.5	10.9
hypothetical protein	-	CJA_0365	8.9	8.9	8.9	9.6
hypothetical protein	-	CJA_0366	9.3	9.2	9.9	9.8
serine/threonine protein kinase	-	CJA_0367	9.7	10.2	9.6	9.9
ATPase, ParA family	-	CJA_0368	11.5	11.0	11.9	10.1
hypothetical protein	-	CJA_0369	12.5	12.6	13.9	12.8
Fic family protein	-	CJA_0370	11.7	11.7	12.5	11.3
RND efflux transporter, permease protein	-	CJA_0371	10.4	10.8	10.0	9.9
RND transporter, Hydrophobe/Amphiphile Efflux family	-	CJA_0372	10.2	11.1	10.1	10.1
HlyD family secretion protein	-	CJA_0373	11.6	11.6	11.4	10.5
cellulase, putative, cel45A	cel45A	CJA_0374	12.0	11.8	10.5	9.7
AhpC	ahpC	CJA_0375	11.8	11.1	11.0	10.2
AhpF	ahpF	CJA_0376	10.4	10.4	10.2	9.4
beta-1, 4-galactosyltransferase, putative, gt2a	-	CJA_0377	10.3	10.0	11.8	9.0
Alpha/Beta hydrolase family of unknown function (DUF1234) family	-	CJA_0378	10.7	10.2	11.9	9.2
probable homoserine/homoserine lactone efflux protein	-	CJA_0379	10.9	11.8	10.9	9.2
hypothetical protein	-	CJA_0380	10.8	10.0	11.4	9.5
hypothetical protein	-	CJA_0381	11.1	10.8	10.6	9.0
hypothetical protein	-	CJA_0382	9.1	9.3	9.2	8.8
putative lipoprotein	-	CJA_0383	11.5	11.7	11.2	9.2
pectate lyase, putative, pel10C	pel10C	CJA_0384	11.7	11.4	12.7	10.7
3-methyl-2-oxobutanoate hydroxymethyltransferase	panB	CJA_0385	11.9	12.1	11.8	12.1
predicted deoxypurine kinase	-	CJA_0386	10.7	10.6	10.9	10.9
2-amino-4-hydroxy-6- hydroxymethylidihydropteridine pyrophosphokinase	folK	CJA_0387	10.0	10.8	9.8	10.8
polynucleotide adenyltransferase	pcnB	CJA_0388	11.7	11.7	11.1	11.5
galR two-component system response regulator	-	CJA_0389	10.9	11.1	12.2	11.9
galS His Kinase A (phosphoacceptor) domain	galS	CJA_0390	10.9	11.3	10.4	9.7
hypothetical protein	-	CJA_0391	12.3	12.3	12.8	11.9
glutamyl- and glutaminyl-tRNA synthetase	-	CJA_0392	10.0	10.5	9.8	9.9
DnaK suppressor protein	-	CJA_0393	9.5	9.5	9.2	12.0
Permeases of the drug/metabolite transporter (DMT) superfamily	-	CJA_0394	11.7	12.9	11.7	10.5
sugar fermentation stimulation protein A	sfsA	CJA_0395	11.6	11.8	10.8	10.5
putative lipoprotein	-	CJA_0396	11.0	12.3	10.8	10.7
undecaprenyl-diphosphatase UppP	uppP	CJA_0397	11.5	12.1	12.5	10.9

alpha amylase, putative, amy13F	amy13F	CJA_0398	10.9	10.9	10.4	9.1
hypothetical protein	-	CJA_0399	10.3	9.5	11.2	12.9
cytochrome b561 family protein	-	CJA_0400	11.8	10.9	12.3	13.1
hypothetical protein	-	CJA_0401	10.9	11.0	10.6	10.9
hypothetical protein	-	CJA_0402	12.8	12.6	13.4	13.1
hypothetical protein	-	CJA_0403	8.8	8.8	8.8	8.8
ATP-dependent protease ATP-binding subunit HslU	hslU	CJA_0404	11.2	11.0	11.0	12.8
ATP-dependent protease peptidase subunit	-	CJA_0405	10.1	10.1	10.2	12.5
Sporulation related repeat family	-	CJA_0406	12.1	13.0	11.2	11.0
primosomal protein N'	priA	CJA_0407	10.1	10.1	9.9	9.6
High potential iron-sulfur protein (HiPIP)	hip	CJA_0408	10.0	10.2	9.9	9.2
50S ribosomal subunit protein L31	rpmE	CJA_0409	9.7	9.2	9.7	12.8
staphylococcal nuclease homolog	-	CJA_0410	10.2	10.1	9.9	11.0
murein polymerase, putative, gt51D	gt51D	CJA_0411	10.2	10.6	10.1	10.4
type IV pilus assembly protein PilM	pilM	CJA_0412	11.2	11.3	12.6	12.3
type 4 fimbrial biogenesis protein PilN	pilN	CJA_0413	9.8	9.2	10.3	11.3
pilO	pilO	CJA_0414	10.1	9.8	11.3	11.5
type IV pilus biogenesis protein PilP	pilP	CJA_0415	10.5	10.4	12.0	11.8
fimbrial assembly protein PilQ	-	CJA_0416	10.4	10.2	12.2	12.3
shikimate kinase	-	CJA_0417	11.8	11.1	12.9	11.9
3-dehydroquinate synthase	aroB	CJA_0418	10.9	10.9	11.5	12.2
hypothetical protein	-	CJA_0419	10.7	11.6	10.1	10.6
glycine cleavage system protein H	gcvH	CJA_0420	9.8	9.6	9.8	11.5
glycine cleavage system aminomethyltransferase T	gcvT	CJA_0421	10.7	10.4	10.0	12.5
YbcL	-	CJA_0422	10.1	10.1	10.9	10.6
hypothetical protein	-	CJA_0423	10.6	10.4	10.5	10.9
trypsin domain protein	-	CJA_0424	13.2	12.9	12.8	12.0
competence protein ComF	-	CJA_0425	10.8	11.2	10.3	9.2
biotin synthase	bioB	CJA_0426	10.9	10.8	11.4	12.2
8-amino-7-oxononanoate synthase	bioF	CJA_0427	10.4	10.0	10.0	10.9
biotin biosynthesis protein BioC	bioC	CJA_0428	9.6	9.6	9.4	10.2
dethiobiotin synthase	bioD	CJA_0429	9.4	9.3	9.3	10.1
putative lipoprotein	-	CJA_0430	10.2	9.9	10.1	10.0
Domain of unknown function (DUF1078) family	-	CJA_0431	8.9	8.8	9.0	9.5
srpA-related protein	-	CJA_0432	10.7	10.2	11.5	10.2
Uncharacterized BCR, YhbC family	-	CJA_0434	11.7	12.1	12.3	13.2
transcription elongation factor NusA	nusA	CJA_0435	11.1	10.4	11.1	13.9
translation initiation factor IF-2	infB	CJA_0436	10.5	10.2	10.0	13.2
ribosome-binding factor A	rbfA	CJA_0437	10.0	9.9	9.5	12.7
tRNA pseudouridine synthase B	truB	CJA_0438	11.8	12.1	10.9	12.9

ribosomal protein S15	rpsO	CJA_0439	11.0	9.5	12.9	13.6
polynucleotide phosphorylase/polyadenylase	-	CJA_0440	12.0	11.1	10.8	13.9
hypothetical protein	-	CJA_0441	10.0	9.6	10.4	10.1
AmpG protein, beta-lactamase induction signal transducer	-	CJA_0442	12.6	11.9	12.2	13.1
inorganic pyrophosphatase	ppa	CJA_0443	13.9	12.5	13.5	14.6
FHA domain protein	-	CJA_0444	12.5	12.7	11.8	11.7
Selenoprotein W-related family	-	CJA_0445	11.0	11.4	11.2	10.3
hypothetical protein	-	CJA_0446	11.3	10.9	12.0	11.1
hypothetical protein	-	CJA_0448	13.4	13.6	11.7	10.4
hypothetical protein	-	CJA_0449	12.1	12.2	11.8	10.3
xylan esterase, putative, axe2C	axe2C	CJA_0450	10.8	10.6	11.5	10.3
mucin-desulfating sulfatase (N-acetylglucosamine-6-sulfatase)	-	CJA_0451	11.6	11.9	11.5	10.4
DNA polymerase III subunit delta	holA	CJA_0452	9.8	9.6	9.7	10.3
putative rare lipoprotein B precursor	-	CJA_0453	11.5	11.3	11.5	12.8
leucyl-tRNA synthetase	leuS	CJA_0454	10.8	10.9	10.8	12.9
hypothetical protein	-	CJA_0455	11.2	12.0	14.3	10.2
endo-1,4-beta-xylanase B	-	CJA_0456	12.6	13.2	13.3	11.2
aqualysin precursor	aql	CJA_0457	10.5	11.1	10.4	9.3
ribosomal protein L21	rplU	CJA_0458	11.2	9.8	10.8	14.2
50S ribosomal protein L27	rpmA	CJA_0459	9.1	9.0	9.5	12.2
GTPase ObgE	obgE	CJA_0460	11.4	11.1	11.9	13.0
gamma-glutamyl kinase	proB	CJA_0461	11.7	12.0	12.4	12.6
hypothetical protein	-	CJA_0462	11.4	10.6	12.7	12.5
putative lipoprotein	-	CJA_0463	9.9	10.1	10.5	11.8
HAD-superfamily subfamily IB hydrolase, TIGR01490	-	CJA_0464	11.7	11.6	11.8	12.2
hydrolase, NUDIX family	-	CJA_0465	12.2	11.6	12.9	12.6
phosphoenolpyruvate-protein phosphotransferase PtsP	-	CJA_0466	10.4	10.1	10.6	11.8
prolipoprotein diacylglycerol transferase	lgt	CJA_0467	11.3	10.9	12.2	11.8
thymidylate synthase	thyA	CJA_0468	10.6	10.2	12.2	12.6
dihydrofolate reductase	folA	CJA_0469	10.7	10.3	11.1	13.6
hypothetical protein	-	CJA_0470	9.4	8.9	10.8	14.1
hypothetical protein	-	CJA_0471	12.9	9.3	13.5	14.9
MotA/TolQ/ExbB proton channel family protein	-	CJA_0472	14.3	10.6	13.8	15.3
TonB system transport protein ExbB2	-	CJA_0473	13.7	11.4	13.3	15.1
TonB system transport protein ExbD2	-	CJA_0474	12.8	10.0	11.3	14.7
putative tonB2 protein	-	CJA_0475	11.1	9.7	11.2	14.3
TPR domain protein	-	CJA_0476	10.5	9.6	11.7	14.1
dihydroxy-acid dehydratase	ilvD	CJA_0477	10.6	10.4	10.9	12.6
acetyltransferase, GNAT family	-	CJA_0478	10.7	10.6	11.4	10.5
N-acetylglutamate synthase	argA	CJA_0479	10.3	10.2	10.8	11.2

acetylnithine deacetylase	argE	CJA_0480	11.6	11.9	11.3	11.1
pho4 family protein	-	CJA_0481	10.1	10.6	10.2	11.8
conserved hypothetical protein TIGR00153	-	CJA_0482	9.4	9.3	9.3	11.5
type IV pilus biogenesis protein	-	CJA_0483	10.7	11.4	10.2	10.5
putative glutathione S-transferase	-	CJA_0484	10.8	11.7	10.4	10.3
twin arginine-targeting protein translocase, TatA/E family	-	CJA_0485	9.2	9.1	9.1	9.1
PEP-CTERM putative exosortase interaction domain protein	-	CJA_0486	10.4	10.3	9.4	9.1
Tat (twin-arginine translocation) pathway signal sequence domain protein	-	CJA_0487	9.9	10.0	9.5	9.0
Sec-independent protein translocase TatC	-	CJA_0488	11.0	10.4	11.0	10.0
TatB	-	CJA_0489	9.7	9.7	9.8	9.5
hypothetical protein	-	CJA_0490	10.8	10.4	11.2	9.8
arabinogalactan endo-1,4-beta-galactosidase, putative, gal53A	gal53A-1	CJA_0491	9.7	9.5	9.6	8.9
arabinogalactan endo-1,4-beta-galactosidase, putative, gal53B	gal53B	CJA_0492	10.8	10.7	12.0	9.2
hypothetical protein	-	CJA_0493	10.4	10.1	12.9	9.1
carbohydrate binding protein, cbp35C	cbp35C	CJA_0494	11.2	11.4	11.4	9.3
hypothetical protein	-	CJA_0495	10.6	10.3	11.4	9.7
beta-galactosidase, putative, bgl2A	bgl2A	CJA_0496	10.0	10.7	9.6	9.3
Arabinogalactan endo-1,4-beta-galactosidase gal53A	gal53A-2	CJA_0497	10.9	11.6	11.4	9.2
putative TonB-dependent receptor	-	CJA_0498	12.4	12.9	12.1	9.6
hypothetical protein	-	CJA_0499	9.4	9.1	10.4	9.2
glutamate-ammonia-ligase adenyllyltransferase	glnE	CJA_0500	10.9	10.4	10.5	11.2
branched-chain amino acid aminotransferase	ilvE	CJA_0501	11.4	11.3	10.5	12.7
glycosyl transferase, putative, gt9A	gt9A	CJA_0502	11.3	12.2	10.4	11.6
lipopolysaccharide core biosynthesis protein WaaP	waaP	CJA_0503	9.3	9.4	9.1	9.9
glycosyl transferase, putative, gt4E	gt4E	CJA_0504	9.2	9.2	9.1	9.7
O-antigen polymerase family protein	-	CJA_0505	13.8	14.2	13.1	11.7
glycosyl transferase, putative, gt4D	gt4D	CJA_0506	9.7	9.6	9.4	10.1
hypothetical protein	-	CJA_0507	10.3	10.8	10.0	9.9
lipid A export permease/ATP-binding protein MsbA	msbA	CJA_0508	11.3	11.2	11.3	10.9
LPS biosynthesis protein RfaE	rfaE	CJA_0509	11.7	12.0	11.3	11.8
methyl-accepting chemotaxis protein	-	CJA_0510	11.4	11.6	11.1	10.7
methyl-accepting chemotaxis protein	-	CJA_0511	10.4	10.9	10.0	9.8
methyl-accepting chemotaxis transducer	-	CJA_0512	11.4	11.4	11.3	11.1
NADH-dependent butanol dehydrogenase	-	CJA_0513	11.6	12.7	12.0	11.9
hypothetical protein	-	CJA_0514	10.6	10.6	10.6	11.2
iron-sulfur cluster-binding protein, Rieske family	-	CJA_0515	9.8	9.9	9.5	10.5
hypothetical protein	-	CJA_0516	10.1	10.2	9.6	11.4
heat shock protein HtpX	htpX	CJA_0517	9.5	9.6	9.6	11.6
cAMP-dependent protein kinase	-	CJA_0518	10.8	11.1	11.1	9.5
TfoX C-terminal domain superfamily	-	CJA_0519	10.5	10.1	10.7	10.4

D-alanyl-D-alanine carboxypeptidase	-	CJA_0520	10.7	10.2	11.2	10.6
transporter	-	CJA_0521	11.8	12.5	11.5	10.4
serine acetyltransferase	-	CJA_0522	11.4	11.5	10.5	10.7
hypothetical protein	-	CJA_0523	12.0	13.1	11.4	10.6
hypothetical protein	-	CJA_0524	10.9	11.4	11.6	10.7
AsmA family superfamily	-	CJA_0525	10.2	10.1	12.2	10.3
hypothetical protein	-	CJA_0526	9.3	9.2	10.3	9.2
hypothetical protein	-	CJA_0527	8.8	8.9	9.0	8.9
nitrate ABC transporter permease protein	-	CJA_0528	12.0	12.7	13.0	9.1
nitrate-binding protein nrtA precursor, periplasmic	-	CJA_0529	11.3	10.5	13.5	9.1
A / G specific adenine glycosylase	mutY	CJA_0530	9.6	10.3	9.4	10.7
hypothetical protein	-	CJA_0531	9.4	9.6	9.4	10.0
beta-galactosidase, putative, bgl2B	bgl2B	CJA_0532	10.3	10.3	9.9	9.1
pectate lyase, putative, pel1B	pel1B	CJA_0533	11.8	11.5	12.2	8.9
Transcriptional regulator family	-	CJA_0534	9.1	9.2	9.1	9.2
hypothetical protein	-	CJA_0535	9.7	10.2	9.1	9.3
2-hydroxychromene-2-carboxylate isomerase family protein	-	CJA_0536	9.6	10.4	9.2	9.5
cholesterol oxidase	choB	CJA_0537	11.1	11.4	11.3	9.7
hypothetical protein	-	CJA_0538	11.9	11.7	12.5	9.4
hypothetical protein	-	CJA_0539	9.2	9.2	9.6	9.1
hydroxydechloroatrazine ethylaminohydrolase	-	CJA_0540	11.2	11.8	10.9	9.9
transcriptional regulator, TetR family	-	CJA_0541	11.3	11.4	12.1	10.9
bmp family protein	-	CJA_0542	11.7	12.1	13.0	9.4
ABC transporter, permease protein	-	CJA_0543	9.5	9.6	9.4	9.1
permease protein of sugar ABC transporter	-	CJA_0544	9.9	10.4	9.9	9.0
ABC transporter, ATP-binding protein	-	CJA_0545	9.4	9.4	10.0	8.9
xanthine dehydrogenase, XdhA subunit	xdhA	CJA_0546	9.3	9.4	9.9	8.9
xanthine dehydrogenase	xdhB	CJA_0547	10.6	10.2	11.3	9.1
putative xanthine dehydrogenase accessory factor XdhC	-	CJA_0548	9.6	9.5	9.5	9.0
putative OHCU decarboxylase	-	CJA_0549	8.9	8.9	9.0	9.0
Transthyretin-like protein precursor	-	CJA_0550	10.0	9.4	9.8	9.2
guanine aminohydrolase	-	CJA_0551	10.6	10.6	10.8	9.4
hypothetical protein	-	CJA_0552	10.7	11.7	11.1	9.5
hypothetical protein	-	CJA_0553	9.0	9.3	9.1	9.0
hypothetical protein	-	CJA_0554	9.9	9.7	10.9	9.7
transposase	-	CJA_0555	11.8	11.2	11.6	9.7
transposase	-	CJA_0556	10.2	9.9	10.9	10.0
hypothetical protein	-	CJA_0557	8.9	8.8	8.9	9.0
hypothetical protein	-	CJA_0558	8.8	8.8	8.8	8.8
carbohydrate binding protein, putative, cbp35B	cbp35B	CJA_0559	10.1	9.6	10.9	9.5

outer membrane ferric siderophore receptor	-	CJA_0560	11.1	11.4	11.4	9.9
polysaccharide deacetylase protein, putative, pda4B	pda4B	CJA_0561	10.0	10.3	10.2	9.1
hypothetical protein	-	CJA_0562	9.7	9.8	9.6	8.8
putative adenosine deaminase	-	CJA_0563	10.4	10.1	11.1	8.9
hypothetical protein	-	CJA_0564	8.9	8.8	8.9	8.8
putative TonB-dependent receptor	-	CJA_0565	10.7	10.8	13.8	9.3
hypothetical protein	-	CJA_0566	10.8	10.2	12.1	9.2
ToIR	-	CJA_0567	10.3	10.1	10.7	9.2
TonB system transport protein ExbB2	-	CJA_0568	9.2	9.2	9.3	8.9
TonB system transport protein ExbD2	-	CJA_0569	10.1	9.6	9.8	9.0
TonB2 protein	-	CJA_0570	9.3	9.3	9.2	9.0
tetratricopeptide repeat domain protein	-	CJA_0571	10.1	9.7	10.2	9.1
methythioadenosine phosphorylase	-	CJA_0572	11.9	11.7	12.1	9.4
putative purine nucleoside permease	-	CJA_0573	10.8	11.1	11.1	9.4
amidase	-	CJA_0574	10.4	10.0	10.0	9.6
gamma-glutamyltranspeptidase	-	CJA_0575	9.6	9.4	9.2	9.1
hypothetical integral membrane protein	-	CJA_0576	10.5	11.4	10.1	9.1
purine catabolism protein	pucG	CJA_0577	9.6	9.5	9.4	9.3
adenosine deaminase	-	CJA_0578	11.1	10.6	10.4	9.7
allantoate amidohydrolase	amaB	CJA_0579	11.9	12.6	10.9	9.8
hypoxanthine-guanine phosphoribosyltransferase	hpt-1	CJA_0580	12.7	13.3	12.3	10.4
hypothetical protein	-	CJA_0581	9.9	9.8	10.8	9.7
hypothetical protein	-	CJA_0582	9.4	9.3	11.3	9.4
putative purine nucleoside permease	-	CJA_0583	11.4	11.9	11.2	9.5
adenosine deaminase	-	CJA_0584	10.2	10.0	10.6	9.0
hypothetical protein	-	CJA_0585	9.2	9.3	9.7	8.8
hypothetical protein	-	CJA_0587	11.1	10.7	11.7	9.8
hypothetical protein	-	CJA_0588	13.0	14.0	13.0	9.5
Putative Ig domain family	-	CJA_0589	11.7	11.9	10.8	10.7
Sulfotransferase domain superfamily	-	CJA_0590	11.0	11.3	11.2	10.8
hypothetical protein	-	CJA_0591	11.6	10.7	11.9	9.8
microcystin dependent protein; MdpB	-	CJA_0592	9.7	10.0	9.2	9.1
microcystin dependent protein; MdpB	-	CJA_0593	11.5	11.2	10.5	9.6
hypothetical protein	-	CJA_0594	10.8	10.4	10.1	9.7
hypothetical protein	-	CJA_0595	9.1	9.1	9.0	9.1
acetyltransferase, GNAT family	-	CJA_0596	10.1	9.7	9.5	9.1
hypothetical protein	-	CJA_0597	11.1	11.2	10.8	9.4
GumN protein superfamily	-	CJA_0598	9.9	9.9	9.8	10.2
ABC transporter, ATP-binding protein	-	CJA_0599	9.9	10.1	9.6	10.0
hypothetical protein	-	CJA_0600	10.9	11.0	12.0	10.8

transcriptional regulator, GntR family	-	CJA_0601	8.9	9.1	8.9	9.3
hydrolase, alpha/beta fold family domain protein	-	CJA_0602	10.9	11.7	9.9	9.9
sodium ABC transporter ATP-binding protein	natA	CJA_0603	11.2	11.3	10.9	10.1
ABC-2 type transporter	-	CJA_0604	11.1	10.9	10.6	9.8
hypothetical protein	-	CJA_0605	11.5	11.5	10.3	10.0
hypothetical protein	-	CJA_0606	10.1	10.0	9.6	9.8
hypothetical protein	-	CJA_0607	10.2	10.8	10.0	9.0
putative lipoprotein	-	CJA_0608	11.9	12.4	12.5	10.6
hypothetical protein	-	CJA_0609	13.4	12.2	13.6	12.4
capsular polysaccharide biosynthesis protein	cpsA	CJA_0610	10.7	10.7	10.1	9.0
hypothetical protein	-	CJA_0611	9.6	9.7	9.3	9.1
hypothetical protein	-	CJA_0612	10.7	10.0	10.1	9.1
hypothetical protein	-	CJA_0613	11.4	11.2	11.1	9.3
glycosyl transferase, putative, gt25A	gt25A	CJA_0614	10.6	11.0	9.8	9.1
hypothetical protein	-	CJA_0615	11.0	10.3	9.9	9.0
glycosyl transferase, putative, gt4J	gt4J-1	CJA_0616	11.6	11.1	10.8	9.1
glycosyl transferase, putative, gt26A	gt26A	CJA_0617	10.1	10.3	9.4	9.0
UDP-GlcA beta-glucuronosyltransferase, putative, gt70A	gt70A	CJA_0618	11.8	12.5	11.4	9.2
endo-1,4-beta glucanase, putative, cel5H	cel5H	CJA_0619	11.1	11.3	10.2	9.3
glycosyl transferase, putative, gt4J	gt4J-2	CJA_0620	10.6	10.3	9.5	9.1
putative GumE protein	-	CJA_0621	9.3	9.5	9.0	8.9
EpsG	epsG	CJA_0622	9.7	9.8	9.6	9.0
putative chain length determinant protein EpsF	-	CJA_0623	11.1	11.2	10.3	9.1
EpsE	epsE	CJA_0624	9.9	10.3	9.8	9.2
hypothetical protein	-	CJA_0625	9.6	9.7	9.6	9.0
3-phosphoshikimate 1-carboxyvinyltransferase	aroA	CJA_0627	11.4	12.3	10.4	12.2
thioesterase family protein domain protein	-	CJA_0628	10.2	10.5	10.0	11.4
PEP-CTERM putative exosortase interaction domain protein	-	CJA_0629	10.5	10.7	10.7	11.2
hypothetical protein	-	CJA_0630	10.4	10.8	10.1	9.8
Domain of unknown function (306) family	-	CJA_0631	10.1	10.1	9.9	9.6
putative DNA helicase II	-	CJA_0632	11.0	10.7	10.8	9.7
Piwi domain protein	-	CJA_0633	10.3	10.2	9.8	9.7
hypothetical protein	-	CJA_0635	11.2	11.5	10.4	10.4
type I restriction-modification system, S subunit	-	CJA_0636	10.6	10.8	10.2	10.8
RhuM-like protein	rhuM	CJA_0637	11.2	10.9	10.3	10.9
type I restriction-modification system, M subunit	hsdM	CJA_0638	12.2	12.2	11.8	11.5
type I restriction-modification system, R subunit	-	CJA_0639	11.8	11.9	11.0	11.2
hypothetical protein	-	CJA_0640	10.4	10.3	10.2	10.5
GTP-binding protein YchF	ychF	CJA_0641	12.7	12.9	11.4	12.9
peptidyl-tRNA hydrolase	pth	CJA_0642	9.8	10.2	9.5	10.1

50S ribosomal protein L25/general stress protein Ctc	-	CJA_0643	12.5	12.4	11.6	13.5
ribose-phosphate pyrophosphokinase	prs	CJA_0644	9.9	10.1	9.1	12.3
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	ipk	CJA_0646	10.0	9.6	9.8	10.8
outer membrane lipoprotein LolB	lolB	CJA_0647	10.8	10.6	11.6	9.7
TPR domain protein	-	CJA_0648	10.1	10.6	9.7	9.4
hypothetical protein	-	CJA_0649	10.8	11.6	9.3	9.7
hypothetical protein	-	CJA_0650	10.4	10.7	9.2	9.2
glutamyl-tRNA reductase	hemA	CJA_0651	11.3	11.5	10.0	10.6
peptide chain release factor 1	prfA	CJA_0652	11.3	11.2	9.9	11.6
methyltransferase, HemK family	-	CJA_0653	12.0	11.6	10.7	11.7
molybdopterin biosynthesis MoeB protein	moeB	CJA_0654	11.0	10.9	9.9	10.6
hypothetical protein	-	CJA_0655	10.9	10.6	10.2	12.0
peptidase, M48 family	-	CJA_0656	10.6	10.3	10.1	10.5
kinase, pfkB family	-	CJA_0657	11.2	11.5	9.8	11.6
hypothetical protein	-	CJA_0658	9.9	9.7	10.0	10.1
murein polymerase, putative, gt51C	gt51C	CJA_0659	9.9	10.1	9.4	9.8
hypothetical protein	-	CJA_0660	12.2	12.2	11.7	10.9
RNA polymerase ECF-type sigma factor	algT	CJA_0661	9.2	9.3	9.2	9.9
hypothetical protein	-	CJA_0662	11.2	10.5	11.0	9.8
hypothetical protein	-	CJA_0663	11.0	10.2	11.4	10.5
acetolactate synthase 3 catalytic subunit	ilvB	CJA_0664	10.7	10.4	9.8	13.2
acetolactate synthase 3 regulatory subunit	ilvH	CJA_0665	10.9	10.7	10.1	13.0
possible DNA-3-methyladenine glycosidase	-	CJA_0666	11.4	11.9	10.4	10.6
DNA-binding transcriptional regulator IlvY	-	CJA_0667	10.9	11.1	9.9	10.2
ketol-acid reductoisomerase	ilvC	CJA_0668	10.8	10.0	9.6	13.2
phosphatidylserine synthase	pssA	CJA_0669	12.4	11.3	11.7	12.5
alanine racemase	alr	CJA_0676	10.1	9.8	10.0	11.6
biotin-[acetyl-CoA-carboxylase] ligase	-	CJA_0677	10.6	10.4	10.3	12.1
transcriptional activator, putative, Baf family	-	CJA_0678	11.5	11.0	11.3	12.7
Sporulation related repeat family	-	CJA_0679	10.0	9.8	10.1	10.9
elongation factor Tu	-	CJA_0684	14.9	12.3	12.6	15.3
preprotein translocase, SecE subunit	secE	CJA_0686	11.4	10.0	10.2	14.5
transcription termination/antitermination factor NusG	nusG	CJA_0687	9.8	9.1	9.2	14.1
ribosomal protein L11	rplK	CJA_0688	11.0	9.6	9.9	14.8
ribosomal protein L1	rplA	CJA_0689	10.9	10.0	9.8	14.6
50S ribosomal protein L10	-	CJA_0690	10.6	9.4	9.5	14.5
ribosomal protein L7/L12	rplL	CJA_0691	9.6	9.1	9.3	14.3
DNA-directed RNA polymerase subunit beta	rpoB	CJA_0692	10.7	10.3	10.3	14.3
DNA-directed RNA polymerase subunit beta'	rpoC	CJA_0693	10.5	10.0	10.9	14.0
30S ribosomal protein S12	rpsL	CJA_0694	10.0	9.0	9.2	14.3

30S ribosomal protein S7	rpsG	CJA_0695	10.7	9.3	9.9	14.6
translation elongation factor G	-	CJA_0696	10.9	10.3	10.2	14.7
ribosomal protein S10	rpsJ	CJA_0698	9.9	9.0	9.0	14.6
ribosomal protein L3	rplC	CJA_0699	12.3	10.1	10.2	15.4
ribosomal protein L4/L1 family	rplD	CJA_0700	11.1	9.7	10.4	15.1
ribosomal protein L23	rplW	CJA_0701	10.8	9.5	9.5	14.9
50S ribosomal protein L2	rplB	CJA_0702	12.4	10.2	10.3	15.4
ribosomal protein S19	rpsS	CJA_0703	12.3	10.5	10.5	15.4
50S ribosomal protein L22	rplV	CJA_0704	12.3	10.3	9.9	15.3
30S ribosomal protein S3	rpsC	CJA_0705	10.5	9.2	9.2	14.8
50S ribosomal protein L16	rplP	CJA_0706	13.0	10.3	10.6	15.4
ribosomal protein L29	rpmC	CJA_0707	9.2	8.9	8.9	14.4
30S ribosomal protein S17	rpsQ	CJA_0708	11.8	9.5	9.6	15.3
50S ribosomal protein L14	rplN	CJA_0709	10.4	9.1	9.2	14.8
ribosomal protein L24	rplX	CJA_0710	9.1	8.9	8.9	14.0
50S ribosomal protein L5	rplE	CJA_0711	11.8	9.7	10.6	15.4
30S ribosomal protein S14	rpsN	CJA_0712	10.9	9.9	9.4	15.1
ribosomal protein S8	rpsH	CJA_0713	10.2	9.5	9.6	14.9
50S ribosomal protein L6	rplF	CJA_0714	11.3	9.6	10.1	15.2
ribosomal protein L18	rplR	CJA_0715	12.8	11.0	10.3	15.5
30S ribosomal protein S5	rpsE	CJA_0716	11.7	10.6	10.2	15.1
ribosomal protein L30	rpmD	CJA_0717	11.5	10.4	10.1	15.0
ribosomal protein L15	rplO	CJA_0718	10.4	9.4	10.3	14.9
preprotein translocase, SecY subunit	-	CJA_0719	11.2	10.2	11.4	15.0
ribosomal protein L36	-	CJA_0720	10.3	9.3	10.5	14.5
30S ribosomal protein S13	rpsM	CJA_0721	10.1	9.0	10.0	14.6
30S ribosomal protein S11	rpsK	CJA_0722	11.5	9.2	11.3	14.9
ribosomal protein S4	rpsD	CJA_0723	12.9	10.4	13.2	15.2
DNA-directed RNA polymerase subunit alpha	rpoA	CJA_0724	10.3	9.5	11.0	14.7
ribosomal protein L17	rplQ	CJA_0725	11.6	10.6	12.2	14.0
excinuclease ABC, A subunit	uvrA	CJA_0726	12.4	12.5	11.9	12.3
major facilitator family transporter	-	CJA_0727	11.3	11.5	10.8	11.0
single-stranded DNA-binding protein	ssb	CJA_0728	11.8	11.1	12.5	13.0
transcriptional regulator, LacI family	-	CJA_0729	10.6	10.3	10.6	11.7
transporter, major facilitator family	-	CJA_0730	11.4	11.3	10.4	9.5
glucan 1,4-alpha-glucosidase, putative, gla15A	gla15	CJA_0731	9.5	9.7	9.2	9.1
oligo-1,6-glucosidase, putative, glu13A	glu13A	CJA_0732	9.8	9.7	9.5	9.5
TonB-dependent receptor	-	CJA_0733	11.2	11.2	10.7	9.8
tryptophan halogenase	-	CJA_0734	10.4	10.0	9.8	9.2
alpha-amylase, putative, amy13E	amy13E	CJA_0735	10.3	10.3	9.9	9.2

alpha-glucosidase, putative, adg97B	adg97B	CJA_0736	10.7	10.8	10.6	10.4
alpha amylase, putative, amy13D	amy13D	CJA_0737	10.0	10.0	9.6	9.4
hypothetical protein	-	CJA_0738	8.8	8.9	9.0	8.8
Adenylate cyclase	-	CJA_0739	10.6	10.5	10.0	10.0
predicted membrane protein	-	CJA_0740	10.9	11.0	10.7	10.2
Sec-independent protein translocase TatC	-	CJA_0741	10.4	10.1	10.3	10.8
TatB	-	CJA_0742	12.5	12.1	12.1	12.9
twin arginine-targeting protein translocase, TatA/E family	-	CJA_0743	11.2	10.7	11.4	12.8
phosphoribosyl-ATP pyrophosphohydrolase	-	CJA_0744	9.1	9.0	9.1	11.3
bifunctional protein phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP	hisIE	CJA_0745	9.1	9.1	9.1	11.3
oxidoreductase, aldo/keto reductase family	-	CJA_0746	9.8	10.2	9.4	10.5
oxidoreductase, FAD-binding	-	CJA_0747	9.7	10.1	9.3	9.9
dTDP-4-rhamnose reductase-related protein	-	CJA_0748	10.2	10.2	10.0	10.4
beta-ketoacyl-ACP synthase I	fabB	CJA_0749	10.1	10.4	9.7	12.7
3-hydroxydecanoyl-(acyl carrier protein) dehydratase	fabA	CJA_0750	11.5	11.4	10.6	13.6
octaprenyl-diphosphate synthase	ispB	CJA_0751	9.4	9.8	9.2	10.7
HetI	mtaA	CJA_0752	9.9	10.1	9.5	9.3
peptidyl-prolyl cis-trans isomerase, FkpP family	-	CJA_0753	11.7	10.7	11.2	12.6
two-component hybrid sensor and regulator	-	CJA_0754	11.1	10.9	10.3	10.2
TonB-dependent receptor	-	CJA_0755	10.4	10.6	11.0	10.0
putative citrate synthase I	-	CJA_0756	9.6	9.6	9.6	10.9
putative signal transduction protein	-	CJA_0757	12.3	12.8	11.5	11.1
hypothetical protein	-	CJA_0758	10.7	10.8	11.4	11.3
putative acetolactate synthase large subunit	-	CJA_0759	12.6	13.2	12.8	11.3
hypothetical protein	-	CJA_0760	11.1	11.7	10.2	9.5
transcriptional regulator, AraC family	-	CJA_0761	10.3	10.7	10.6	9.4
Molybdopterin biosynthesis enzyme	-	CJA_0762	10.8	11.6	10.0	11.0
transcription initiation factor sigma 70	rpoD	CJA_0764	10.2	9.9	9.9	13.2
DNA primase	dnaG	CJA_0765	11.3	12.0	10.5	10.2
GatB/Yqey domain superfamily	-	CJA_0766	9.7	9.6	9.6	12.5
ribosomal protein S21	rpsU	CJA_0767	9.0	8.9	9.1	12.8
O-sialoglycoprotein endopeptidase	gcp	CJA_0768	10.9	11.2	10.4	11.6
dihydroneopterin aldolase	folB	CJA_0769	11.1	11.1	10.4	11.6
2-amino-4-hydroxy-6- hydroxymethylidihydropteridine pyrophosphokinase	folK-2	CJA_0770	10.7	10.6	11.0	11.0
putative magnesium and cobalt transport protein CorA	-	CJA_0771	9.9	10.5	9.7	9.8
pteridine reductase	-	CJA_0772	9.5	9.6	9.9	10.2
tRNA nucleotidyltransferase	cca	CJA_0773	9.2	9.3	9.5	10.3
Integral membrane protein DUF6 domain protein	-	CJA_0774	10.5	10.1	11.5	9.7
hypothetical protein	-	CJA_0775	9.2	9.2	15.4	10.1
hypothetical protein	-	CJA_0776	9.7	9.6	10.1	10.9

UDP-glucose 4-epimerase	-	CJA_0777	9.7	10.1	9.7	11.6
carbohydrate binding protein, putative, cbp32A	cbp32A	CJA_0778	10.8	10.6	10.3	9.1
hypothetical protein	-	CJA_0779	9.6	9.4	9.6	9.1
Sensory transduction histidine kinase	phoQ	CJA_0781	10.3	10.2	9.6	9.6
DNA-binding response regulator	phoP	CJA_0782	10.3	10.9	10.2	11.0
hypothetical protein	-	CJA_0783	13.6	14.0	12.9	12.3
hypothetical protein	-	CJA_0784	11.3	11.6	11.2	11.3
gamma-glutamyl phosphate reductase	proA	CJA_0785	11.1	10.9	10.8	12.4
nicotinate (nicotinamide) nucleotide adenyltransferase	nadD	CJA_0786	10.0	9.9	9.5	11.3
iojap domain protein	-	CJA_0787	9.9	10.2	9.8	11.5
conserved hypothetical protein TIGR00246	-	CJA_0788	11.2	10.5	11.9	12.3
penicillin-binding protein 2	mrda-2	CJA_0789	9.6	9.8	9.3	9.5
rod shape-determining protein RodA	rodA	CJA_0790	10.6	10.9	10.0	10.0
peptidoglycan lytic transglycosylase, putative, plt103A	plt103A	CJA_0791	11.4	11.8	11.6	11.6
Six5	-	CJA_0792	11.7	12.2	11.5	11.0
D-alanyl-D-alanine carboxypeptidase family	-	CJA_0793	10.8	11.5	10.7	11.5
thioredoxin family protein	-	CJA_0794	11.2	11.1	12.2	10.6
hypothetical protein	-	CJA_0795	11.1	13.0	10.1	11.4
lipoate-protein ligase B	lipB	CJA_0796	10.6	10.9	10.2	11.2
lipoyl synthase	lipA	CJA_0797	9.6	9.8	9.3	10.7
putative acetyltransferase, GNAT family	-	CJA_0798	9.3	9.3	9.5	9.4
beta-xylosidase/alpha-L-arabinofuranosidase, putative, gly43E	gly43E	CJA_0799	9.8	10.3	10.2	9.4
putative TonB-dependent receptor	-	CJA_0800	9.6	9.7	9.8	9.3
methyl-accepting chemotaxis protein	-	CJA_0801	10.8	10.8	11.3	10.5
hypothetical protein	-	CJA_0802	9.4	9.3	9.7	9.4
hypothetical protein	-	CJA_0803	10.3	10.3	10.0	9.0
hypothetical protein	-	CJA_0804	9.7	9.9	10.0	9.1
arabinanase and alpha-L-arabinofuranosidase, arb43A	arb43A	CJA_0805	10.3	11.4	10.0	9.2
alpha-L-arabinofuranosidase, putative, abf43L	abf43L	CJA_0806	10.9	12.0	10.4	9.3
aldose 1-epimerase	-	CJA_0807	10.2	11.1	9.8	10.5
Peptidase C39 family superfamily	-	CJA_0808	9.0	9.0	9.1	9.8
hypothetical protein	-	CJA_0809	9.1	9.2	9.2	9.6
hypothetical protein	-	CJA_0810	9.0	9.0	9.1	9.6
hypothetical protein	-	CJA_0811	8.8	8.8	8.8	9.4
hypothetical protein	-	CJA_0812	9.1	9.0	9.2	10.4
hypothetical protein	-	CJA_0813	8.8	8.8	8.9	9.4
hypothetical protein	-	CJA_0814	9.0	9.0	9.2	9.7
hypothetical protein	-	CJA_0815	8.9	8.8	9.1	9.7
beta-xylosidase/alpha-L-arabinofuranosidase, putative, gly43C	gly43C	CJA_0816	10.2	11.1	10.1	9.0
alpha-glucosidase, putative, agd97A	agd97A	CJA_0817	9.8	9.6	9.4	9.0

beta-xylosidase/alpha-L-arabinofuranosidase, putative, gly43D	gly43D	CJA_0818	9.3	9.5	9.4	9.0
alpha-L-arabinofuranosidase, putative, abf43M	abf43M	CJA_0819	10.0	10.2	9.6	9.1
hypothetical protein	-	CJA_0820	9.5	9.9	9.5	8.9
hypothetical protein	-	CJA_0821	9.2	9.1	9.7	8.9
transposase	-	CJA_0823	10.2	9.9	11.0	9.9
hypothetical protein	-	CJA_0824	9.0	8.9	9.1	9.2
hypothetical protein	-	CJA_0825	9.5	9.3	10.3	9.4
ParB-like nuclease domain	-	CJA_0826	9.2	9.1	9.2	9.1
ParB-like nuclease domain	-	CJA_0827	9.7	9.9	10.1	9.6
putative lipoprotein	-	CJA_0828	9.8	10.2	9.9	9.6
hypothetical protein	-	CJA_0829	11.7	12.3	11.8	9.6
fibronectin type III domain protein	-	CJA_0830	11.7	12.2	10.5	9.2
Cellulose or protein binding domain	-	CJA_0831	11.2	11.3	11.1	9.3
Cip2	-	CJA_0832	10.2	10.0	10.1	9.2
transcriptional regulator, GntR family	-	CJA_0833	10.4	10.0	10.4	10.6
Diguanylate cyclase/phosphodiesterase domain 2 (EAL)	-	CJA_0834	9.4	9.7	9.2	9.3
NADH dehydrogenase	ndh	CJA_0835	12.5	12.8	11.2	11.7
hypothetical protein	-	CJA_0836	9.8	9.7	9.5	9.9
hypothetical protein	-	CJA_0837	11.7	12.1	11.1	11.3
hypothetical protein	-	CJA_0838	11.2	11.9	9.6	11.7
oxidoreductase, short chain dehydrogenase/reductase family	-	CJA_0839	10.3	11.3	9.3	10.8
transcriptional regulator, AraC family	oruR	CJA_0840	9.5	9.3	9.1	9.0
GGDEF domain protein	-	CJA_0841	10.7	10.8	10.0	8.9
TonB-dependent receptor	cirA	CJA_0842	11.2	11.8	10.6	9.0
phytase domain protein	-	CJA_0843	10.3	10.8	9.3	9.2
Tat (twin-arginine translocation) pathway signal sequence domain protein	-	CJA_0844	10.3	10.2	10.1	9.4
putative lipoprotein	-	CJA_0845	9.8	9.6	10.4	10.7
gluconokinase	idnK	CJA_0846	11.5	11.6	9.9	10.0
transcriptional regulatory protein	-	CJA_0847	11.3	11.4	10.3	10.3
cation symporter	-	CJA_0848	12.3	12.4	10.6	9.7
cyclic beta-1, 2- glucan synthetase, putative, cgs94A	cgs94A	CJA_0849	11.3	11.5	10.4	10.0
hypothetical protein	-	CJA_0850	11.2	11.0	10.1	10.1
hypothetical protein	-	CJA_0851	11.8	10.8	11.5	12.3
ribosomal protein S20	rpsT	CJA_0852	9.6	9.3	9.4	11.9
hypothetical protein	-	CJA_0853	9.1	9.0	9.6	12.3
serine/threonine kinase	-	CJA_0854	10.4	10.6	9.6	9.8
hypothetical protein	-	CJA_0855	9.8	9.5	9.5	9.5
nucleotidyltransferase family protein	-	CJA_0856	10.1	10.7	9.2	9.6
Domain of unknown function DUF227	-	CJA_0857	10.3	11.8	9.2	10.4
putative organic solvent tolerance protein	-	CJA_0858	9.9	9.8	9.4	10.6

peptidyl-prolyl cis-trans isomerase SurA	surA	CJA_0859	11.2	9.9	12.6	12.5
4-hydroxythreonine-4-phosphate dehydrogenase	pdxA	CJA_0860	12.1	12.6	10.2	11.6
dimethyladenosine transferase	ksgA	CJA_0861	10.1	9.9	9.7	11.3
ApaG	apaG	CJA_0862	11.6	11.4	10.7	12.3
diadenosine tetraphosphatase	apaH	CJA_0863	10.4	10.3	10.0	11.3
PEP-CTERM putative exosortase interaction domain protein	-	CJA_0864	10.1	10.0	9.8	10.0
cytochrome c oxidase, subunit II	-	CJA_0865	10.1	10.2	9.4	9.0
cytochrome c oxidase, subunit I	-	CJA_0866	12.1	11.2	11.4	9.1
cytochrome oxidase assembly factor	coxG	CJA_0867	10.5	9.9	10.1	9.1
Cytochrome c oxidase subunit III	-	CJA_0868	12.6	11.3	12.3	9.3
hypothetical protein	-	CJA_0869	12.4	12.5	12.2	9.8
hypothetical protein	-	CJA_0870	11.5	11.5	11.3	9.4
hypothetical protein	-	CJA_0871	9.8	9.6	9.4	9.1
uncharacterized protein required for cytochrome oxidase assembly	-	CJA_0872	11.5	11.3	10.8	9.1
protoheme IX farnesyltransferase	cyoE	CJA_0873	10.6	10.4	9.6	9.0
hypothetical protein	-	CJA_0874	11.1	11.5	9.7	9.2
SCO1/SenC superfamily	-	CJA_0875	10.8	10.5	10.0	9.1
hypothetical protein	-	CJA_0876	11.5	10.2	11.1	9.1
hypothetical protein	-	CJA_0877	9.4	9.3	9.5	13.1
hypothetical protein	-	CJA_0878	10.6	9.5	10.4	12.9
glutamate-1-semialdehyde aminotransferase	hemL	CJA_0880	10.5	10.3	9.7	10.9
thiamine-phosphate pyrophosphorylase	thiE	CJA_0881	11.2	10.6	10.1	11.1
Uncharacterised protein family (UPF0093) superfamily	-	CJA_0882	9.8	9.9	9.2	9.5
hypothetical protein	-	CJA_0883	11.2	11.1	10.6	9.6
voltage-gated chloride channel	-	CJA_0884	10.5	10.7	9.7	10.1
N-acetyl-gamma-glutamyl-phosphate reductase	argC	CJA_0885	11.2	10.7	10.9	13.0
hypothetical protein	-	CJA_0886	10.2	10.0	9.6	11.3
putative cell morphology protein	-	CJA_0887	12.3	10.7	13.5	13.3
HesB/YadR/YfhF family protein	-	CJA_0888	11.7	10.8	12.9	13.2
anhydro-N-acetylmuramic acid kinase	anmK	CJA_0889	11.9	11.8	11.2	11.3
peptidase, M23/M37 family	trg3	CJA_0890	12.4	11.5	11.6	11.7
tyrosyl-tRNA synthetase	tyrS	CJA_0891	10.7	9.9	9.3	12.4
hypothetical protein	-	CJA_0893	8.9	8.8	8.9	12.0
hypothetical protein	-	CJA_0905	12.5	10.7	10.4	12.7
ribosomal-protein-alanine acetyltransferase	rimI	CJA_0906	10.3	9.3	9.4	11.4
DNA-binding response regulator	-	CJA_0907	11.3	9.9	9.9	11.3
sensor histidine kinase	-	CJA_0908	12.2	11.4	10.3	10.9
Na+-driven multidrug efflux pump	-	CJA_0909	12.6	11.4	10.6	10.9
peptide chain release factor 3	prfC	CJA_0910	11.9	10.8	10.8	12.8
hypothetical protein	-	CJA_0911	9.2	9.0	9.0	10.4

hypothetical protein	-	CJA_0912	12.0	10.7	10.3	10.8
TonB family C-terminal domain protein	-	CJA_0913	10.9	10.4	9.7	11.8
cyclic nucleotide-binding domain protein	-	CJA_0914	10.9	10.4	10.3	11.3
hypothetical protein	-	CJA_0915	10.8	10.1	10.3	10.6
hypothetical protein	-	CJA_0916	12.7	9.0	15.0	13.8
hypothetical protein	-	CJA_0917	9.1	8.9	8.9	9.0
hypothetical protein	-	CJA_0918	9.2	9.0	9.2	9.3
TonB system transport protein ExbD2	-	CJA_0919	13.0	12.0	14.0	13.7
YbaK / prolyl-tRNA synthetases associated domain protein	-	CJA_0920	10.2	9.9	11.9	9.3
aspartate transaminase	aspC	CJA_0921	14.0	12.6	12.2	14.6
Zn-dependent protease with chaperone function	-	CJA_0922	10.2	10.0	9.4	9.9
hypothetical protein	-	CJA_0923	10.7	10.6	10.9	10.8
21 kDa hemolysin precursor	-	CJA_0924	11.0	11.2	10.9	10.8
phosphoheptose isomerase	gmhA	CJA_0925	10.8	10.7	10.1	10.8
conserved hypothetical protein TIGR00252	-	CJA_0926	9.9	9.9	9.2	9.7
LppC putative lipoprotein	-	CJA_0927	10.9	10.6	10.1	11.5
conserved hypothetical protein TIGR00096	-	CJA_0928	12.0	12.2	10.5	11.3
putative TonB-dependent receptor	-	CJA_0929	10.1	9.8	9.3	9.5
hypothetical protein	-	CJA_0930	9.4	9.1	9.3	9.3
hypothetical protein	-	CJA_0931	11.5	11.4	10.6	9.8
hypothetical protein	-	CJA_0932	12.7	13.8	11.9	10.3
hypothetical protein	-	CJA_0933	9.5	9.6	9.3	9.1
predicted transcriptional regulator	-	CJA_0934	10.0	9.8	9.5	10.1
glyoxylase I family protein	-	CJA_0935	10.7	10.8	9.8	10.5
hypothetical protein	-	CJA_0936	9.7	9.6	9.4	9.6
hypothetical protein	-	CJA_0937	10.4	10.2	10.0	10.7
hypothetical protein	-	CJA_0938	10.4	10.0	10.2	9.4
nitrate transporter system, ATPase component	-	CJA_0939	11.4	11.1	13.2	9.1
hypothetical protein	-	CJA_0940	9.1	9.0	9.0	8.8
putative TPR domain protein	-	CJA_0941	9.4	9.7	9.1	9.1
Domain of Unknown Function (DUF1080) superfamily	-	CJA_0942	10.8	10.7	11.0	10.3
putative glutathione peroxidase	-	CJA_0943	10.0	10.0	10.0	10.0
hypothetical protein	-	CJA_0944	10.1	11.2	9.7	9.7
transmembrane protein	-	CJA_0945	9.6	9.8	9.8	8.9
sulfatase	-	CJA_0946	10.2	10.7	9.5	9.0
hypothetical protein	-	CJA_0947	10.5	10.2	9.2	9.1
RHS Repeat family	-	CJA_0948	9.3	9.8	8.9	9.1
hypothetical protein	-	CJA_0949	10.5	11.0	9.5	9.5
hypothetical protein	-	CJA_0950	11.7	11.0	11.7	10.1
beta-hydroxylase	lpxO	CJA_0951	11.9	12.3	10.4	10.9

hypothetical protein	-	CJA_0952	9.6	9.4	9.5	9.5
two-component transcriptional regulator, LuxR family	-	CJA_0953	10.8	11.2	10.1	9.6
two-component hybrid sensor and regulator	-	CJA_0954	11.4	12.0	10.1	9.3
hypothetical protein	-	CJA_0955	9.4	9.3	9.3	8.8
amide-urea binding protein	-	CJA_0956	11.0	11.1	9.8	9.1
amino acid/sugar ABC transporter, permease protein	-	CJA_0957	10.4	10.2	9.5	8.9
ABC transporter permease protein	fmdF	CJA_0958	11.3	11.6	9.7	9.1
ABC transporter ATP-binding protein	-	CJA_0959	9.9	11.2	9.1	9.0
ABC transporter ATP-binding protein	-	CJA_0960	10.8	10.3	9.9	9.1
hypothetical protein	-	CJA_0961	12.3	12.7	10.3	9.7
hypothetical protein	-	CJA_0962	12.1	12.4	10.3	9.1
amidase	fmdA	CJA_0963	11.3	10.8	10.1	9.4
putative formamidase regulatory protein FmdB	-	CJA_0964	9.5	9.4	9.2	9.1
putative transcriptional regulator	-	CJA_0965	10.1	10.0	9.3	10.4
nodulin 21-like protein	-	CJA_0966	12.8	13.2	11.5	10.1
conserved protein conserved protein	-	CJA_0967	11.2	12.0	10.5	10.6
LPXTG-motif cell wall anchor domain protein	-	CJA_0968	9.7	9.7	9.5	11.4
ATP-dependent RNA helicase RhlB	-	CJA_0969	9.5	9.6	9.1	11.2
hypothetical protein	-	CJA_0970	10.8	11.2	10.0	10.4
Catalytic LigB subunit of aromatic ring-opening dioxygenase	-	CJA_0971	9.8	10.6	9.3	9.6
putative sulfate transporter	-	CJA_0972	9.5	9.8	9.4	9.8
response regulator protein	rrpX	CJA_0973	10.3	10.3	10.4	9.8
peptidase, rhomboid family	-	CJA_0974	10.9	11.8	10.0	10.6
von Willebrand factor type A domain protein	-	CJA_0975	9.4	9.6	9.2	9.5
hypothetical protein	-	CJA_0976	9.2	9.1	9.3	9.8
hypothetical protein	-	CJA_0977	8.9	8.9	8.9	10.0
hypothetical protein	-	CJA_0978	8.9	8.8	9.1	9.6
hypothetical protein	-	CJA_0979	8.9	8.9	9.0	9.1
hypothetical protein	-	CJA_0980	9.1	9.1	9.6	9.6
peptidase, M56 family	-	CJA_0981	9.9	10.0	10.5	9.5
TonB2	-	CJA_0982	9.7	10.0	9.3	9.0
hypothetical protein	-	CJA_0983	9.4	9.6	9.4	10.3
coproporphyrinogen III oxidase	hemN	CJA_0984	9.6	9.7	9.5	9.8
SM-20 domain protein	-	CJA_0985	9.4	9.5	9.3	10.1
Domain of unknown function (DUF404) family	-	CJA_0986	9.7	9.6	13.2	9.8
Bacterial domain of unknown function (DUF403) superfamily	-	CJA_0987	9.3	9.4	11.7	9.3
endo-chitinase, putative, chi18B	chi18B	CJA_0988	10.2	10.5	9.4	9.0
hypothetical protein	-	CJA_0989	8.9	8.9	9.0	8.9
hypothetical protein	-	CJA_0990	9.5	9.3	9.7	9.0
cardiolipin synthase	-	CJA_0991	9.8	9.7	9.5	9.2

hypothetical protein	-	CJA_0992	10.0	10.0	10.2	9.6
cytosolic long-chain acyl-CoA thioester hydrolase family protein	-	CJA_0993	9.8	9.8	9.4	10.5
Transglutaminase-like superfamily domain protein	-	CJA_0994	11.7	12.1	11.6	11.8
Domain of unknown function (DUF404) family	-	CJA_0995	11.9	12.3	11.5	11.5
chitinase, putative, chi19A	chi19A	CJA_0996	11.8	11.6	10.5	9.2
hypothetical protein	-	CJA_0997	9.2	9.1	10.1	8.9
putative lipoprotein	-	CJA_0998	10.5	10.4	9.9	9.1
Transglutaminase-like superfamily domain protein	-	CJA_0999	10.0	9.9	10.0	9.4
membrane protein, PerM family	-	CJA_1000	11.6	12.4	10.6	9.9
hypothetical protein	-	CJA_1001	11.8	12.0	11.4	11.9
small-conductance mechanosensitive channel	-	CJA_1002	11.3	11.2	10.9	11.1
electron transport complex RsxE subunit	-	CJA_1003	13.1	13.2	12.0	11.9
rnfE	-	CJA_1004	10.4	11.1	9.8	11.1
Electron transport complex protein rnfD	-	CJA_1005	9.9	10.1	9.4	10.6
electron transport complex protein RnfC	-	CJA_1006	10.3	10.2	9.3	11.1
Electron transport complex protein rnfB	-	CJA_1007	10.7	11.7	9.4	10.5
RnfA-related protein	-	CJA_1008	9.0	9.0	9.0	10.4
methionyl-tRNA synthetase	metG	CJA_1009	11.0	10.9	10.1	12.5
hypothetical protein	-	CJA_1010	12.0	12.0	12.9	12.1
transcription elongation factor GreB	greB	CJA_1011	9.5	9.2	9.4	10.0
prevent-host-death family protein	-	CJA_1012	10.3	9.5	12.0	11.8
addiction module toxin, Txe/YoeB family	-	CJA_1013	9.0	8.9	9.5	10.3
hypothetical protein	-	CJA_1014	9.7	9.4	10.0	10.5
prolyl oligopeptidase family	-	CJA_1015	11.9	13.3	11.0	10.8
mesJ protein	mesJ	CJA_1016	10.6	10.4	10.0	10.5
putative lipoprotein	-	CJA_1017	10.9	10.7	10.0	12.1
Y4ij	-	CJA_1018	10.3	11.0	9.9	9.3
hypothetical protein	-	CJA_1019	10.1	9.6	12.0	11.5
hypothetical protein	-	CJA_1020	9.9	9.7	11.0	11.0
hypothetical protein	-	CJA_1021	10.0	9.6	10.5	10.9
hypothetical protein	-	CJA_1022	11.2	10.9	10.6	10.5
rieske [2Fe-2S] domain protein	-	CJA_1023	11.3	11.9	10.8	10.6
hypothetical protein	-	CJA_1024	11.3	11.3	12.2	11.3
murein polymerase, putative, gt51A	gt51A	CJA_1025	11.8	12.1	12.0	10.3
hypothetical protein	-	CJA_1026	11.0	10.2	10.9	13.0
aspartyl-tRNA synthetase	aspS	CJA_1027	11.3	10.7	10.6	13.4
conserved hypothetical protein TIGR01033	-	CJA_1028	10.1	10.0	9.9	11.2
Holliday junction resolvase	ruvC	CJA_1029	11.7	11.3	11.2	11.4
Holliday junction DNA helicase RuvA	ruvA	CJA_1030	9.8	9.6	9.8	10.5
Holliday junction DNA helicase RuvB	ruvB	CJA_1031	10.6	10.5	10.4	12.3

tolQ protein	tolQ-2	CJA_1032	9.1	8.9	9.1	10.5
ToIR protein	tolR	CJA_1033	9.7	9.3	10.8	11.8
putative biopolymer transport protein TolA	-	CJA_1034	10.9	10.1	12.2	12.2
tolB protein	tolB	CJA_1035	11.7	11.4	12.3	13.1
outer membrane protein	-	CJA_1036	12.2	11.1	13.5	13.9
putative 34 kDa outer membrane protein	-	CJA_1037	10.4	10.0	11.0	12.9
hypothetical protein	-	CJA_1038	11.3	11.1	13.7	11.5
hypothetical protein	-	CJA_1039	9.6	10.0	9.4	10.4
inactive regulatory protein	-	CJA_1040	10.0	10.2	9.7	11.1
nucleoid-associated protein NdpA superfamily	ndpA	CJA_1041	12.2	12.5	10.6	11.3
endoribonuclease L-PSP family protein	-	CJA_1042	12.8	12.7	11.2	11.3
histone deacetylase family protein	hda	CJA_1043	9.5	9.2	9.4	9.5
acetyltransferase, GNAT family	-	CJA_1044	10.4	10.5	10.0	10.0
sulfatase	-	CJA_1045	10.3	10.3	10.1	9.1
hypothetical protein	-	CJA_1046	11.4	11.4	10.1	10.4
hypothetical protein	-	CJA_1047	10.7	10.2	10.0	10.1
hypothetical protein	-	CJA_1048	11.0	10.7	10.3	10.2
tryptophan halogenase	rebH	CJA_1049	11.6	11.2	10.8	9.7
TonB-dependent receptor	-	CJA_1050	10.5	10.9	10.0	9.2
amino acid permease	-	CJA_1051	11.1	10.5	10.7	9.5
hypothetical protein	-	CJA_1052	11.7	11.5	12.5	10.8
hypothetical protein	-	CJA_1053	9.6	9.3	9.5	9.0
hypothetical protein	-	CJA_1054	10.5	10.7	9.8	9.1
hypothetical protein	-	CJA_1055	9.1	9.1	9.0	9.0
putative ankyrin G	-	CJA_1056	9.3	9.3	9.2	9.2
cytochrome c''	cycP	CJA_1057	9.5	9.2	9.2	10.0
CybP	cybP	CJA_1058	10.6	10.1	10.4	11.0
putative hydrolase	-	CJA_1059	9.5	9.3	9.2	9.3
elongation factor G	-	CJA_1060	12.2	11.6	11.3	14.2
glycine dehydrogenase	gcvP	CJA_1061	12.5	13.0	10.9	12.3
metabolite transport protein-like protein	-	CJA_1062	12.7	13.1	11.9	10.8
general secretion pathway protein a	gspA	CJA_1063	10.8	10.7	10.4	10.4
hypothetical protein	-	CJA_1064	12.5	12.6	11.2	10.9
bacterioferritin	bfr	CJA_1065	11.8	11.0	12.9	12.3
bacterioferritin-associated ferredoxin-related protein	-	CJA_1066	9.4	9.3	9.2	9.5
probable peroxidase	-	CJA_1067	10.4	10.3	9.8	13.4
uracil-DNA glycosylase	ung	CJA_1068	10.6	10.2	9.7	11.0
putative TonB-dependent receptor	-	CJA_1069	15.0	10.3	15.0	14.9
tryptophan halogenase	-	CJA_1070	11.2	10.4	11.2	12.2
phosphoserine aminotransferase	-	CJA_1071	13.8	13.0	13.2	14.4

D-isomer specific 2-hydroxyacid dehydrogenase	-	CJA_1072	11.1	10.9	10.7	13.4
hypothetical protein	-	CJA_1073	9.8	9.6	9.8	12.6
hydrolase, NUDIX family	-	CJA_1074	10.6	10.6	10.9	11.9
long-chain-fatty-acid--CoA ligase	fadD1	CJA_1075	11.3	10.6	11.8	12.0
hypothetical protein	-	CJA_1076	11.1	10.7	11.7	12.1
hypothetical protein	-	CJA_1077	12.5	11.4	12.8	12.3
Uvs083	uvs083	CJA_1078	9.9	9.7	9.6	10.5
hypothetical protein	-	CJA_1079	10.9	10.3	10.4	12.9
sulphite reductase	cysI	CJA_1080	10.8	10.3	10.6	13.7
hypothetical protein	-	CJA_1081	11.6	11.5	11.2	9.5
ribosomal large subunit pseudouridine synthase A	-	CJA_1082	12.0	12.5	11.5	10.3
hypothetical protein	-	CJA_1083	10.8	11.0	10.4	9.6
Integral membrane protein DUF6 domain protein	-	CJA_1084	10.6	10.4	10.7	9.9
sodium:solute symporter family protein	-	CJA_1085	11.2	11.2	11.0	10.6
hypothetical protein	-	CJA_1086	11.0	11.6	10.3	10.4
DNA-binding response regulator, LuxR family	-	CJA_1087	10.9	10.6	10.8	10.5
two-component system sensor protein	-	CJA_1088	11.6	11.3	10.7	10.2
conserved hypothetical protein TIGR00645	-	CJA_1089	11.8	12.3	11.7	11.8
FAD binding domain protein	-	CJA_1090	11.1	10.6	10.1	9.9
succinyl-diaminopimelate desuccinylase	dapE	CJA_1091	11.1	11.3	10.2	11.3
small heat shock protein	hspC2	CJA_1092	11.5	11.3	10.5	10.3
16 kDa heat shock protein A	-	CJA_1093	9.9	9.7	9.5	10.3
ABC transporter domain protein	-	CJA_1094	11.0	10.8	10.3	12.2
hypothetical protein	-	CJA_1095	11.8	10.8	10.4	11.9
hypothetical protein	-	CJA_1096	9.4	9.3	9.2	10.6
hypothetical protein	-	CJA_1097	9.3	9.1	9.3	9.3
hypothetical protein	-	CJA_1098	9.4	9.1	9.4	10.0
hypothetical protein	-	CJA_1099	12.2	11.7	11.2	13.0
tetrahydrodipicolinate N-succinyltransferase	dapD	CJA_1100	10.2	10.1	9.5	12.4
Protein yffB	-	CJA_1101	10.5	10.5	10.3	11.9
endonuclease III	-	CJA_1102	12.4	12.8	11.4	12.0
succinyl-diaminopimelate transaminase	-	CJA_1103	10.8	10.7	10.8	11.6
PII uridylyl-transferase	glnD	CJA_1104	11.0	10.6	10.2	11.3
methionine aminopeptidase, type I	map	CJA_1105	10.7	10.8	9.7	12.1
hypothetical protein	-	CJA_1106	10.0	9.9	10.1	9.2
superoxide dismutase	-	CJA_1107	11.4	10.7	11.0	9.6
gufA protein	-	CJA_1108	11.7	12.0	10.6	9.7
mannonate dehydratase	uxuA	CJA_1109	10.8	11.0	10.2	9.7
ribosomal protein S2	rpsB	CJA_1110	10.7	9.5	9.5	13.9
elongation factor Ts	tsf	CJA_1111	10.5	9.8	10.0	13.7

hypothetical protein	-	CJA_1112	11.6	11.4	11.1	12.4
hypothetical protein	-	CJA_1113	11.0	11.4	10.4	11.0
uridylate kinase	pyrH	CJA_1114	12.0	11.6	11.6	13.3
ribosome recycling factor	frr	CJA_1115	13.6	13.3	13.3	14.2
undecaprenyl diphosphate synthase	uppS	CJA_1116	10.5	10.6	9.7	11.9
phosphatidate cytidyltransferase	cdsA	CJA_1117	12.3	12.4	11.9	12.1
1-deoxy-D-xylulose 5-phosphate reductoisomerase	dxr	CJA_1118	10.5	10.8	10.0	10.7
putative membrane-associated zinc metalloprotease	-	CJA_1119	10.0	9.6	9.8	10.7
outer membrane protein, bacterial surface antigen family	-	CJA_1120	12.6	12.2	12.3	13.1
putative outer membrane protein OmpH	-	CJA_1121	9.9	9.4	9.5	12.4
UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	lpxD	CJA_1122	10.4	10.3	9.8	12.0
(3R)-hydroxymyristoyl-ACP dehydratase	fabZ	CJA_1123	11.0	10.4	10.6	13.1
UDP-N-acetylglucosamine acyltransferase	lpxA	CJA_1124	10.9	11.1	10.5	12.4
lipid-A-disaccharide synthase, putative, lpx19A	lpx19A	CJA_1125	9.7	9.7	9.8	11.1
ribonuclease HII	rnhB	CJA_1126	12.6	12.6	12.1	12.1
DNA polymerase III subunit alpha	dnaE	CJA_1127	12.1	12.0	11.3	11.9
CBS domain protein	-	CJA_1128	10.8	10.3	13.3	10.2
acetyl-CoA carboxylase, carboxyl transferase, alpha subunit	accA	CJA_1129	11.4	11.0	10.3	13.2
hypothetical protein	-	CJA_1130	8.9	8.9	9.0	8.9
L-lactate dehydrogenase	lldD	CJA_1131	10.4	11.3	9.5	9.1
L-fucose permease	fucP	CJA_1132	11.1	11.5	11.0	9.2
Amidohydrolase family superfamily	-	CJA_1133	10.6	12.0	10.0	9.2
transcriptional regulator kdgR	kdgR	CJA_1134	11.4	11.7	11.1	9.9
D-threo-aldose 1-dehydrogenase-like protein	-	CJA_1135	10.9	12.5	10.0	9.0
hydrolase, UxaA family	-	CJA_1136	11.9	12.9	10.3	9.1
hydrolase, UxaA family	uxaA	CJA_1137	10.5	10.2	9.9	9.1
oxidoreductase UCPA	-	CJA_1138	9.8	9.9	9.8	9.3
putative fumarylacetoacetate hydrolase family protein	-	CJA_1139	10.6	10.4	9.9	9.6
putative 1,4-beta-D-glucan glucohydrolase cel3D	cel3D	CJA_1140	11.7	11.6	11.1	10.4
hypothetical protein	-	CJA_1141	11.1	10.4	11.7	11.4
OmpA family protein	-	CJA_1142	11.2	11.9	10.8	9.2
hypothetical protein	-	CJA_1143	11.2	12.5	10.9	11.5
phosphoribosylaminoimidazole carboxylase ATPase subunit	purK	CJA_1144	11.8	12.6	10.8	12.2
phosphoribosylaminoimidazole carboxylase, catalytic subunit	purE	CJA_1145	10.4	9.7	9.7	12.2
sodium bicarbonate cotransporter	-	CJA_1146	11.4	11.9	10.5	9.0
rubisco operon transcriptional regulator	rbcR	CJA_1147	10.6	11.1	10.5	9.6
apbE family protein	-	CJA_1148	10.7	10.1	10.1	11.2
putative sulfate transporter YchM	sul1	CJA_1149	10.5	11.0	10.3	9.9
recombination associated protein	rdgC	CJA_1150	10.0	9.6	10.2	12.0
peptidylprolyl cis-trans isomerase	fkfB	CJA_1151	11.8	12.3	10.2	13.0

hypothetical protein	-	CJA_1152	12.3	12.2	11.4	10.8
hypothetical protein	-	CJA_1153	11.7	12.0	11.1	9.6
ferrous iron transport protein B	feoB	CJA_1154	9.7	9.7	9.7	10.6
ferrous iron transport protein	-	CJA_1155	9.5	9.5	9.4	10.2
hypothetical protein	-	CJA_1156	11.1	10.3	12.3	11.1
TonB-dependent receptor	-	CJA_1157	10.0	10.2	9.7	9.1
hypothetical protein	-	CJA_1158	10.8	10.6	11.2	9.9
tryptophan halogenase	-	CJA_1159	10.0	9.8	10.6	9.3
BadF/BadG/BcrA/BcrD ATPase family superfamily	-	CJA_1160	11.9	12.1	11.9	10.6
glucose/galactose transporter	gluP	CJA_1161	12.1	12.2	11.3	10.0
hypothetical protein	-	CJA_1162	11.8	12.2	11.1	9.5
N-acetylhexosamine 6-phosphate deacetylase, putative, nag9A	nag9A	CJA_1163	9.4	9.6	9.3	9.6
glucosamine-6-phosphate isomerase	nagB	CJA_1164	9.3	9.5	9.2	9.5
transcriptional regulator, LacI family	-	CJA_1165	12.5	12.7	12.4	12.2
periplasmic ATP/GTP-binding protein	-	CJA_1166	9.4	9.5	9.6	9.5
hypothetical protein	-	CJA_1167	9.7	9.5	10.0	10.4
RDD family domain protein	-	CJA_1168	13.0	12.6	12.3	11.8
chaperone protein hscC	hscC	CJA_1169	11.5	11.4	10.6	11.9
chemotaxis motA protein	motA1	CJA_1170	11.2	11.3	11.4	11.1
chemotaxis protein MotB	motB	CJA_1171	10.8	11.5	11.5	10.5
hypothetical protein	-	CJA_1172	9.7	9.6	9.8	10.7
transporter, monovalent cation:proton antiporter-2 (CPA2) family	-	CJA_1173	12.7	12.3	12.0	12.8
von Willebrand factor type A domain protein	-	CJA_1174	10.5	10.3	10.5	9.6
RNA polymerase sigma-24 factor	-	CJA_1175	9.6	9.8	9.3	9.2
transglutaminase-like domain protein	-	CJA_1176	11.0	11.0	10.3	9.4
hypothetical protein	-	CJA_1177	10.3	10.5	9.7	9.2
MoxR protein	-	CJA_1178	11.6	11.7	10.5	10.0
putative Capsule biosynthesis protein capA	-	CJA_1179	11.0	10.9	10.6	9.7
GGDEF domain protein	-	CJA_1180	9.8	10.4	9.4	9.2
endo-chitinase, putative, chi18A	chi18A	CJA_1182	10.6	11.3	9.9	9.7
Mg-dependent DNase	-	CJA_1183	10.0	11.0	9.3	9.3
hypothetical protein	-	CJA_1184	11.9	12.2	11.3	10.5
ThiF family protein	-	CJA_1185	10.9	10.6	10.2	10.9
Response regulator receiver domain protein	-	CJA_1186	9.7	9.5	9.9	9.5
methyl-accepting chemotaxis protein	-	CJA_1187	10.8	10.7	10.7	9.5
chemotaxis protein methyltransferase CheR	-	CJA_1188	10.8	10.9	10.1	9.5
response regulator	-	CJA_1189	11.2	11.4	10.6	9.7
Response regulator receiver domain protein	-	CJA_1190	9.9	10.3	9.6	9.0
carbohydrate binding protein, putative, cbp6A	cbp6A	CJA_1191	10.1	10.6	10.9	9.4
transcriptional regulator, GntR family/aminotransferase class-I	-	CJA_1192	10.0	10.7	10.0	9.9

transporter, LysE family	-	CJA_1193	11.0	12.2	10.9	9.6
DGPF domain family	-	CJA_1194	11.0	11.0	11.3	9.9
hypothetical protein	-	CJA_1195	9.2	9.4	9.5	9.0
EF hand domain protein	-	CJA_1196	10.3	10.4	10.6	9.4
hypothetical heme receptor	hupA	CJA_1197	9.9	9.7	10.0	9.3
azurin	azu	CJA_1198	9.4	9.4	10.1	10.7
2-nitropropane dioxygenase	-	CJA_1199	9.6	10.1	9.7	9.2
hypothetical protein	-	CJA_1200	9.4	9.5	9.5	9.0
transcriptional regulator, LysR family	-	CJA_1201	10.2	9.9	11.2	11.4
hypothetical protein	-	CJA_1202	10.0	10.1	10.3	10.3
GGDEF domain protein	-	CJA_1203	9.2	9.3	9.4	9.6
hypothetical protein	-	CJA_1204	9.0	9.1	9.1	9.5
hypothetical protein	-	CJA_1205	9.1	9.8	9.1	9.2
hypothetical protein	-	CJA_1206	9.9	9.9	10.7	9.2
Domain of unknown function (DUF955) family	-	CJA_1207	9.4	9.3	10.1	10.9
Helix-turn-helix motif	sinR	CJA_1208	9.0	9.0	9.1	10.6
hypothetical protein	-	CJA_1209	9.5	9.4	9.6	9.9
hypothetical protein	-	CJA_1210	9.3	9.3	9.4	9.7
Fic family protein	-	CJA_1211	10.4	10.7	10.5	9.7
DNA-binding protein	-	CJA_1212	10.8	10.5	12.0	10.2
hypothetical protein	-	CJA_1213	8.9	9.0	9.0	9.6
hypothetical protein	-	CJA_1214	9.1	9.0	9.3	10.4
hypothetical protein	-	CJA_1215	8.8	8.8	8.8	9.2
hypothetical protein	-	CJA_1216	9.1	9.0	9.3	9.8
antirestriction protein family protein	-	CJA_1217	9.1	9.2	9.3	8.9
putative lipoprotein	-	CJA_1218	9.0	9.1	9.2	8.9
hypothetical protein	-	CJA_1221	9.1	9.0	9.2	8.9
hypothetical protein	-	CJA_1222	8.9	8.9	9.0	8.9
hypothetical protein	-	CJA_1223	10.5	11.8	10.1	8.9
putative lipoprotein	-	CJA_1224	10.6	11.2	10.5	9.0
hypothetical protein	-	CJA_1225	9.0	9.0	9.1	8.8
invertase/recombinase like protein	-	CJA_1226	9.8	10.0	9.7	9.2
putative lipoprotein	-	CJA_1227	9.1	9.1	10.0	9.0
hypothetical protein	-	CJA_1228	8.9	8.9	9.6	8.9
hypothetical protein	-	CJA_1229	9.2	9.2	9.5	9.0
putative two-component transcriptional regulator, LuxR family	-	CJA_1230	9.0	9.0	9.3	9.1
hypothetical protein	-	CJA_1231	10.5	10.3	11.1	9.7
hypothetical protein	-	CJA_1232	9.3	9.4	9.4	9.0
TraG/TraD family	-	CJA_1233	9.3	9.9	9.2	9.0
hypothetical protein	-	CJA_1234	9.0	9.0	9.0	8.9

Site-specific recombinase	ccrB	CJA_1236	9.2	9.3	9.4	9.2
putative branched-chain amino acid transport protein (ABC superfamily, ATP_	-	CJA_1237	9.2	9.2	9.4	9.0
branched-chain amino acid ABC transporter, ATP-binding protein	-	CJA_1238	10.1	10.2	10.4	9.4
possible permease of ABC transporter	-	CJA_1239	9.9	10.0	11.1	9.3
Branched-chain amino acid transport system / permease component domain	-	CJA_1240	10.6	10.3	11.6	9.2
ABC transporter, substrate-binding protein	-	CJA_1241	10.3	10.2	14.7	9.3
GntR-family transcriptional regulator	gntR	CJA_1242	10.4	9.9	11.5	9.0
urea amidolyase	-	CJA_1243	10.4	10.7	12.3	9.0
urea amidolyase	-	CJA_1244	9.6	10.0	13.0	9.0
Fic family protein	-	CJA_1245	9.4	9.1	9.9	10.2
deoxyguanosinetriphosphate triphosphohydrolase-like protein	-	CJA_1246	10.9	10.6	11.7	10.9
hypothetical protein	-	CJA_1248	11.4	12.1	11.8	10.6
hypothetical protein	-	CJA_1249	11.9	12.0	12.7	12.0
possible ribosomal protein S6 modification protein	-	CJA_1250	9.3	9.4	9.3	10.4
ribosomal protein S6 modification protein	-	CJA_1251	9.4	9.5	9.3	10.2
hypothetical protein	-	CJA_1252	14.6	13.8	14.1	9.9
hypothetical protein	-	CJA_1253	13.9	12.2	13.7	9.7
IS66 family element, transposase	-	CJA_1254	9.4	9.5	10.4	10.4
IS66 family element, transposase	-	CJA_1257	11.7	11.1	13.2	11.5
hypothetical protein	-	CJA_1258	8.8	8.9	8.8	8.8
ParB-like nuclease domain	-	CJA_1259	9.5	9.8	9.6	9.1
hypothetical protein	-	CJA_1263	9.3	9.4	9.5	9.1
hypothetical protein	-	CJA_1264	9.6	9.4	10.3	9.3
sensory box/GGDEF family protein	-	CJA_1265	10.6	11.4	10.6	11.5
hypothetical protein	-	CJA_1266	10.5	11.0	10.6	9.4
hypothetical protein	-	CJA_1267	11.2	11.2	11.5	11.6
hypothetical protein	-	CJA_1268	10.4	10.1	11.0	10.4
DNA repair protein RadA	radA	CJA_1269	9.9	10.0	10.6	11.4
hypothetical protein	-	CJA_1270	9.6	9.4	9.4	9.7
hypothetical protein	-	CJA_1271	10.6	11.2	10.4	10.1
probable NAGC-like transcription regulator yajF	-	CJA_1272	10.1	10.6	10.1	11.0
hypothetical protein	-	CJA_1273	9.2	9.4	9.6	10.8
oxidoreductase	-	CJA_1274	10.1	10.0	10.3	11.1
hypothetical protein	-	CJA_1275	8.9	9.0	9.0	9.4
hypothetical protein	-	CJA_1276	10.8	10.4	11.4	10.9
pectate lyase III	pelC	CJA_1277	10.6	10.6	9.6	9.5
oxidoreductase, short chain dehydrogenase/reductase family	-	CJA_1278	11.2	11.4	11.9	11.1
flavodoxin	-	CJA_1279	9.9	9.4	9.9	10.0
hypothetical protein	-	CJA_1280	10.5	11.0	10.2	10.0
hypothetical protein	-	CJA_1281	10.3	10.2	10.1	9.7

hypothetical protein	-	CJA_1282	10.1	10.2	9.4	9.2
hypothetical protein	-	CJA_1283	10.3	10.3	11.6	9.7
Spore Coat Protein U domain protein	-	CJA_1284	9.6	9.4	9.3	9.1
putative type 1 pili pilus subunit	-	CJA_1285	9.7	9.5	9.6	9.0
type 1 pilus chaperone FimC	fimC	CJA_1286	11.8	12.6	10.6	9.3
type 1 pili usher protein FimD	fimD	CJA_1287	10.4	10.4	10.3	9.3
putative type 1 pili tip component	-	CJA_1288	10.7	10.9	9.8	9.1
polysaccharide deacetylase	-	CJA_1289	11.9	11.3	12.1	10.8
putative type 1 pili tip component	-	CJA_1290	10.1	10.3	11.0	9.0
Uvs045	uvs045	CJA_1291	11.3	10.9	10.0	9.6
cartilage oligomeric matrix protein	-	CJA_1292	10.8	12.2	9.4	9.2
outer membrane protein A	ompA	CJA_1293	11.8	11.2	11.6	8.9
Regulatory P domain of the subtilisin-like proprotein	-	CJA_1294	10.2	10.5	10.4	9.4
hypothetical protein	-	CJA_1295	10.2	10.4	9.9	9.3
Uncharacterized iron-regulated membrane protein DUF337	-	CJA_1296	10.6	10.7	10.1	9.3
conserved membrane-spanning domain protein	-	CJA_1297	10.5	11.0	10.1	9.4
ferripyoverdine receptor	-	CJA_1298	10.9	11.8	10.9	10.3
ExbD	exbD	CJA_1299	10.7	12.0	10.3	9.8
ExbB	exbB	CJA_1300	11.3	11.8	10.9	12.0
Uvs044	uvs044	CJA_1301	9.4	9.7	9.3	10.3
alpha amylase, putative, amy13J	amy13J	CJA_1302	11.2	11.0	10.9	9.3
hypothetical protein	-	CJA_1303	11.0	11.5	13.1	10.0
hypothetical protein	-	CJA_1304	14.3	12.8	15.0	11.6
hypothetical protein	-	CJA_1305	11.1	9.5	14.3	11.3
TonB-dependent receptor	-	CJA_1306	13.6	11.9	14.9	11.7
chromate transporter	chrA	CJA_1307	11.4	12.5	10.6	9.3
TonB-dependent receptor	-	CJA_1308	11.8	11.9	11.6	11.2
hypothetical protein	-	CJA_1309	9.7	10.0	9.8	9.1
hypothetical protein	-	CJA_1310	11.2	10.8	10.4	9.2
IS66 family element, Orf2 protein	-	CJA_1312	11.8	10.4	12.4	9.1
putative ABC transporter ATP-binding protein	-	CJA_1314	11.6	11.8	10.2	13.3
transport protein	-	CJA_1315	10.7	11.5	9.7	8.9
beta-xylosidase/alpha-L-arabinofuranosidase, putative, gly43F	gly43F	CJA_1316	10.4	10.5	9.9	9.1
putative lipoprotein	-	CJA_1317	11.5	11.2	12.6	10.1
septum site-determining protein MinC	minC	CJA_1318	11.3	12.4	10.3	11.5
septum site-determining protein MinD	minD	CJA_1319	11.5	11.6	11.2	13.0
cell division topological specificity factor MinE	minE	CJA_1320	9.1	9.0	9.0	10.5
ycel-like protein, ycel4	ycel4	CJA_1321	10.9	11.2	10.8	11.4
hypothetical protein	-	CJA_1322	10.2	10.3	10.3	10.7
radical SAM domain protein	-	CJA_1323	10.9	11.5	10.3	11.1

hypothetical protein	-	CJA_1324	12.1	12.2	11.8	11.8
phage shock protein	-	CJA_1325	10.5	11.1	11.0	11.0
hypothetical protein	-	CJA_1326	10.4	10.5	13.0	10.7
hypothetical protein	-	CJA_1327	10.5	10.7	10.0	10.5
putative translation initiation factor SUI1	-	CJA_1328	9.6	9.8	9.6	10.2
beta-lactamase	-	CJA_1329	10.6	10.6	10.0	10.6
host factor for lysis of phiX174 infection-related protein	-	CJA_1330	9.6	10.0	10.0	10.6
sensory box/GGDEF domain/EAL domain protein	-	CJA_1331	10.9	10.9	10.9	9.4
Peptidase family M48 family	-	CJA_1332	11.4	11.7	11.3	11.0
Uncharacterized protein family UPF0033 family	-	CJA_1333	9.8	9.7	9.5	10.7
putative peptidase, insulinase family	-	CJA_1334	9.7	9.9	9.3	9.4
hypothetical protein	-	CJA_1335	9.2	9.2	9.0	9.8
pyruvate dehydrogenase subunit E1	aceE	CJA_1336	9.9	9.6	9.7	13.2
glycosyl transferase, putative, gt4H	gt4H	CJA_1337	10.8	10.4	9.5	13.3
hypothetical protein	-	CJA_1338	9.4	9.8	9.4	9.4
hypothetical protein	-	CJA_1339	9.5	9.6	9.6	9.6
molybdopterin-guanine dinucleotide biosynthesis protein A	mobA	CJA_1340	11.6	12.3	11.2	10.6
pyridoxamine 5'-phosphate oxidase	pdxH	CJA_1341	11.0	10.9	10.5	11.4
alcohol dehydrogenase, zinc-containing	-	CJA_1342	9.4	9.4	9.3	10.6
CAIB/BAIF family protein	-	CJA_1343	11.3	11.9	10.9	11.9
hypothetical protein	-	CJA_1344	12.8	13.3	11.5	11.6
Cytidine and deoxycytidylate deaminase zinc-binding region domain protein	-	CJA_1345	10.7	10.4	10.4	10.4
decarboxylase family protein	-	CJA_1346	11.2	11.2	13.4	11.7
hyaluronidase, putative, hyl84A	hyl84	CJA_1347	11.5	11.6	10.8	10.4
glucose-6-phosphate isomerase	pgi	CJA_1348	10.7	10.8	10.5	13.7
phosphogluconate dehydratase	edd	CJA_1349	10.3	10.3	10.1	12.9
glucose-6-phosphate 1-dehydrogenase	zwf	CJA_1350	10.6	10.2	10.4	13.5
6-phosphogluconolactonase	pgl	CJA_1351	10.4	10.5	10.1	13.4
KHG/KDPG aldolase	kdgA	CJA_1352	11.5	11.4	10.7	13.8
glyceraldehyde-3-phosphate dehydrogenase, type I	gap	CJA_1353	12.0	10.7	10.8	14.1
pyruvate kinase	pyk	CJA_1354	10.2	9.9	9.6	13.6
hypothetical protein	-	CJA_1355	10.7	10.8	11.5	11.8
peptidase, M23/M37 family	-	CJA_1356	11.5	12.0	12.6	12.0
MORN repeat family protein	-	CJA_1357	13.3	13.0	14.3	12.3
Tetraacyldisaccharide-1-P 4-kinase	-	CJA_1358	9.8	9.5	10.7	12.3
alanyl-tRNA synthetase	alaS	CJA_1359	10.3	10.1	10.1	12.4
aspartate kinase, monofunctional class	lysC	CJA_1360	9.8	9.5	9.5	13.0
carbon storage regulator	csrA	CJA_1361	9.2	9.1	9.3	10.6
valyl-tRNA synthetase	valS	CJA_1363	10.4	10.1	10.5	12.3
capsular polysaccharide synthesis	lcbA	CJA_1364	9.8	9.7	9.9	10.1

hypothetical protein	-	CJA_1365	10.5	10.5	10.3	10.7
glycosyl transferase, putative, gt4F	gt4F	CJA_1366	10.4	11.0	10.1	11.3
glycosyl transferase, putative, gt2F	gt2F	CJA_1367	10.7	10.4	11.7	12.4
hypothetical protein	-	CJA_1368	10.0	10.7	9.5	10.7
lipopolysaccharide heptosyltransferase, putative, gt9B	gt9B	CJA_1369	10.3	10.0	9.9	11.8
hypothetical protein	-	CJA_1370	9.6	9.6	9.5	11.8
metallo-beta-lactamase family protein	-	CJA_1371	10.9	11.6	11.0	10.3
hypothetical protein	-	CJA_1372	10.0	10.2	9.6	9.8
sulfurtransferase	-	CJA_1373	12.1	11.8	12.0	11.0
transcriptional activator	-	CJA_1374	9.9	9.9	10.0	9.5
cyd operon protein YbgT	-	CJA_1375	9.4	10.0	9.3	8.9
hypothetical protein	-	CJA_1376	10.5	10.8	10.0	9.1
Lactoylglutathione lyase	-	CJA_1377	10.2	10.3	10.8	10.1
antibiotic biosynthesis monooxygenase family protein	-	CJA_1378	10.9	10.9	10.5	10.1
glutamyl-tRNA synthetase	gltX	CJA_1379	11.0	10.9	10.3	12.5
hypothetical protein	-	CJA_1381	10.0	9.7	10.4	10.6
methyl-accepting chemotaxis protein	-	CJA_1382	9.7	9.8	9.9	9.2
hypothetical protein	-	CJA_1383	9.2	9.2	9.2	9.1
hypothetical protein	-	CJA_1384	11.3	11.1	11.5	9.3
hypothetical protein	-	CJA_1385	11.4	12.0	12.6	9.8
dihydrouridine synthase family protein	-	CJA_1386	10.5	10.6	9.9	10.4
ATP-dependent RNA helicase, DEAD box family	-	CJA_1387	10.6	10.7	10.6	11.4
hypothetical protein	-	CJA_1388	10.7	9.5	15.4	10.8
PhoH-like protein	phoH	CJA_1389	12.0	10.6	15.4	10.6
hypothetical protein	-	CJA_1390	9.0	9.0	9.5	9.0
rRNA guanine-N1-methyltransferase	rrmA	CJA_1391	10.4	10.6	10.4	10.6
probable agglutination protein	-	CJA_1392	9.8	9.6	10.6	11.9
toxin secretion ATP-binding protein	-	CJA_1393	10.8	11.0	10.4	10.0
HlyD-family secretion protein	-	CJA_1394	10.7	10.9	10.6	10.5
putative two-component response regulator	-	CJA_1395	9.8	10.4	9.4	9.5
putative hemolysin	-	CJA_1396	9.7	10.4	9.6	10.9
hypothetical protein	-	CJA_1397	9.8	10.1	9.5	10.1
EAL domain protein	-	CJA_1398	12.4	12.2	11.1	9.9
hypothetical protein	-	CJA_1399	10.1	10.2	9.5	9.3
GGDEF domain protein	-	CJA_1400	10.4	10.2	10.4	9.0
Bacterial extracellular solute-binding protein domain protein	-	CJA_1401	10.3	10.6	10.3	9.1
alpha amylase, putative, amy13C	amy13C	CJA_1402	10.8	11.7	10.1	9.1
alkaline phosphatase III	-	CJA_1403	9.8	10.3	9.5	9.1
oxidoreductase alpha (molybdopterin) subunit	-	CJA_1404	10.4	11.0	10.4	9.6
regulator protein PecM	-	CJA_1405	10.7	11.8	10.4	9.1

DNA-binding response regulator CreB	-	CJA_1406	10.5	11.0	9.6	9.4
sensory histidine kinase CreC	creC	CJA_1407	9.5	9.7	9.4	9.1
hypothetical protein	creD	CJA_1408	10.7	10.8	10.3	9.0
oxidoreductase, aldo/keto reductase family	-	CJA_1409	9.5	9.5	9.6	10.8
hypothetical protein	-	CJA_1410	10.7	10.7	11.0	9.9
trans-2-enoyl-CoA reductase	-	CJA_1411	10.9	11.1	10.2	13.3
putative acyltransferase	-	CJA_1412	9.6	9.6	9.6	10.7
hypothetical protein	-	CJA_1413	9.0	9.0	9.0	9.1
putative outer membrane protein	-	CJA_1414	9.6	10.0	10.2	12.1
lipid A biosynthesis lauroyl acyltransferase	-	CJA_1415	11.1	11.3	10.7	11.3
hypothetical protein	-	CJA_1416	8.9	8.9	8.9	9.6
hypothetical protein	-	CJA_1417	9.3	9.1	9.5	10.5
hypothetical protein	-	CJA_1418	8.8	8.9	9.0	9.4
Transposase IS4 family	-	CJA_1419	10.9	10.7	11.6	11.0
hypothetical protein	-	CJA_1420	8.9	8.9	9.0	9.1
IS3 family element, transposase orfB	-	CJA_1421	10.5	11.6	10.0	9.4
relative of glycosyl transferase family GT1, gt*A	-	CJA_1422	9.8	9.9	10.6	10.4
hypothetical protein	-	CJA_1423	9.3	9.3	9.6	10.1
SapC family protein	-	CJA_1424	10.4	10.0	10.2	13.4
hypothetical protein	-	CJA_1425	9.1	9.2	14.0	9.2
putative sigma 54 modulation protein	-	CJA_1426	10.4	10.2	15.4	10.4
conserved hypothetical protein TIGR01777	-	CJA_1429	10.3	10.6	11.3	11.2
16 kDa heat shock protein A	-	CJA_1430	10.6	10.4	13.4	12.1
transcriptional regulator, AraC family	-	CJA_1431	10.1	10.4	10.8	10.4
probable beta-ketoacyl synthase	-	CJA_1432	10.7	10.9	10.9	13.3
ribosomal protein S16	rpsP	CJA_1433	9.4	9.4	9.3	13.7
16S rRNA processing protein RimM	rimM	CJA_1434	10.3	10.3	9.3	13.9
tRNA (guanine-N1)-methyltransferase	trmD	CJA_1435	10.1	10.8	9.3	13.6
ribosomal protein L19	rplS	CJA_1436	9.1	9.0	8.9	10.7
tyrosine recombinase XerD	xerD	CJA_1437	12.7	11.8	12.4	13.1
thiol:disulfide interchange protein DsbC	dsbC	CJA_1438	11.9	10.3	12.3	13.2
homoserine dehydrogenase	hom	CJA_1439	10.5	10.4	10.1	13.3
threonine synthase	thrC	CJA_1440	9.5	9.4	9.2	11.7
thioredoxin-like protein	-	CJA_1441	10.3	10.5	10.0	12.0
hypothetical protein	-	CJA_1442	9.9	10.3	9.5	9.9
ribosomal biogenesis GTPase	rbgA	CJA_1443	10.7	10.8	10.7	11.0
hypothetical protein	-	CJA_1444	11.0	10.7	10.1	10.9
hypothetical protein	-	CJA_1445	10.3	10.2	10.5	10.7
Sugar efflux transporter A	-	CJA_1446	10.3	11.2	10.8	9.6
DNA polymerase III, chi subunit	holC	CJA_1447	10.1	10.4	10.1	11.2

cytosol aminopeptidase	-	CJA_1448	10.9	11.5	11.1	11.6
putative permease, YjgP/YjgQ family superfamily	-	CJA_1449	11.4	12.2	10.6	10.8
putative permease, YjgP/YjgQ family	-	CJA_1450	10.1	10.3	9.8	9.9
putative RDD family	-	CJA_1451	10.1	10.5	9.6	9.6
hypothetical protein	-	CJA_1452	11.8	12.2	11.3	11.0
hypothetical protein	-	CJA_1453	11.5	11.6	10.4	10.2
S-adenosylmethionine:tRNA ribosyltransferase-isomerase	queA	CJA_1456	9.9	10.2	9.8	11.0
queuine tRNA-ribosyltransferase	tgt	CJA_1457	9.9	10.1	9.4	10.6
protein-export membrane protein SecD	secD	CJA_1458	10.6	10.3	10.1	13.4
protein-export membrane protein SecF	secF	CJA_1459	10.7	10.3	9.7	11.9
hypothetical protein	-	CJA_1460	8.9	8.9	8.9	9.2
two-component hybrid sensor and regulator	-	CJA_1461	11.4	11.2	11.0	10.7
endo-1,4-beta glucanase, cel5A	cel5A	CJA_1462	12.1	10.5	9.9	10.5
extragenic suppressor protein SuhB	suhB	CJA_1463	10.6	10.6	10.3	12.1
RNA methyltransferase, TrmH family, group 1	-	CJA_1464	10.7	11.6	9.4	11.9
iron-sulfur cluster assembly transcription factor IscR	iscR	CJA_1465	9.4	9.8	9.3	11.8
cysteine desulfurase used in synthesis of Fe-S cluster (tRNA 4-thiouridine sulfu	-	CJA_1466	9.6	10.4	9.2	11.4
cysteine desulfurase activator complex subunit SufB	sufB	CJA_1467	11.3	11.2	11.1	13.0
FeS assembly ATPase SufC	sufC	CJA_1468	11.6	11.4	11.7	13.4
FeS assembly protein SufD	sufD	CJA_1469	9.4	9.6	9.3	12.6
selenocysteine lyase	-	CJA_1470	10.3	10.1	10.3	13.1
HesB protein	-	CJA_1471	10.7	10.7	12.3	12.5
Domain of unknown function domain protein	-	CJA_1472	11.2	12.2	11.1	12.0
transcriptional regulator, TetR family	-	CJA_1473	9.9	10.2	9.6	10.6
AcrB/AcrD/AcrF family protein	acrB	CJA_1474	10.9	11.3	9.8	12.2
multidrug resistance protein	acrA	CJA_1475	11.1	11.3	10.6	12.6
Fe-S metabolism associated domain protein	-	CJA_1476	9.8	9.9	9.4	10.9
nucleotide diphosphate kinase	ndk	CJA_1477	9.1	9.1	9.0	11.8
radical SAM enzyme, Cfr family	-	CJA_1478	11.0	11.0	10.1	12.5
type IV pilus biogenesis protein PilF	pilF	CJA_1479	9.8	9.7	9.3	11.2
putative DNA-binding protein	-	CJA_1480	10.8	11.0	10.1	11.3
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	ispG	CJA_1481	11.2	10.6	10.8	13.0
histidyl-tRNA synthetase	hisS	CJA_1482	9.5	9.4	9.6	12.2
hypothetical protein	-	CJA_1483	11.9	11.0	13.4	13.9
PQQ enzyme repeat domain protein	-	CJA_1484	12.3	12.0	11.8	13.1
GTP-binding protein EngA	engA	CJA_1485	11.1	10.9	10.5	12.6
response regulator	-	CJA_1486	11.1	11.8	10.4	12.0
anti-anti-sigma factor	-	CJA_1487	9.3	9.5	9.2	10.6
hypothetical protein	-	CJA_1488	10.2	10.5	9.5	11.4
transaldolase B	tal	CJA_1489	10.4	10.7	10.2	12.8

tRNA-dihydrouridine synthase A	-	CJA_1490	10.2	11.0	9.6	11.1
molybdenum cofactor biosynthesis protein C	moaC	CJA_1491	9.9	10.1	9.5	10.2
molybdenum cofactor biosynthesis protein D/E	moaDE	CJA_1492	11.5	11.4	11.0	11.2
molybdenum cofactor biosynthesis protein E	-	CJA_1493	10.1	10.4	10.7	10.7
Glucose/galactose transporter	-	CJA_1494	10.8	11.5	10.0	12.3
transcriptional regulator, LacI family	-	CJA_1495	11.9	11.4	13.0	12.2
glucokinase	glk	CJA_1496	11.5	11.3	10.6	13.7
glucan 1,4-beta-glucosidase, putative, cel3B	cel3B	CJA_1497	13.6	12.5	14.9	13.8
hypothetical protein	-	CJA_1498	10.4	10.6	11.5	10.2
citrate synthase I	gltA	CJA_1499	11.4	10.7	10.6	13.9
hypothetical protein	-	CJA_1500	9.2	9.0	9.5	9.1
Succinate dehydrogenase cytochrome b subunit	-	CJA_1501	9.5	9.4	9.2	13.2
succinate dehydrogenase hydrophobic membrane anchor protein	-	CJA_1502	10.9	10.3	11.4	14.2
succinate dehydrogenase flavoprotein subunit	sdhA	CJA_1503	9.9	9.6	9.4	13.6
succinate dehydrogenase iron-sulfur subunit	sdhB	CJA_1504	8.9	8.9	8.9	12.9
2-oxoglutarate dehydrogenase E1 component	sucA	CJA_1505	9.9	9.7	9.7	13.4
dihydrolipoamide succinyltransferase	sucB	CJA_1506	9.6	9.5	9.5	13.5
dihydrolipoamide dehydrogenase	-	CJA_1507	11.2	10.5	10.6	14.4
succinyl-CoA synthetase beta chain	sucC	CJA_1508	13.4	10.9	13.9	15.0
hypothetical protein	-	CJA_1509	9.0	8.9	8.9	9.6
succinyl-CoA synthetase alpha chain	-	CJA_1510	11.7	9.8	10.9	14.1
arginine decarboxylase	speA	CJA_1511	9.6	9.4	9.2	13.1
saccharopine dehydrogenase	-	CJA_1512	9.8	9.6	9.8	13.7
carboxynorspermidine decarboxylase	nspC	CJA_1513	9.8	9.4	9.5	12.9
Na ⁺ /H ⁺ antiporter	-	CJA_1514	9.6	9.8	9.3	10.5
putative membrane-fusion protein	-	CJA_1515	9.0	8.9	9.0	8.9
putative toxin secretion ABC transporter, ATP-binding subunit/permease prot	-	CJA_1516	9.0	8.9	9.0	8.9
hypothetical protein	-	CJA_1517	9.2	8.9	9.2	9.5
hypothetical protein	-	CJA_1518	8.8	8.8	8.8	9.0
hypothetical protein	-	CJA_1519	8.8	8.8	8.8	9.0
hypothetical protein	-	CJA_1520	8.8	8.8	8.8	9.1
hypothetical protein	-	CJA_1521	8.9	8.9	8.9	9.6
alpha amylase, putative, amy13B	amy13B	CJA_1522	8.9	8.9	8.9	9.7
ABC-type multidrug efflux pump	-	CJA_1523	9.6	9.5	9.2	10.6
hypothetical protein	-	CJA_1524	9.9	10.7	10.1	11.3
hypothetical protein	-	CJA_1525	9.0	9.2	9.0	10.2
hypothetical protein	-	CJA_1526	9.5	9.6	9.1	10.1
hypothetical protein	-	CJA_1527	9.5	9.4	9.5	9.9
acetaldehyde dehydrogenase	nahO	CJA_1528	10.0	10.6	9.9	9.2
hypothetical protein	-	CJA_1529	10.3	10.3	10.7	11.9

fatty acid cis/trans isomerase	-	CJA_1530	9.8	9.9	10.1	10.7
hypothetical protein	-	CJA_1531	10.1	10.1	10.2	10.3
hypothetical protein	-	CJA_1536	9.2	9.1	8.9	12.1
hypothetical protein	-	CJA_1537	10.0	10.6	9.3	11.8
hypothetical protein	-	CJA_1538	9.5	9.6	9.2	10.7
hypothetical protein	-	CJA_1539	10.9	12.2	10.1	11.1
hypothetical protein	-	CJA_1540	9.8	9.7	9.6	10.7
hypothetical protein	-	CJA_1541	10.8	12.2	9.7	11.8
Putative transcriptional regulator	-	CJA_1542	8.9	8.9	8.9	9.8
hypothetical protein	-	CJA_1543	10.6	10.7	9.9	9.4
dienelactone hydrolase domain protein	-	CJA_1544	9.4	9.4	9.3	9.4
putative HTH-type transcriptional regulator YcjZ	-	CJA_1545	9.5	9.7	9.3	9.7
nitric oxide reductase qNor type	norB	CJA_1546	10.1	10.6	9.9	10.3
hypothetical protein	-	CJA_1547	10.4	11.4	10.0	9.9
NnrS protein superfamily	-	CJA_1548	11.7	12.0	10.8	10.6
rff2 family protein	-	CJA_1549	10.0	9.6	10.5	10.3
hypothetical protein	-	CJA_1550	9.3	9.3	9.9	9.5
putative signaling protein	-	CJA_1551	10.3	10.9	10.2	10.1
ABC transporter, ATP-binding protein	-	CJA_1552	10.0	10.1	9.8	11.4
ABC-type multidrug transport system, permease component	-	CJA_1553	11.2	11.4	11.5	12.6
7-cyano-7-deazaguanine reductase	queF	CJA_1554	11.9	13.3	10.8	11.7
probable adenylate cyclase	-	CJA_1555	9.9	10.3	9.7	10.2
hypothetical protein	-	CJA_1556	9.2	9.0	9.5	9.7
hypothetical protein	-	CJA_1557	9.0	8.9	9.0	8.9
hypothetical protein	-	CJA_1558	9.5	9.4	10.2	9.5
nitroreductase family protein	-	CJA_1559	11.6	11.3	12.2	12.0
hypothetical protein	-	CJA_1562	10.1	10.4	10.0	10.0
Luciferase-like monooxygenase	-	CJA_1563	10.4	10.8	9.7	11.1
hypothetical protein	-	CJA_1564	9.0	9.0	9.0	10.3
hypothetical protein	-	CJA_1565	10.9	10.7	11.2	12.4
putative lipoprotein	-	CJA_1566	9.2	9.2	9.1	9.8
hypothetical protein	-	CJA_1567	9.3	9.3	9.3	10.2
ribonucleotide-diphosphate reductase subunit beta	nrdB	CJA_1568	13.2	13.2	12.9	14.4
ribonucleotide-diphosphate reductase subunit alpha	nrdA	CJA_1569	11.0	11.0	10.4	13.6
Tat (twin-arginine translocation) pathway signal sequence domain protein	-	CJA_1570	10.7	11.4	9.6	9.3
hypothetical protein	-	CJA_1571	12.0	13.2	11.1	10.5
putative TonB dependent receptor	-	CJA_1572	10.1	10.0	9.6	9.0
Ser/Thr protein phosphatase family protein family	-	CJA_1573	10.1	10.3	9.8	9.1
ABC transporter substrate binding protein	-	CJA_1574	9.7	10.5	9.5	9.5
polyphosphate kinase family protein	-	CJA_1575	9.3	9.3	9.2	9.1

PIN (PiIT N terminus) domain	-	CJA_1576	10.7	11.2	9.8	10.0
fic family protein	-	CJA_1577	11.1	11.1	10.2	11.0
putative ATP-dependent DNA helicase	-	CJA_1578	11.0	11.6	11.1	12.4
phage-related regulatory protein cII	-	CJA_1579	10.5	10.9	11.0	11.6
hypothetical protein	-	CJA_1580	10.0	9.6	9.8	9.6
type III restriction-modification system methyltransferase	mod	CJA_1581	10.9	11.6	10.7	9.4
type III restriction system endonuclease	res	CJA_1582	10.6	11.0	9.9	9.1
CRISPR-associated protein, Csm2 family	csm2	CJA_1583	10.4	10.4	10.7	10.8
RloA protein	rloA	CJA_1584	11.4	11.2	11.2	12.0
hypothetical protein	-	CJA_1585	12.0	12.4	10.1	11.5
hypothetical protein	-	CJA_1586	9.7	9.6	9.3	10.5
ATP synthase, Delta/Epsilon chain, long alpha-helix domain	-	CJA_1587	10.8	11.0	10.3	10.6
hypothetical protein	-	CJA_1588	10.0	10.1	9.7	10.1
hypothetical protein	-	CJA_1589	9.7	9.9	9.4	9.2
ABC transporter permease protein	afuB_2	CJA_1590	11.0	11.5	9.7	9.3
ABC transporter, substrate binding protein	-	CJA_1591	11.0	10.9	10.8	9.5
ABC transporter ATP-binding protein	-	CJA_1592	10.7	11.1	9.3	9.1
hypothetical protein	-	CJA_1593	10.8	11.1	10.4	9.6
hypothetical protein	-	CJA_1594	9.8	10.2	9.7	9.2
hypothetical protein	-	CJA_1595	9.5	9.6	9.1	9.1
hypothetical protein	-	CJA_1596	11.6	12.1	10.7	10.5
hypothetical protein	-	CJA_1597	9.4	9.4	9.4	9.5
Auxin Efflux Carrier superfamily	-	CJA_1598	10.2	11.4	10.2	9.5
adenylylsulfate kinase	cysC	CJA_1599	11.9	12.6	11.4	10.7
Aspartyl/Asparaginyl beta-hydroxylase family	-	CJA_1600	10.4	10.9	9.8	9.6
hypothetical protein	-	CJA_1601	9.7	9.6	9.7	9.3
formyltetrahydrofolate deformylase	purU	CJA_1602	11.9	12.1	12.2	12.0
transporter, major facilitator family	-	CJA_1603	10.1	10.8	9.5	9.7
L-lactate permease	lctP	CJA_1604	11.1	11.6	10.4	9.2
carbohydrate phosphosrylase, putative, gt35A	gt35A	CJA_1605	11.5	11.9	11.4	9.7
D-lactate dehydrogenase	-	CJA_1606	10.4	10.5	11.8	9.6
putative lipoprotein	-	CJA_1607	10.8	11.4	11.4	9.7
hypothetical protein	-	CJA_1608	10.8	10.8	11.4	9.9
ABC transporter, ATP-binding protein	-	CJA_1609	10.7	10.7	10.8	9.5
ABC-type transport system, permease component	-	CJA_1610	9.9	10.5	9.7	9.4
putative pseudouridylate synthase	-	CJA_1611	10.4	10.7	9.9	10.6
hypothetical protein	-	CJA_1612	9.8	10.2	9.6	10.0
hypothetical protein	-	CJA_1613	10.4	10.4	9.9	10.8
single-stranded-DNA-specific exonuclease RecJ	recJ	CJA_1614	10.5	10.7	10.2	10.8
acyl-CoA thioesterase I	tesA	CJA_1615	10.1	10.3	11.5	10.7

ABC transporter, ATP-binding protein	-	CJA_1616	9.9	9.8	9.8	10.7
efflux ABC transporter, permease protein	-	CJA_1617	10.1	10.2	10.0	10.7
MATE domain protein	-	CJA_1618	9.9	10.2	10.2	9.8
GtrA-like protein family	-	CJA_1619	10.3	10.5	10.0	11.1
hypothetical protein	-	CJA_1620	10.6	10.2	10.0	12.4
hypothetical protein	-	CJA_1621	10.2	10.4	10.6	10.5
glycosyl transferase, putative, gt2H	gt2H	CJA_1622	11.2	11.8	10.6	11.7
hypothetical protein	-	CJA_1623	10.5	10.5	11.0	10.0
heavy metal regulator HmrR	hmrR	CJA_1624	10.3	10.7	11.0	10.5
deoxycytidine triphosphate deaminase	dcd	CJA_1625	10.3	9.7	11.0	12.7
hypothetical protein	-	CJA_1626	10.0	10.2	9.9	10.0
FKBP-type peptidyl-prolyl cis-trans isomerase	-	CJA_1627	12.7	12.2	14.1	13.3
hypothetical protein	-	CJA_1628	10.7	9.9	13.7	12.2
phosphoribosylglycinamide formyltransferase	purN	CJA_1629	11.1	12.1	10.4	12.3
phosphoribosylformylglycinamide cyclo-ligase	purM	CJA_1630	11.5	12.6	10.6	13.2
hypothetical protein	-	CJA_1631	9.5	9.5	9.5	10.3
DnaA family protein	-	CJA_1632	9.5	9.7	9.3	10.3
endo-1,4-beta glucanase, putative, cel9B	cel9B	CJA_1633	10.6	10.8	9.8	10.2
putative ADA regulatory protein	-	CJA_1634	10.5	11.0	10.2	9.6
apolipoprotein N-acyltransferase	Int	CJA_1635	12.4	12.1	12.4	10.8
magnesium and cobalt efflux protein CorC	-	CJA_1636	11.0	11.4	10.9	10.9
hypothetical protein	-	CJA_1637	11.2	11.9	11.6	12.0
PhoH-like protein	-	CJA_1638	11.6	11.4	12.4	12.3
hypothetical protein	-	CJA_1639	9.8	10.2	9.4	9.8
tRNA-i(6)A37 thiotransferase enzyme MiaB	miaB	CJA_1640	11.0	10.9	10.5	12.1
ATP-dependent RNA helicase, DEAD box family	-	CJA_1641	9.8	10.1	9.5	11.3
hypothetical protein	-	CJA_1642	9.2	9.2	9.4	8.9
hypothetical protein	-	CJA_1643	11.7	10.8	11.8	12.3
putative glycerol kinase	-	CJA_1644	10.7	11.3	9.6	10.2
serine/threonine protein kinase PpkA	ppkA	CJA_1645	11.5	12.6	10.4	9.8
protein phosphatase	-	CJA_1646	9.8	10.5	9.6	10.1
hypothetical protein	-	CJA_1647	11.9	12.6	10.7	11.4
Peptidase M16 inactive domain family	-	CJA_1648	9.8	10.2	9.6	10.7
DTW domain protein	-	CJA_1649	9.6	10.1	9.4	9.7
GIY-YIG catalytic domain protein	-	CJA_1650	11.0	11.5	10.6	11.1
smtA protein	smtA	CJA_1651	9.6	10.0	9.6	10.0
DnaJ domain protein	-	CJA_1652	9.6	9.6	9.5	9.9
putative lipoprotein	-	CJA_1653	10.2	10.0	10.3	9.6
hypothetical protein	-	CJA_1654	10.8	10.8	11.7	11.8
peptidylarginine deiminase-related protein	-	CJA_1655	10.7	10.7	11.4	12.7

glycosyl hydrolase, family 10	-	CJA_1656	10.5	10.5	10.8	12.0
hypothetical protein	-	CJA_1657	9.6	9.7	9.6	10.5
Bcp	bcp	CJA_1658	9.4	9.2	9.3	10.5
transcriptional regulator, AraC family	-	CJA_1659	9.4	8.9	10.5	10.7
preprotein translocase, YajC subunit	-	CJA_1660	9.6	9.5	9.3	10.3
DsrC	-	CJA_1661	11.5	11.4	11.4	11.2
DsrH	dsrH	CJA_1662	10.5	10.6	10.3	11.0
DsrE/DsrF-like family	-	CJA_1663	10.1	10.5	10.1	10.9
dsrE protein	dsrE	CJA_1664	10.0	10.2	9.9	10.9
integral membrane protein	-	CJA_1665	10.9	10.2	14.1	12.1
ribonuclease, Rne/Rng family protein	-	CJA_1667	11.0	10.0	10.6	13.3
hypothetical protein	-	CJA_1668	9.4	9.7	10.5	11.0
pseudouridine synthase, RluA family subfamily	-	CJA_1669	10.5	10.5	10.4	11.3
HAD-superfamily hydrolase	-	CJA_1670	10.3	10.4	10.2	11.5
septum formation protein Maf	-	CJA_1671	9.9	10.6	9.9	10.6
predicted metal-binding/nucleic acid-binding protein	-	CJA_1672	10.3	10.9	9.1	13.0
ribosomal protein L32	rpmF	CJA_1673	9.0	8.9	8.9	11.9
putative glycerol-3-phosphate acyltransferase PlsX	plsX	CJA_1674	10.2	10.1	10.1	12.2
malonyl CoA-acyl carrier protein transacylase	fabD	CJA_1675	11.3	10.8	11.3	13.2
3-oxoacyl-(acyl-carrier-protein) reductase	fabG	CJA_1676	10.2	10.2	10.6	13.3
acyl carrier protein	acpP	CJA_1677	9.3	9.0	9.2	12.4
Beta-ketoacyl synthase, N-terminal domain protein	-	CJA_1678	10.0	9.9	9.7	12.5
4-amino-4-deoxychorismate lyase	pabC	CJA_1679	11.0	10.4	11.1	11.7
Uncharacterized BCR, YceG family	-	CJA_1680	11.7	11.5	11.3	11.4
glutaminyl-tRNA synthetase	glnS	CJA_1681	11.6	11.6	11.5	13.2
cysteinyl-tRNA synthetase	cysS	CJA_1682	10.5	10.0	10.2	12.1
hypothetical protein	-	CJA_1683	9.4	9.2	10.4	12.1
cytochrome C assembly protein	-	CJA_1684	12.4	12.6	11.5	11.7
signal recognition particle protein	ffh	CJA_1685	10.8	10.4	9.7	12.4
conserved hypothetical protein TIGR00149	-	CJA_1686	12.0	10.8	11.3	11.8
type III effector HopPmaJ(Pto)	-	CJA_1687	11.5	11.3	11.7	12.4
malate dehydrogenase	sfcA1	CJA_1688	10.9	10.7	11.1	12.0
yecA family protein subfamily	-	CJA_1689	9.2	9.0	9.9	11.0
hypothetical protein	-	CJA_1690	9.7	9.2	10.4	11.7
aldehyde dehydrogenase	-	CJA_1691	12.2	11.8	11.7	12.2
3-ketoacyl-CoA thiolase	fadA	CJA_1693	11.2	10.8	12.5	10.9
hypothetical protein	-	CJA_1694	11.4	11.5	10.7	10.6
hypothetical protein	-	CJA_1695	9.9	10.1	9.9	10.8
hypothetical protein	-	CJA_1696	10.7	11.4	10.7	11.0
LexA repressor	lexA	CJA_1697	9.7	10.0	10.6	11.3

putative lipoprotein	-	CJA_1698	10.9	10.2	11.7	10.4
hypothetical protein	-	CJA_1699	10.8	10.5	11.4	10.5
oxidoreductase, short chain dehydrogenase/reductase family	-	CJA_1700	11.0	10.6	11.1	10.7
flagellar protein FliS	-	CJA_1701	12.5	12.3	14.7	12.0
hypothetical protein	-	CJA_1702	11.0	11.2	13.4	11.5
flagellar protein FliS	-	CJA_1703	10.3	10.6	10.4	10.5
regulatory protein	fleQ	CJA_1704	11.1	11.0	11.0	11.6
Superfamily II DNA and RNA helicase	-	CJA_1706	10.1	10.1	9.8	12.0
bicyclomycin resistance protein	-	CJA_1707	10.8	11.4	10.6	10.4
two-component sensor	fleS	CJA_1708	10.9	10.6	13.2	11.0
transcriptional activator	fleR	CJA_1709	11.3	11.2	12.6	11.4
hypothetical protein	-	CJA_1710	9.5	9.3	9.4	9.1
hypothetical protein	-	CJA_1711	9.8	9.8	9.3	8.9
flagellar hook-basal body complex protein (FlIE)	fliE	CJA_1712	10.0	10.1	12.1	10.5
flagellar MS-ring protein	fliF	CJA_1713	10.7	10.7	13.2	10.3
flagellar motor switch protein G	fliG	CJA_1714	10.0	10.1	11.1	10.7
Flagellar assembly protein FliH	fliH	CJA_1715	10.0	10.3	9.8	10.4
flagellum-specific ATP synthase	fliI	CJA_1716	11.5	11.7	11.0	11.3
putative flagellar protein FliJ	-	CJA_1717	10.0	10.0	10.3	9.9
hypothetical protein	-	CJA_1718	10.7	10.2	13.8	11.2
response regulator	-	CJA_1719	11.3	11.8	11.5	11.2
Hpt domain protein	-	CJA_1720	10.6	10.8	11.8	11.1
putative flagellar hook-length control protein FliK	-	CJA_1721	10.5	10.5	10.4	10.6
Flagellar basal body-associated protein FliL	-	CJA_1722	10.8	10.2	13.7	11.6
flagellar motor switch protein FliM	fliM	CJA_1723	11.9	11.5	13.8	11.9
flagellar protein	fliN	CJA_1724	9.4	9.3	10.1	10.7
flagellar protein FliO	-	CJA_1725	10.5	10.2	10.5	10.5
flagellar biosynthesis protein FliP	fliP	CJA_1726	10.5	10.3	9.8	9.3
flagellar biosynthetic protein FliQ	fliQ	CJA_1727	10.1	10.0	10.4	9.8
flagellar biosynthetic protein FliR	fliR	CJA_1728	10.0	9.8	10.6	9.5
flagellar biosynthesis protein FliB	fliB	CJA_1729	10.0	10.1	10.0	9.7
hypothetical protein	-	CJA_1730	9.5	9.4	9.6	9.5
putative lipoprotein	-	CJA_1731	10.6	10.5	11.7	11.4
hypothetical protein	-	CJA_1732	10.6	10.7	10.6	10.8
Response regulator receiver domain protein	-	CJA_1733	10.1	10.1	10.1	10.6
exonuclease III	xth	CJA_1734	9.0	8.9	9.0	10.2
tail-specific protease	prc	CJA_1735	11.2	10.9	12.7	12.6
hypothetical protein	-	CJA_1736	10.8	10.9	11.1	9.9
hypothetical protein	-	CJA_1737	10.2	10.2	11.3	10.6
hypothetical protein	-	CJA_1738	9.7	9.8	11.4	10.7

hypothetical protein	-	CJA_1739	9.0	9.0	9.2	9.1
phospho-2-dehydro-3-deoxyheptonate aldolase	-	CJA_1740	10.3	10.2	9.7	12.2
phospholipase, patatin family	-	CJA_1741	10.2	10.7	10.6	10.4
putative lipoprotein	-	CJA_1742	11.4	11.2	11.3	11.9
transcriptional regulator, LysR family	-	CJA_1743	12.5	12.7	12.0	10.8
isopropylmalate isomerase large subunit	leuC	CJA_1744	11.2	11.8	10.7	12.9
3-isopropylmalate dehydratase, small subunit	leuD	CJA_1745	9.5	9.7	9.5	11.8
3-isopropylmalate dehydrogenase	leuB	CJA_1746	11.8	11.3	11.5	13.6
aspartate-semialdehyde dehydrogenase	asd	CJA_1747	10.5	10.3	10.5	12.6
hypothetical protein	-	CJA_1748	11.5	11.4	13.0	12.7
tRNA pseudouridine synthase A	truA	CJA_1749	10.9	11.0	10.2	11.0
N-(5'phosphoribosyl)anthranilate isomerase	trpF	CJA_1750	10.7	10.6	10.1	11.9
tryptophan synthase subunit beta	trpB	CJA_1751	9.9	9.8	9.5	12.4
tryptophan synthase, alpha subunit	trpA	CJA_1752	10.8	11.0	10.3	12.9
acetyl-CoA carboxylase, carboxyl transferase, beta subunit	accD	CJA_1753	11.3	10.3	11.4	13.6
folylpolyglutamate synthetase	folC	CJA_1754	10.5	11.0	10.1	12.1
Sporulation related repeat family	-	CJA_1755	10.1	10.2	10.6	10.2
CvpA family protein	cvpA	CJA_1756	10.8	10.7	10.4	11.7
amidophosphoribosyltransferase	purF	CJA_1757	9.9	10.0	9.4	12.1
O-succinylhomoserine sulfhydrylase	metZ	CJA_1758	9.5	9.6	9.3	11.5
heat shock protein 90	-	CJA_1760	10.1	9.7	10.1	13.6
methylglyoxal synthase	mgsA	CJA_1761	10.3	10.5	10.3	12.4
cold-shock domain family protein	-	CJA_1762	10.9	10.3	12.3	12.1
putative lipoprotein	-	CJA_1763	12.0	11.8	11.8	12.0
transcription-repair coupling protein Mfd	mfd	CJA_1764	10.4	11.4	9.8	11.5
Na(+)-translocating NADH-quinone reductase subunit A	nqrA	CJA_1765	10.5	10.4	10.3	14.4
Na(+)-translocating NADH-quinone reductase subunit B	nqrB	CJA_1766	12.4	12.0	11.1	14.8
Na(+)-translocating NADH-quinone reductase subunit C	nqrC	CJA_1767	11.3	9.7	10.1	14.4
Na(+)-translocating NADH-quinone reductase subunit D	nqrD	CJA_1768	11.0	10.6	10.3	14.3
NADH:ubiquinone oxidoreductase, Na(+)-translocating, E subunit	nqrE	CJA_1769	12.3	11.4	11.8	14.8
Na(+)-translocating NADH-quinone reductase subunit F	nqrF	CJA_1770	11.6	10.8	10.4	14.0
hypothetical protein	-	CJA_1771	12.7	11.9	12.8	13.4
soluble pyridine nucleotide transhydrogenase	-	CJA_1772	10.7	10.7	10.9	13.0
hypothetical protein	-	CJA_1773	10.2	10.1	11.9	9.9
hypothetical protein	-	CJA_1774	10.9	10.5	11.1	10.5
efflux ABC transporter, permease protein	-	CJA_1775	11.4	12.3	10.5	10.6
insulin-like growth factor I	-	CJA_1776	11.2	12.1	9.9	10.8
lipoprotein releasing system, permease protein	-	CJA_1777	9.5	9.9	9.5	9.7
DNA internalization-related competence protein ComEC/Rec2	-	CJA_1778	12.2	12.5	12.1	9.6
MotA/TolQ/ExbB proton channel family domain protein	-	CJA_1779	10.7	11.3	10.4	11.6

ExbD/ToIR family protein	-	CJA_1780	11.9	13.3	10.2	11.1
tetraacyldisaccharide 4'-kinase	-	CJA_1781	10.4	10.9	10.1	10.4
3-deoxy-manno-octulosonate cytidyltransferase	kdsB	CJA_1782	10.0	10.4	9.6	11.3
protein-tyrosine-phosphatase	-	CJA_1783	10.7	10.5	11.3	12.3
UDP-N-acetylpyruvoylglucosamine reductase	murB	CJA_1784	11.2	11.3	10.3	11.4
GacA	gacA	CJA_1785	10.2	10.6	11.4	11.5
excinuclease ABC, C subunit	uvrC	CJA_1786	11.8	12.9	11.4	11.3
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	pgsA	CJA_1787	12.2	12.1	12.0	11.4
RNA methyltransferase, TrmH family	-	CJA_1790	10.5	11.0	10.5	10.8
pyridoxine 5'-phosphate synthase	pdxJ	CJA_1791	11.8	11.7	11.2	12.4
peptidyl-prolyl cis-trans isomerase A (PPIaseA) (Rotamase A) (Cyclophilin A)	-	CJA_1792	11.6	11.2	11.9	12.5
hypothetical protein	-	CJA_1793	10.4	10.6	10.4	12.2
YCII-related domain family	-	CJA_1794	10.1	10.0	10.1	11.9
hypothetical protein	-	CJA_1795	9.8	10.0	10.2	11.2
PHP domain protein	-	CJA_1796	11.5	12.3	11.9	11.8
Sua5/YciO/YrdC/YwC family protein	-	CJA_1797	13.2	14.3	12.9	11.8
segregation and condensation protein A	scpA	CJA_1798	9.9	11.0	9.6	11.1
segregation and condensation protein B	-	CJA_1799	10.9	10.6	10.7	12.3
RNA pseudouridylate synthase family protein	-	CJA_1800	11.3	11.4	11.7	12.5
abfX GGDEF domain protein	abfX	CJA_1801	9.5	9.4	10.7	9.6
abfS arabinofuranosidase two component system sensor protein	abfS	CJA_1802	11.3	12.2	10.4	10.1
abfR arabinofuranosidase two component system response regulator	abfR	CJA_1803	9.7	9.7	9.7	10.9
putative periplasmic protein CpxP	-	CJA_1804	9.5	9.2	10.3	9.6
putative methyltransferase	-	CJA_1805	12.1	12.8	10.8	11.7
flavodoxin	-	CJA_1806	9.4	10.2	9.2	11.0
putative methyltransferase	-	CJA_1807	10.9	11.1	9.8	11.0
EAL domain/GGDEF domain protein	-	CJA_1808	10.1	10.5	9.9	9.4
putative response regulator/TPR domain protein	-	CJA_1809	10.3	10.2	10.4	9.7
sensor histidine kinase	-	CJA_1810	10.2	10.0	10.2	10.4
FHA domain protein	-	CJA_1811	9.7	10.2	9.8	11.3
hypothetical protein	-	CJA_1812	10.7	10.6	13.0	11.9
hypothetical protein	-	CJA_1813	11.4	11.9	10.5	10.3
putative signal transduction protein containing EAL and modified HD-GYP don	-	CJA_1814	9.3	9.7	9.1	9.1
hypothetical protein	-	CJA_1815	9.9	9.8	10.1	9.5
hypothetical protein	-	CJA_1816	9.3	9.3	9.4	9.1
hypothetical protein	-	CJA_1817	9.5	9.4	9.4	9.1
hypothetical protein	-	CJA_1818	10.2	9.9	10.6	9.7
hypothetical protein	-	CJA_1819	10.3	10.4	10.3	9.7
hypothetical protein	-	CJA_1820	9.3	9.4	9.3	9.5
gp68	-	CJA_1821	10.4	10.6	11.1	10.9

TnpT protein	tnpT	CJA_1822	9.9	10.0	10.4	10.4
hypothetical protein	-	CJA_1823	10.5	10.0	11.2	10.7
hypothetical protein	-	CJA_1824	10.5	11.1	9.8	9.3
copper resistance protein A	-	CJA_1825	11.4	11.5	10.5	10.2
hypothetical protein	copB	CJA_1826	9.7	10.4	9.3	9.6
hypothetical protein	-	CJA_1827	9.7	9.4	9.4	10.0
cytochrome c family protein	-	CJA_1828	12.7	12.8	11.7	10.7
Haloacid dehalogenase/epoxide hydrolase family:E1-E2 ATPase	copF	CJA_1829	10.8	10.9	9.8	9.4
heavy metal RND efflux membrane fusion protein, CzcB family	-	CJA_1830	10.0	10.8	9.7	9.6
heavy metal RND efflux transporter, CzcA family	-	CJA_1831	10.0	10.7	10.3	9.9
hypothetical protein	-	CJA_1832	9.3	9.4	9.3	10.1
putative cytoplasmic protein	-	CJA_1833	10.3	10.2	10.1	10.7
putative lipoprotein	-	CJA_1834	9.5	9.5	9.8	9.6
periplasmic metal-binding protein-related protein	-	CJA_1835	9.2	9.4	9.0	9.1
copper transporter	cueA	CJA_1836	10.9	11.5	10.3	11.5
Cu(I)-responsive transcriptional regulator	cueR	CJA_1837	9.2	9.2	9.3	10.2
Cd(II)/Pb(II)-responsive transcriptional regulator	cadR	CJA_1838	10.8	11.4	10.6	10.4
cation efflux family protein	-	CJA_1839	11.3	11.7	11.1	10.7
hypothetical protein	-	CJA_1840	9.8	10.8	9.6	9.2
cation efflux system protein	czcC	CJA_1841	9.6	9.6	9.2	9.2
possible RND divalent metal cation efflux membrane fusion protein CzcB precursor	-	CJA_1842	9.9	9.9	9.3	9.3
heavy metal efflux pump, CzcA family subfamily	-	CJA_1843	10.1	10.4	9.6	9.5
Nitrogen regulatory protein P-II	-	CJA_1844	10.0	10.0	9.5	9.5
PbrT protein	pbrT	CJA_1845	10.2	10.4	9.6	9.4
helix-turn-helix domain protein	-	CJA_1846	9.0	9.1	8.9	8.9
hypothetical protein	-	CJA_1847	10.5	10.6	9.6	9.5
FOG: GGDEF domain	-	CJA_1848	11.1	11.6	10.5	10.2
TnpS	tnpS	CJA_1849	9.9	10.0	9.7	9.8
Mpr protein	mpr	CJA_1850	9.8	9.7	9.9	10.2
Transposase	-	CJA_1851	9.4	9.3	9.2	8.9
chemotaxis protein CheV	cheV-2	CJA_1853	9.5	9.3	9.7	8.9
DNA-binding response regulator	kdpE	CJA_1855	9.8	9.6	10.0	11.7
two-component sensor KdpD	kdpD	CJA_1856	10.6	10.0	9.9	10.0
potassium uptake protein TrkH	trkH-2	CJA_1857	10.2	10.1	9.7	9.6
phosphorylase kinase alpha subunit	-	CJA_1858	10.1	10.1	10.6	10.9
hypothetical protein	-	CJA_1859	10.4	10.4	10.3	9.1
N-acetyltransferase and Transcription factor-like protein	-	CJA_1860	9.3	9.3	9.1	9.0
probable transmembrane sensor	-	CJA_1861	9.4	9.3	10.1	10.2
penicillin amidase family protein	-	CJA_1862	9.2	9.2	9.2	9.3
N6-hydroxylysine acetyl transferase	vbsA	CJA_1863	9.1	9.1	9.0	8.9

hypothetical protein	-	CJA_1864	9.2	9.1	9.2	9.0
hypothetical protein	-	CJA_1865	9.3	9.2	9.3	8.9
renal dipeptidase family protein	-	CJA_1866	9.6	9.3	9.2	8.9
pyoverdine ABC transporter, permease/ATP-binding protein	pvdE	CJA_1867	9.3	9.3	9.2	8.9
TonB-dependent receptor protein	-	CJA_1868	9.7	9.6	9.6	9.6
lipase/esterase family protein	-	CJA_1869	9.1	9.1	9.0	9.4
peptide synthase	-	CJA_1870	9.4	9.4	9.3	9.8
amino acid adenylation domain protein	-	CJA_1871	9.3	9.2	9.1	9.0
putative syrP protein	-	CJA_1872	9.7	10.2	9.3	9.1
thioesterase	-	CJA_1873	9.5	9.8	9.3	9.3
MbtH-like protein-related protein	-	CJA_1874	9.7	9.5	10.0	9.4
diaminobutyrate--2-oxoglutarate aminotransferase	-	CJA_1875	10.6	11.8	10.5	9.1
hypothetical protein	-	CJA_1876	9.8	10.1	9.3	8.9
hypothetical protein	-	CJA_1877	8.8	8.8	8.8	8.8
peptide synthase	-	CJA_1878	10.0	11.0	9.3	9.1
hypothetical protein	-	CJA_1879	9.2	9.1	9.4	8.9
PsbS	psbS	CJA_1880	9.7	9.7	9.9	9.4
hypothetical protein	-	CJA_1881	9.4	9.4	11.4	9.3
4-alpha-glucanotransferase, putative, mal77	mal77Q	CJA_1882	9.1	9.2	9.4	9.3
glycoside hydrolase, putative, gly57A	gly57A	CJA_1883	10.2	10.0	11.6	10.0
glucose-1-phosphate adenylyltransferase	glgC	CJA_1884	10.9	11.4	13.4	11.1
glycogen branching enzyme	gbe13A	CJA_1885	10.6	12.0	11.3	10.8
ADP-glucose:starch glucosyltransferase, gt5A	gt5A	CJA_1886	11.2	12.0	11.9	10.9
phosphoglucomutase	pgm	CJA_1887	11.8	11.7	10.8	12.0
Uvs037	uvs037	CJA_1888	11.0	11.0	10.9	11.8
cupin-fold protein	-	CJA_1889	11.2	11.8	11.0	11.0
possible hydrolase	-	CJA_1890	11.9	11.8	12.0	11.9
glutaredoxin NrdH-related protein	-	CJA_1891	9.3	9.1	9.3	10.0
P(-)rp(+) fimbrial protein	-	CJA_1892	10.2	11.7	9.9	10.5
hypothetical protein	-	CJA_1893	10.4	10.3	11.0	10.9
MiaB-like tRNA modifying enzyme YliG, TIGR01125	-	CJA_1894	10.4	11.2	10.1	11.6
hypothetical protein	-	CJA_1895	9.6	10.0	9.7	9.9
Aminotransferases class-I	patB	CJA_1896	11.1	11.5	10.7	10.6
response regulator	-	CJA_1897	10.8	11.2	10.3	10.6
putative sensory box histidine kinase/response regulator	-	CJA_1898	10.8	10.7	10.2	10.4
Generic methyltransferase	-	CJA_1899	10.2	10.4	10.4	11.5
hypothetical protein	-	CJA_1900	10.6	10.9	11.1	12.1
chemotaxis protein CheY	-	CJA_1901	10.3	9.8	11.5	11.3
hypothetical protein	-	CJA_1902	9.8	10.0	9.7	11.4
hypothetical protein	-	CJA_1903	10.3	10.9	9.8	11.0

hypothetical protein	-	CJA_1904	10.7	10.8	10.3	11.4
hypothetical protein	-	CJA_1905	11.4	11.2	11.9	12.1
delta-aminolevulinic acid dehydratase	hemB	CJA_1906	11.0	11.0	10.5	11.8
hypothetical protein	-	CJA_1907	9.9	10.1	9.8	10.7
lytic murein transglycosylase, putative, slt23E	slt23E	CJA_1908	9.6	9.7	9.5	10.5
DNA ligase, NAD-dependent	ligA	CJA_1909	11.0	11.1	10.6	11.7
cell division protein ZipA	zipA	CJA_1910	10.2	10.5	9.9	11.5
chromosome segregation protein SMC	smc	CJA_1911	10.1	10.3	9.8	11.7
cytochrome c-type biogenesis protein CcmI	ccmI	CJA_1912	11.7	12.3	11.5	11.5
Cytochrome c-type biogenesis protein cycL precursor	-	CJA_1913	10.2	10.0	9.9	10.6
Flagellar hook-associated protein 2	fliD	CJA_1916	11.9	10.9	14.3	11.5
flagellin	flaA	CJA_1917	13.1	11.9	14.4	12.6
FlaG	-	CJA_1918	9.2	9.0	10.2	10.2
flagellin	-	CJA_1919	15.2	10.2	15.4	14.0
hypothetical protein	-	CJA_1920	10.6	10.4	10.1	9.8
flagellar hook-associated protein type 3 FlgL	flgL	CJA_1921	9.9	9.9	11.5	10.3
flagellar hook-associated protein 1 FlgK	flgK	CJA_1922	10.3	10.4	10.3	10.8
endo-beta-N-acetylglucosaminidase, putative, acm73B	acm73B	CJA_1923	10.6	10.0	12.4	10.9
flagellar basal body P-ring protein	flgI	CJA_1924	10.2	10.3	12.7	10.7
flagellar L-ring protein FlgH	flgH	CJA_1925	11.4	10.8	14.6	11.5
flagellar basal body rod protein FlgG	flgG	CJA_1926	11.9	11.2	15.0	12.2
flagellar basal-body rod protein FlgF	flgF	CJA_1927	9.9	10.1	11.6	10.8
flagellar hook protein FlgE	flgE	CJA_1928	10.0	10.0	10.5	11.1
flagellar basal-body rod modification protein FlgD	flgD	CJA_1929	12.7	12.9	14.9	12.6
flagellar basal body rod protein FlgC	flgC	CJA_1930	10.5	10.2	14.6	12.1
flagellar basal-body rod protein FlgB	flgB	CJA_1931	9.7	9.7	11.9	10.8
hypothetical protein	-	CJA_1932	9.0	9.0	9.0	9.2
chemotaxis protein methyltransferase CheR	-	CJA_1933	10.5	10.3	10.5	9.8
chemotaxis protein CheV	-	CJA_1934	10.4	9.8	13.4	10.9
putative flagella basal body P-ring formation protein FlgA	-	CJA_1935	9.4	9.3	10.3	9.6
putative negative regulator of flagellin synthesis FlgM	-	CJA_1936	10.3	9.7	14.5	12.0
FlgN protein superfamily	-	CJA_1937	9.6	9.7	12.9	11.0
16S ribosomal RNA methyltransferase RsmE	-	CJA_1939	11.4	11.8	11.4	11.2
thiosulfate sulfurtransferase	-	CJA_1940	9.6	9.6	9.5	9.2
hypothetical protein	-	CJA_1941	11.3	11.2	12.3	11.3
deoxyribodipyrimidine photolyase	phrB	CJA_1942	10.3	10.1	9.9	10.2
hypothetical protein	-	CJA_1943	10.1	10.4	9.8	10.1
hypothetical protein	-	CJA_1944	8.9	8.9	9.0	9.0
transcriptional regulator CysB	cysB	CJA_1945	10.2	9.3	12.9	11.4
5-nucleotidase	ushA	CJA_1946	11.4	11.4	11.4	11.5

carbon-nitrogen hydrolase family protein	-	CJA_1947	10.7	11.3	10.6	11.2
putative transporter	-	CJA_1948	10.4	10.5	11.3	10.4
chorismate synthase	aroC	CJA_1949	9.8	10.0	9.5	11.3
modification methylase, HemK family	-	CJA_1950	10.5	11.1	10.1	11.5
GTP cyclohydrolase I	folE	CJA_1951	10.5	10.6	10.3	12.2
Serine/threonine protein phosphatase	-	CJA_1952	12.5	12.6	11.7	11.5
hypothetical protein	-	CJA_1953	10.3	10.3	10.4	11.1
hydrolase, alpha/beta fold family	-	CJA_1954	10.8	10.8	10.8	11.5
phosphohistidine phosphatase SixA	sixA	CJA_1955	10.1	10.3	10.1	11.7
possible lipase	-	CJA_1956	9.7	9.4	11.8	12.1
NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	gpsA	CJA_1957	11.0	10.9	10.9	12.0
Potential flavoprotein oxygenase, DIM6/NTAB family	-	CJA_1958	10.3	10.1	9.8	11.6
outer membrane iron(III) dicitrate receptor	-	CJA_1963	9.9	10.2	10.0	10.4
bifunctional protein 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-m	fold	CJA_1964	12.7	12.6	12.3	13.4
RNA pseudouridine synthase family protein	-	CJA_1965	11.1	11.4	10.6	11.6
ribosomal small subunit pseudouridine synthase A	rsuA1	CJA_1966	12.8	12.6	12.1	11.6
putative ribosomal RNA small subunit methyltransferase C	-	CJA_1967	9.9	10.1	9.6	10.0
hypothetical protein	-	CJA_1969	10.3	10.4	9.5	10.7
hydrolase, alpha/beta fold family domain protein	-	CJA_1970	11.0	11.2	10.9	9.9
pseudouridine synthase Rlu family protein	-	CJA_1971	10.1	10.6	10.4	10.5
acetyltransferase, CysE/LacA/LpxA/NodL family	lacA	CJA_1972	9.5	9.7	9.4	9.8
Ferredoxin-dependent glutamate synthase	-	CJA_1973	10.7	11.0	10.9	10.1
hypothetical protein	-	CJA_1974	10.3	9.7	11.1	10.9
Uncharacterized protein family UPF0016 family	-	CJA_1975	10.3	10.9	9.9	10.4
HIT-like protein	-	CJA_1976	10.6	10.2	10.8	10.8
4-alpha-glucanotransferase, putative, mal77A	mal77A	CJA_1977	10.4	10.2	10.2	10.6
Yail/YqxD family protein superfamily	-	CJA_1978	9.9	10.8	9.7	9.7
ATP-dependent RNA helicase DeaD	deaD-1	CJA_1979	9.7	9.5	9.2	12.3
hypothetical protein	-	CJA_1980	10.1	9.5	10.3	10.1
ATP-dependent helicase HepA	hepA	CJA_1981	9.5	9.6	9.3	11.7
aldose 1-epimerase family protein	-	CJA_1982	10.2	10.6	9.9	11.1
malate dehydrogenase	mdh	CJA_1983	10.5	9.8	9.8	13.6
dUTPase	dut	CJA_1984	10.5	10.2	11.3	12.2
sensory box/GGDEF family protein	-	CJA_1985	11.3	11.9	10.6	10.9
deoxyribonuclease, TatD family	-	CJA_1986	9.6	9.9	9.5	11.6
hypothetical protein	-	CJA_1987	11.2	12.1	10.2	11.8
type 4 fimbrial biogenesis protein PilZ	pilZ	CJA_1988	9.5	9.4	9.7	10.5
DNA polymerase III, delta prime subunit	holB	CJA_1989	9.5	10.0	9.4	9.8
hypothetical protein	-	CJA_1990	12.7	13.3	12.3	9.8
ribosomal large subunit pseudouridine synthase A	-	CJA_1991	12.4	13.3	11.5	11.1

putative traF	-	CJA_1992	11.4	10.4	10.6	12.1
thymidylate kinase	tmk	CJA_1993	10.2	10.2	9.9	10.7
peptidyl-prolyl cis-trans isomerase B	ppiB-1	CJA_1994	10.3	10.1	9.8	12.5
UDP-2,3-diacetylglucosamine hydrolase	lpxH	CJA_1995	9.7	9.7	9.5	10.3
hypothetical protein	-	CJA_1996	11.2	11.2	11.4	11.5
tRNA-(MS[2]IO[6]A)-hydroxylase subfamily	miaE	CJA_1997	9.2	9.0	9.3	10.7
hypothetical protein	-	CJA_1998	9.9	10.0	9.9	11.7
trehalase, putative, tre37B	tre37B	CJA_1999	10.8	11.1	11.2	13.0
gluconolactonase precursor	gnl	CJA_2000	12.5	13.1	12.2	13.5
bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	acnB	CJA_2001	10.9	10.5	10.5	13.6
putative peptidyl-prolyl cis-trans isomerase D	-	CJA_2002	9.5	9.2	9.3	13.0
DNA-binding protein HU superfamily	-	CJA_2003	9.4	9.3	9.4	13.0
ATP-dependent protease La	lon	CJA_2004	11.1	11.1	13.9	13.5
ATP-dependent protease ATP-binding subunit ClpX	clpX	CJA_2005	9.6	9.8	12.0	12.7
ATP-dependent Clp protease proteolytic subunit	clpP	CJA_2006	10.3	10.2	13.6	13.7
trigger factor	tig	CJA_2007	10.3	10.0	10.0	13.6
hypothetical protein	-	CJA_2009	11.2	11.2	10.9	11.9
DNA topoisomerase I	-	CJA_2010	10.9	11.0	10.1	12.2
hypothetical protein	-	CJA_2011	9.2	9.7	9.1	9.5
hypothetical protein	-	CJA_2012	10.1	10.4	10.6	10.1
hypothetical protein	-	CJA_2013	9.7	10.3	9.8	9.8
universal stress protein family	-	CJA_2014	10.7	11.3	13.8	10.8
ABC transporter, ATP-binding protein	-	CJA_2015	9.8	10.1	10.0	11.2
hypothetical protein	-	CJA_2016	11.9	11.9	12.5	10.9
lytic murein transglycosylase, putative, lmt23A	lmt23A	CJA_2017	10.8	11.1	12.0	10.9
hypothetical protein	-	CJA_2019	9.4	9.4	10.9	11.7
peptidyl-prolyl cis-trans isomerase, cyclophilin-type domain protein	-	CJA_2020	10.8	10.5	11.4	12.3
HPP family	-	CJA_2021	10.8	11.4	10.3	11.6
hypothetical protein	-	CJA_2022	9.9	9.8	9.8	9.1
hypothetical protein	-	CJA_2023	10.4	11.8	9.9	10.2
copper-translocating P-type ATPase	-	CJA_2024	10.2	11.0	10.0	10.1
MerR-family transcriptional regulator	hmrR2	CJA_2025	10.3	10.9	10.1	10.2
outer membrane efflux protein	-	CJA_2026	9.7	9.8	9.5	9.5
multicopper oxidase	-	CJA_2027	12.1	13.8	10.9	10.2
hypothetical protein	-	CJA_2028	9.0	9.0	8.9	8.9
possible msrA, pms peptide methionine sulfoxide reductase	-	CJA_2029	10.0	9.9	11.5	9.6
assimilatory nitrate reductase	narB	CJA_2030	9.0	9.1	9.1	8.8
TonB-dependent outer membrane receptor	prrrA	CJA_2031	10.4	10.5	10.6	9.4
putative regulatory lipoprotein	-	CJA_2032	9.3	9.8	9.1	9.0
Predicted thiol oxidoreductase	-	CJA_2033	9.7	9.9	9.4	9.1

hypothetical protein	-	CJA_2034	10.3	9.7	10.8	10.1
putative lipoprotein	-	CJA_2035	9.6	10.0	9.5	9.7
hypothetical protein	-	CJA_2036	11.2	12.2	10.8	10.4
hypothetical protein	-	CJA_2037	9.6	9.8	9.5	10.1
para-aminobenzoate synthase, component I	pabB	CJA_2038	10.6	10.8	10.2	10.8
carboxymethylenebutenolidase	-	CJA_2039	11.6	11.8	11.3	11.5
pectate lyase, putative, pel10B	pel10B	CJA_2040	10.2	10.8	9.9	9.4
phosphoserine phosphatase	thrH	CJA_2041	10.1	10.5	9.9	12.2
phosphoadenosine phosphosulfate reductase	cysH	CJA_2042	11.8	12.3	11.6	11.8
protein-methionine-S-oxide reductase	-	CJA_2043	9.7	10.3	10.5	10.1
putative periplasmic protease	-	CJA_2044	9.5	9.3	9.5	10.6
hypothetical protein	-	CJA_2045	9.5	9.4	9.6	10.5
hydrolase, NUDIX family	-	CJA_2046	10.2	10.3	9.9	10.3
PA1822-like protein	-	CJA_2047	10.6	10.6	10.7	11.2
DNA polymerase III, epsilon subunit	dnaQ	CJA_2048	10.5	10.5	10.7	11.5
RNase H	rnhA	CJA_2049	10.4	10.8	10.9	11.2
Generic methyl-transferase	-	CJA_2050	9.9	10.3	10.2	9.9
hypothetical protein	-	CJA_2051	9.5	9.8	9.7	9.8
hydroxyacylglutathione hydrolase	-	CJA_2052	11.3	12.3	10.6	9.8
lytic murein transglycosylase, putative, lmt23B	lmt23B	CJA_2053	11.2	10.7	10.8	11.9
peptide ABC transporter, ATP-binding protein	-	CJA_2054	11.2	11.3	11.0	11.8
oligopeptide ABC transporter, permease protein	oppC	CJA_2055	10.8	10.5	11.3	11.9
oligopeptide transport system permease protein oppB	oppB	CJA_2056	10.5	10.9	10.7	10.9
oligopeptide ABC transporter periplasmic oligopeptide-binding protein	-	CJA_2057	10.3	10.4	12.6	11.9
oligopeptide ABC transporter periplasmic oligopeptide-binding protein	-	CJA_2058	10.7	10.9	11.8	11.8
Peptidase family M3	-	CJA_2059	10.3	10.3	10.8	11.6
hypothetical protein	-	CJA_2060	10.9	11.7	11.0	9.8
sensory box/GGDEF family protein	-	CJA_2061	10.3	10.3	11.1	9.7
hypothetical protein	-	CJA_2062	10.1	10.9	10.1	9.9
Uvs015	uvs015	CJA_2063	10.6	11.1	10.3	10.9
cytochrome c-type biogenesis protein CcmF	ccmF	CJA_2064	10.9	10.7	11.6	11.6
CycJ	-	CJA_2065	9.8	9.6	9.8	10.5
heme exporter protein CcmD	ccmD	CJA_2066	10.0	10.0	10.0	10.6
heme exporter protein C	-	CJA_2067	10.5	10.6	10.0	11.4
heme exporter protein CcmB	ccmB	CJA_2068	10.4	11.2	10.1	10.2
heme ABC exporter, ATP-binding protein CcmA	ccmA	CJA_2069	11.4	12.0	10.7	11.7
hypothetical protein	-	CJA_2070	9.9	10.6	9.7	9.6
FlhB domain protein	-	CJA_2071	9.2	9.6	9.1	9.3
sensory box protein	-	CJA_2072	10.5	10.7	10.4	10.0
alanine dehydrogenase	ald	CJA_2073	11.6	12.4	11.8	9.6

hypothetical protein	-	CJA_2074	10.4	10.8	11.9	10.3
hypothetical protein	-	CJA_2075	9.6	10.2	9.4	10.5
hypothetical protein	-	CJA_2076	13.2	14.2	12.7	9.8
hypothetical protein	-	CJA_2077	9.3	9.4	9.5	9.8
aerotaxis receptor Aer-2	aer-2	CJA_2078	10.9	11.0	12.2	11.1
adenosylmethionine-8-amino-7-oxononanoate transaminase	bioA	CJA_2079	10.9	11.8	11.2	10.9
tryptophanyl-tRNA synthetase	trpS	CJA_2080	10.7	10.7	10.2	11.7
cyclic nucleotide-binding domain protein	-	CJA_2081	10.6	10.5	10.7	10.0
putative aminopeptidase 2	-	CJA_2082	10.5	11.3	10.1	11.4
glycoprotease family protein	-	CJA_2083	11.3	11.7	10.7	12.6
adenylate kinase	adk	CJA_2084	11.9	11.3	11.6	13.9
transcriptional regulator, AsnC family	-	CJA_2085	10.3	9.9	11.5	12.1
methyl-accepting chemotaxis protein	-	CJA_2086	10.9	11.6	11.1	9.5
succinate-semialdehyde dehydrogenase	gabD	CJA_2087	10.0	11.1	9.8	10.6
potassium/proton antiporter	-	CJA_2088	11.1	11.3	11.2	12.3
exoribonuclease II	rnb	CJA_2089	9.9	9.7	9.6	11.9
Family of unknown function (DUF589) superfamily	-	CJA_2090	9.5	9.6	9.3	10.3
hypothetical protein	-	CJA_2091	8.9	8.9	8.9	9.0
hypothetical protein	-	CJA_2092	9.0	9.0	9.1	9.1
Rhs family protein	-	CJA_2093	9.2	9.0	9.1	9.0
RHS Repeat family	-	CJA_2096	9.4	9.3	9.4	9.1
IS66 family element, Orf2 protein	-	CJA_2099	13.4	11.9	13.5	9.6
putative cytoplasmic membrane protein	-	CJA_2101	9.6	9.6	9.5	9.6
Predicted deacylase	-	CJA_2102	9.6	10.3	9.2	10.9
GMP synthase	guaA	CJA_2103	10.3	10.5	10.5	13.0
inosine-5'-monophosphate dehydrogenase	guaB	CJA_2104	10.8	10.7	10.6	12.9
exodeoxyribonuclease VII, large subunit	xseA	CJA_2105	10.1	10.2	9.8	10.8
glycine oxidase ThiO	thiO	CJA_2106	10.3	10.9	9.8	11.0
thiamine biosynthesis protein ThiS	thiS	CJA_2107	9.5	9.7	9.5	10.5
thiazole synthase	thiG	CJA_2108	9.7	10.6	9.3	10.1
hypothetical protein	-	CJA_2109	10.5	10.3	11.0	10.4
putative HD-GYP hydrolase domain containing protein	-	CJA_2110	9.7	9.6	9.8	9.8
Auxin Efflux Carrier superfamily	-	CJA_2111	10.1	10.0	11.2	10.1
ammonium transporter	-	CJA_2112	11.3	11.6	12.4	10.4
himD/ihfB	himD	CJA_2113	9.7	9.5	10.5	12.1
30S ribosomal protein S1	rpsA	CJA_2114	10.2	9.8	9.7	14.3
mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	-	CJA_2115	11.4	11.6	11.6	13.3
UTP-glucose-1-phosphate uridylyltransferase	galU	CJA_2116	9.8	9.8	9.9	12.8
putative phosphomannomutase	-	CJA_2117	10.2	10.2	10.4	12.8
cytidylate kinase	cmk	CJA_2118	9.7	9.9	9.7	12.1

Orotidine 5'-phosphate decarboxylase	-	CJA_2119	11.2	11.2	11.5	13.3
integral membrane protein	comEA	CJA_2120	8.9	8.8	8.9	9.5
sulfate adenylyltransferase subunit 1	cysN	CJA_2121	11.3	11.1	10.7	13.1
sulfate adenylyltransferase subunit 2	cysD	CJA_2122	9.6	9.5	9.6	13.0
Prephenate dehydrogenase	-	CJA_2123	10.5	11.0	10.4	12.2
chorismate mutase/prephenate dehydratase	pheA	CJA_2124	11.1	11.3	10.9	13.1
DNA gyrase, A subunit	gyrA	CJA_2125	9.1	9.3	9.0	12.1
hypothetical protein	-	CJA_2126	10.4	10.5	10.6	9.4
N-ethylammelline chlorohydrolase	-	CJA_2127	10.9	11.9	10.1	11.3
3-demethylubiquinone-9 3-methyltransferase	ubiG	CJA_2128	11.0	11.6	10.4	11.8
HAD-superfamily hydrolase, subfamily IA, variant 3	-	CJA_2129	10.7	11.3	10.2	11.6
oxidoreductase, short chain dehydrogenase/reductase family	-	CJA_2130	10.5	10.6	10.4	10.8
hypothetical protein	-	CJA_2131	9.6	9.6	9.5	9.7
CheW	-	CJA_2132	9.9	10.2	10.5	10.5
CheW domain protein	-	CJA_2133	9.9	10.6	10.1	10.4
ParA family protein	-	CJA_2134	9.5	9.6	10.5	10.7
hypothetical protein	-	CJA_2135	9.5	9.6	9.8	9.6
flagellar motor protein	motC	CJA_2136	10.8	10.9	12.2	10.6
chemotaxis-specific methylesterase	cheB	CJA_2137	9.9	10.0	10.1	10.5
histidine kinase	cheA	CJA_2138	9.8	9.8	10.7	11.3
chemotaxis protein CheZ	cheZ	CJA_2139	10.4	10.2	12.5	12.2
CheY	-	CJA_2140	9.3	9.1	10.9	11.7
FliA	-	CJA_2141	10.1	10.4	10.4	11.2
flagellar number regulator FleN	fleN	CJA_2142	10.5	10.5	12.6	11.7
flagellar biosynthesis protein FlhF	flhF	CJA_2143	9.6	9.7	12.8	10.5
flagellar biosynthesis protein FlhA	flhA	CJA_2144	9.5	9.9	9.8	9.5
hypothetical protein	-	CJA_2145	10.5	11.5	10.6	10.6
hypothetical protein	-	CJA_2146	10.6	10.8	10.6	10.5
cyclopropane fatty acyl phospholipid synthase	cfa1	CJA_2147	10.0	9.7	11.4	9.6
hypothetical protein	-	CJA_2148	10.1	10.9	9.8	10.1
elongation factor P	efp	CJA_2149	10.8	10.0	10.2	13.8
hydrolase, NUDIX family domain protein	-	CJA_2150	10.2	10.0	11.8	11.2
hypothetical protein	-	CJA_2151	8.9	8.8	9.0	9.0
glutamate dehydrogenase	gdhA	CJA_2152	10.5	10.0	10.7	14.0
'Cold-shock' DNA-binding domain protein	-	CJA_2153	9.8	9.4	10.6	11.1
hypothetical protein	-	CJA_2154	8.9	9.0	9.0	9.2
hypothetical protein	-	CJA_2155	8.9	9.0	9.0	9.1
23S rRNA m(2)G2445 methyltransferase	rlmL	CJA_2156	9.9	9.9	10.0	10.7
ribosome modulation factor-related protein	-	CJA_2157	14.2	10.7	15.4	11.8
dihydroorotate dehydrogenase 2	pyrD	CJA_2158	10.4	11.0	10.9	12.4

hypothetical protein	-	CJA_2159	9.7	9.6	9.5	9.3
pullulanase, putative, pul13A	pul13A	CJA_2160	10.3	10.7	9.7	9.0
NAD-specific glutamate dehydrogenase	-	CJA_2161	9.5	9.7	9.6	9.2
MoxR-like protein	-	CJA_2162	11.8	11.6	12.8	13.2
hypothetical protein	-	CJA_2163	10.1	10.1	10.4	12.0
hypothetical protein	-	CJA_2164	10.2	10.4	9.8	11.1
von Willebrand factor type A domain protein	-	CJA_2165	10.5	10.9	10.2	11.0
TPR domain protein	-	CJA_2166	10.9	11.0	11.9	11.5
hypothetical protein	-	CJA_2167	10.1	10.2	10.9	10.9
hypothetical protein	-	CJA_2168	8.8	8.7	8.8	8.8
hypothetical protein	-	CJA_2169	9.8	10.0	10.8	9.6
aminopeptidase N	pepN	CJA_2170	10.1	10.3	10.9	11.5
hypothetical protein	-	CJA_2171	10.5	10.4	12.1	11.6
peptidase, rhomboid family	-	CJA_2172	10.3	10.2	11.3	10.7
serine/threonine protein phosphatase	-	CJA_2173	10.3	10.6	10.5	10.4
inorganic polyphosphate/ATP-NAD kinase	ppnK	CJA_2174	9.9	10.2	10.1	10.7
hypothetical protein	-	CJA_2175	11.0	11.4	10.8	10.2
cyclic nucleotide-binding domain protein	-	CJA_2176	10.1	10.0	10.7	10.0
hypothetical protein	-	CJA_2177	9.2	9.3	9.5	9.8
hypothetical protein	-	CJA_2178	10.0	11.1	10.2	10.3
hypothetical protein	-	CJA_2179	10.7	11.1	10.9	9.9
hypothetical protein	-	CJA_2180	11.0	11.2	10.3	9.9
hypothetical protein	-	CJA_2181	9.1	9.1	10.6	9.5
sensory box histidine kinase	-	CJA_2184	10.5	10.4	10.4	9.6
hypothetical protein	-	CJA_2185	10.4	10.6	10.9	10.3
tRNA (uracil-5-)-methyltransferase	trmA	CJA_2186	10.7	10.5	10.3	11.3
putative acetyltransferase, GNAT family	-	CJA_2187	9.1	9.2	9.1	9.7
hypothetical protein	-	CJA_2188	9.8	9.5	9.8	10.3
RmuC domain protein family	-	CJA_2189	10.8	11.0	11.0	10.6
glutamate racemase	murl	CJA_2190	12.6	14.1	11.1	10.5
carbohydrate binding protein, putative, cpb33A	cpb33A	CJA_2191	11.6	12.3	10.2	9.2
hexuronate transporter	exuT	CJA_2192	10.1	10.1	10.2	9.9
hypothetical protein	-	CJA_2193	10.5	11.3	10.1	10.0
UvrD/REP helicase domain protein	-	CJA_2194	10.4	10.8	9.5	10.4
cold shock protein-related protein	-	CJA_2195	9.2	9.0	9.1	10.0
Transcriptional activator protein anr	anr	CJA_2196	10.9	11.0	11.0	12.3
hypothetical protein	-	CJA_2197	9.6	9.6	9.7	11.0
hypothetical protein	-	CJA_2198	10.4	10.2	11.2	11.9
hypothetical protein	-	CJA_2199	10.8	9.4	11.7	10.4
hypothetical protein	-	CJA_2200	9.9	9.4	10.3	11.3

rhodanese-like domain protein	-	CJA_2201	10.6	10.2	10.9	11.9
hypothetical protein	-	CJA_2202	9.9	9.7	9.4	10.6
cell division protein BolA	-	CJA_2203	9.2	9.2	9.1	10.5
galactokinase	galK	CJA_2204	10.5	10.7	10.1	9.6
galactose-1-phosphate uridylyltransferase	galT	CJA_2205	10.1	11.0	10.0	9.6
diacylglycerol kinase	-	CJA_2206	11.4	11.6	11.9	10.3
membrane-associated phospholipid phosphatase	-	CJA_2207	10.2	10.2	9.8	9.1
glycosyl transferase, putative, gt1A	gt1A	CJA_2208	11.1	10.8	10.8	10.1
peptidyl-tRNA hydrolase domain protein	-	CJA_2209	11.0	11.6	11.3	11.6
positive regulator for alginate biosynthesis MucC	mucC	CJA_2210	10.3	9.9	12.5	12.2
sigma factor algU regulatory protein MucB	mucB	CJA_2211	11.2	10.9	12.4	12.3
mucA	mucA	CJA_2212	10.0	9.2	14.0	12.3
RNA polymerase sigma factor AlgU	algU	CJA_2213	10.1	9.7	11.9	11.9
L-aspartate oxidase	nadB	CJA_2214	9.8	9.9	9.6	10.9
TPR repeat family protein	-	CJA_2215	10.8	10.7	11.1	11.0
hypothetical protein	-	CJA_2216	9.8	9.8	10.2	10.9
hypothetical protein	-	CJA_2217	10.5	10.6	11.4	11.3
RNA polymerase sigma factor RpoS	rpoS	CJA_2218	10.1	9.4	12.5	11.2
lipoprotein NlpD	nlpD	CJA_2219	9.3	9.3	9.3	9.6
protein-L-isoaspartate O-methyltransferase	pcm	CJA_2220	9.2	9.2	9.3	10.4
tRNA pseudouridine synthase D	truD	CJA_2221	10.6	10.1	10.2	11.8
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	ispF	CJA_2222	10.1	10.1	10.5	11.9
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	ispD	CJA_2223	12.6	12.3	12.9	13.9
Septum formation initiator superfamily	-	CJA_2224	9.6	9.2	9.9	13.1
phosphopyruvate hydratase	eno	CJA_2225	11.2	10.3	11.8	14.0
2-dehydro-3-deoxyphosphooctonate aldolase	kdsA	CJA_2226	10.4	9.9	10.6	13.1
CTP synthetase	pyrG	CJA_2227	10.8	10.7	11.0	13.3
Regulatory protein recX	-	CJA_2228	10.4	10.0	10.9	10.9
putative lipoprotein	-	CJA_2229	12.7	11.0	15.0	13.4
recombinase A	recA	CJA_2230	12.5	12.4	14.0	13.4
competence/damage-inducible protein CinA C-terminal domain subfamily	-	CJA_2231	10.3	10.4	10.2	10.5
hypothetical protein	-	CJA_2232	10.3	10.8	10.3	9.2
hypothetical protein	-	CJA_2233	9.7	10.0	9.5	9.1
cysteine desulfurase, SufS subfamily	-	CJA_2234	9.7	9.9	9.7	9.1
major membrane protein I (MMP-I) (35 kDa antigen)	srpI	CJA_2235	9.9	9.8	10.5	9.4
Helix-turn-helix domain protein	-	CJA_2236	10.4	10.1	9.9	9.2
serine acetyltransferase	srpH	CJA_2237	11.3	11.6	10.9	9.2
Rhodanese-like domain protein	-	CJA_2238	9.8	9.5	9.9	9.1
hypothetical protein	-	CJA_2239	10.8	11.3	10.3	8.9
sulfate/thiosulfate import ATP-binding protein cysA 2	cysA-2	CJA_2240	10.1	10.5	9.9	9.6

sulfate ABC transporter, permease protein CysW	-	CJA_2241	10.1	9.9	9.7	9.4
sulfate ABC transporter, permease protein CysT	-	CJA_2242	10.3	10.0	10.1	9.3
sulfate ABC transporter, periplasmic binding protein component	-	CJA_2243	10.3	9.9	11.0	9.5
hypothetical protein	-	CJA_2244	9.3	9.1	9.4	9.2
hypothetical protein	-	CJA_2245	9.6	9.6	9.9	9.2
TonB-dependent receptor	-	CJA_2246	10.1	9.9	9.4	9.1
unidentified transporter-ATP binding	-	CJA_2247	10.6	10.4	10.4	9.4
nitroreductase family protein	-	CJA_2248	10.4	10.1	9.9	9.2
Bacterial extracellular solute-binding protein, family 5 domain protein	-	CJA_2249	10.5	11.0	10.0	9.0
ABC transporter domain protein	-	CJA_2250	10.7	10.7	10.1	9.0
Binding-protein-dependent transport systems inner membrane component dc	-	CJA_2251	10.2	10.4	10.1	9.0
ABC transporter, permease protein	-	CJA_2252	11.2	11.2	11.6	9.0
transcriptional regulator, GntR family	-	CJA_2253	10.9	10.4	10.5	9.4
putative oxidoreductase	-	CJA_2254	11.2	11.7	9.9	9.5
ferredoxin, 4Fe-4S	-	CJA_2255	11.8	11.4	11.2	9.4
ABC transporter substrate-binding protein	-	CJA_2256	12.5	11.9	12.0	9.5
ABC transporter, permease protein	-	CJA_2257	9.5	10.3	9.3	9.0
ABC transporter ATP-binding protein	-	CJA_2258	10.9	11.4	10.6	9.3
HEAT repeat protein	-	CJA_2259	10.7	11.2	10.0	9.4
hypothetical protein	-	CJA_2260	9.7	9.9	9.2	9.1
alanine acetyl transferase-like protein	-	CJA_2261	11.2	10.8	13.2	9.7
protein phosphatase family protein	-	CJA_2262	12.4	12.5	12.6	9.1
formate/nitrate transporter	-	CJA_2263	14.0	14.2	15.2	9.9
hypothetical protein	-	CJA_2264	9.1	9.1	9.1	8.9
putative oligopeptide binding protein (ABC superfamily, peri_bind)(OppA)	-	CJA_2265	10.6	10.6	10.4	9.1
Alkanesulfonate monooxygenase (FMNH2-dependentaliphatic sulfonate mon	-	CJA_2266	12.0	12.5	11.4	9.2
putative TonB dependent receptor	-	CJA_2267	11.0	11.1	10.2	9.0
hypothetical protein	-	CJA_2268	9.1	9.2	9.5	8.9
hypothetical protein	-	CJA_2269	12.1	12.3	11.2	8.9
acyl-CoA dehydrogenase family protein	-	CJA_2270	10.8	11.4	9.9	8.9
putative sulfonate monooxygenase	-	CJA_2271	9.6	9.7	9.6	8.9
hypothetical protein	-	CJA_2272	11.8	10.7	11.4	9.4
putative porin	-	CJA_2273	10.7	11.3	10.3	9.3
Mg(2+) transport ATPase	mgtC	CJA_2274	10.5	11.0	10.2	9.1
probable amidotransferase	-	CJA_2275	10.3	10.4	9.9	9.2
serine/threonine protein kinase	-	CJA_2276	9.7	10.4	9.1	9.0
putative Transcriptional regulator CadC	-	CJA_2277	10.7	10.9	9.6	9.3
4a-hydroxytetrahydrobiopterin dehydratase (PCD)	-	CJA_2278	9.6	10.1	9.8	9.4
hypothetical protein	-	CJA_2279	10.2	9.5	9.4	8.9
valine--pyruvate transaminase	avtA	CJA_2280	10.3	10.8	9.6	9.4

response regulator	-	CJA_2281	11.1	11.6	10.1	9.6
probable ribonuclease	-	CJA_2282	10.7	11.2	11.1	10.0
arsenate reductase	arsC	CJA_2283	10.8	11.2	10.9	11.3
trp repressor binding protein	-	CJA_2284	10.3	11.4	10.0	10.8
hypothetical protein	-	CJA_2285	9.9	10.9	10.0	10.9
signal peptide peptidase SppA, 67K type	sppA	CJA_2286	11.5	11.3	11.0	11.8
putative tonB-dependent receptor protein (outer membrane salicin receptor)	-	CJA_2287	12.0	12.4	11.6	9.3
hypothetical protein	-	CJA_2288	9.0	8.9	9.3	8.9
hypothetical protein	-	CJA_2289	9.8	9.3	10.4	9.0
ABC transporter, permease protein	-	CJA_2290	9.8	9.9	10.1	9.0
Bacterial extracellular solute-binding protein, family 5 domain protein	-	CJA_2291	10.8	10.3	9.9	9.0
TonB-dependent receptor protein	-	CJA_2292	11.0	10.8	10.2	9.4
transmembrane sensor	fecR	CJA_2293	11.0	11.3	10.0	9.8
RNA polymerase sigma factor, sigma-70 family	-	CJA_2294	10.8	11.6	9.9	9.9
TonB-dependent receptor protein	-	CJA_2295	10.7	10.8	10.8	9.2
transmembrane sensor	-	CJA_2296	10.3	11.6	9.6	9.6
Probable fecI Specialized sigma subunits of RNA	fecI	CJA_2297	12.3	13.0	11.0	9.9
TonB-dependent receptor protein	-	CJA_2298	12.1	12.4	11.6	9.4
fagA protein	fagA	CJA_2299	9.3	9.4	9.1	8.9
fumarate hydratase	fumC	CJA_2300	10.5	10.9	9.9	9.3
Ferric-pseudobactin 358 receptor precursor	-	CJA_2301	10.9	10.7	10.8	10.7
transcriptional regulator, LysR family	-	CJA_2302	10.8	10.7	9.7	9.6
oxidoreductase, short chain dehydrogenase/reductase family	-	CJA_2303	10.4	11.4	9.4	9.2
putative polyketide synthase	-	CJA_2304	9.6	9.2	9.2	9.1
hypothetical protein	-	CJA_2305	11.7	12.7	10.5	9.4
hypothetical protein	-	CJA_2306	10.6	10.7	9.8	9.5
hypothetical protein	-	CJA_2309	11.2	11.4	11.0	10.9
PepSY domain protein	-	CJA_2310	11.2	11.7	11.0	10.7
putative iron uptake protein	-	CJA_2311	11.8	11.4	11.8	10.2
ferrisiderophore receptor-like protein	-	CJA_2312	11.2	11.1	10.6	9.4
ABC-transport protein, ATP-binding component	-	CJA_2313	10.8	11.0	10.3	9.0
ABC-transport protein, ATP-binding component	-	CJA_2314	10.2	10.8	9.4	8.9
xenobiotic compound monooxygenase, DszA family, A subunit	-	CJA_2315	11.0	10.7	10.3	9.1
hypothetical protein	-	CJA_2316	10.2	10.0	9.8	8.9
putative dibenzothiophene desulfurization enzyme B	-	CJA_2317	10.8	10.8	10.3	8.9
hypothetical protein	-	CJA_2318	8.9	8.9	8.8	8.8
HlyD family secretion protein	-	CJA_2319	10.2	10.5	9.5	8.9
desulfurizing enzyme	-	CJA_2320	12.6	12.6	11.2	9.0
AtsB	atsB	CJA_2321	11.2	11.4	10.9	9.1
alkanesulfonate monooxygenase	-	CJA_2322	10.9	12.3	9.5	8.9

AtsB	-	CJA_2323	13.5	14.0	13.6	9.3
putative ABC transporter, substrate binding protein	-	CJA_2324	10.8	10.7	10.7	9.0
hypothetical protein	-	CJA_2325	9.4	9.5	9.3	8.8
hypothetical protein	-	CJA_2326	11.6	11.3	10.6	9.2
tonB protein	tonB-2	CJA_2327	10.9	10.9	9.8	9.1
ExbB	exbB1	CJA_2328	9.8	10.0	9.3	9.0
ExbD	exbD1	CJA_2329	9.8	9.8	9.9	9.0
hypothetical protein	-	CJA_2330	11.6	12.2	10.2	9.0
putative dibenzothiophene desulfurization enzyme B	-	CJA_2331	10.0	10.1	9.5	9.0
sigma54-dependent transcriptional regulator	sfnR	CJA_2332	10.0	10.1	9.6	9.1
putative tonB-dependent receptor protein	-	CJA_2333	11.0	11.7	10.2	9.1
putative dibenzothiophene desulfurization enzyme B	-	CJA_2334	11.2	11.6	10.6	9.0
putative alkanesulfonate monooxygenase	-	CJA_2335	10.9	11.8	10.7	9.3
hypothetical protein	-	CJA_2336	9.8	10.1	9.6	9.1
putative dibenzothiophene desulfurization enzyme B	-	CJA_2337	11.2	11.9	9.7	9.0
hypothetical protein	-	CJA_2338	9.4	9.1	9.4	8.9
hypothetical protein	-	CJA_2339	9.0	9.0	9.1	8.8
putative transport protein (ABC superfamily, atp_bind and membrane)	-	CJA_2340	10.1	10.6	9.5	8.9
ABC transporter protein, ATP-binding component	-	CJA_2341	10.2	10.2	9.7	9.0
molybdenum-pterin binding domain protein	-	CJA_2342	11.0	11.3	11.0	9.0
AtsC	-	CJA_2343	11.6	12.0	11.0	9.3
FMN reductase	msuE	CJA_2344	9.7	9.9	9.7	9.1
Rhodanese-like domain protein	-	CJA_2345	11.8	11.5	11.9	9.0
hypothetical protein	-	CJA_2346	11.3	11.3	10.8	9.1
sulfate ABC transporter, permease protein CysW	-	CJA_2347	12.5	12.7	12.9	9.7
sulfate ABC transporter, permease protein CysT	-	CJA_2348	10.8	11.6	11.0	9.8
thiosulfate ABC transporter, periplasmic thiosulfate-binding protein	cysP	CJA_2349	10.6	10.5	12.1	10.5
transporter, major facilitator family subfamily	-	CJA_2350	10.7	10.5	11.0	9.5
hypothetical protein	-	CJA_2351	10.0	9.5	10.5	9.1
antioxidant protein LsfA	-	CJA_2352	9.4	9.4	11.9	9.4
hypothetical protein	-	CJA_2353	10.1	10.9	9.5	10.3
Domain of unknown function domain protein	-	CJA_2354	11.7	12.2	10.9	10.5
hypothetical protein	-	CJA_2355	9.5	9.6	9.5	9.9
DNA mismatch repair protein MutS	mutS	CJA_2356	9.7	9.8	9.6	10.6
7-Fe ferredoxin	fdxA	CJA_2357	10.8	10.3	10.9	12.5
hypothetical protein	-	CJA_2358	10.1	10.1	10.2	10.0
vacJ lipoprotein	vacJ	CJA_2359	11.3	11.7	11.1	11.7
putative lipoprotein	-	CJA_2360	10.6	11.3	10.2	9.1
putative TonB-dependent receptor	-	CJA_2361	10.8	10.2	10.0	9.1
hypothetical protein	-	CJA_2362	12.1	12.0	10.9	10.0

hypothetical protein	-	CJA_2363	11.2	10.4	10.8	11.5
porin signal peptide protein	ifcO	CJA_2364	10.5	9.6	10.1	12.7
hypothetical protein	-	CJA_2365	9.5	9.4	9.5	9.9
hypothetical protein	-	CJA_2366	12.2	11.6	12.3	12.7
ATP-dependent helicase HrpA	hrpA	CJA_2367	10.4	10.5	9.9	10.8
putative lipoprotein	-	CJA_2368	10.0	9.5	9.8	9.6
RND transporter, Hydrophobe/Amphiphile Efflux family	-	CJA_2369	10.8	10.6	10.4	10.5
RND efflux membrane fusion protein	-	CJA_2370	10.0	10.0	10.4	10.4
hypothetical protein	-	CJA_2371	9.9	10.0	10.2	10.0
methionine-R-sulfoxide reductase	msrB	CJA_2372	10.2	10.0	10.7	10.5
aminotransferase AlaT	-	CJA_2373	10.1	10.3	10.2	11.4
predicted SAM-dependent methyltransferase	-	CJA_2374	10.5	10.8	10.6	10.6
NAD(+)/NADH kinase	-	CJA_2375	9.6	9.7	9.7	10.9
erythronate-4-phosphate dehydrogenase	pdxB	CJA_2376	12.2	11.9	12.4	12.5
hypothetical protein	-	CJA_2377	11.2	11.4	14.0	11.0
hypothetical protein	-	CJA_2378	11.2	11.6	11.9	12.7
SirA protein homolog	-	CJA_2379	9.1	9.1	9.2	10.0
hypothetical protein	-	CJA_2380	9.7	9.6	12.4	10.4
putative RNA 2'-O-ribose methyltransferase	-	CJA_2381	9.9	10.0	10.3	11.3
hypothetical protein	-	CJA_2382	9.2	9.2	9.7	11.2
ACT domain protein	-	CJA_2383	9.3	9.6	9.7	10.9
hypothetical protein	-	CJA_2384	9.3	9.7	9.2	9.0
MSHA biogenesis protein MshQ	-	CJA_2385	10.3	10.3	10.1	9.0
putative MSHA biogenesis protein MshP	-	CJA_2386	10.6	10.9	10.7	9.1
hypothetical protein	-	CJA_2387	9.8	10.2	9.9	9.1
MSHA pilin protein MshD	mshD	CJA_2388	11.1	10.9	11.1	9.3
msha pilin protein mshc	-	CJA_2389	10.4	9.5	13.6	10.2
hypothetical protein	-	CJA_2390	11.6	10.3	14.0	10.1
hypothetical protein	-	CJA_2391	9.6	9.9	9.5	9.1
MSHA biogenesis protein MshG	mshG	CJA_2392	11.4	11.1	12.0	9.7
hypothetical protein	-	CJA_2393	9.3	9.6	9.7	9.1
MSHA biogenesis protein MshE	mshE	CJA_2394	11.5	11.7	10.8	9.6
putative MSHA biogenesis protein MshN	-	CJA_2395	12.0	11.7	11.2	9.4
MSHA biogenesis protein MshM	mshM	CJA_2396	10.7	10.8	11.2	9.5
MSHA biogenesis protein MshL	mshL	CJA_2397	10.4	10.8	11.4	9.2
MSHA biogenesis protein MshK	-	CJA_2398	9.8	9.9	9.9	9.1
putative MSHA biogenesis protein MshJ	-	CJA_2399	10.5	10.1	11.3	9.1
MSHA biogenesis protein MshI	-	CJA_2400	11.5	11.9	10.9	9.1
putative MSHA biogenesis protein MshI	-	CJA_2401	11.2	11.7	11.0	9.4
RNA methyltransferase, TrmH family, group 2	-	CJA_2402	9.4	9.4	9.5	10.6

flavodoxin	-	CJA_2403	10.7	10.4	10.5	11.3
flavodoxin FldB	-	CJA_2404	10.2	10.1	9.7	11.2
D-amino acid oxidase family protein	-	CJA_2405	10.5	10.8	9.5	10.4
hypothetical protein	-	CJA_2406	10.1	10.3	10.6	9.7
hypothetical protein	-	CJA_2407	10.2	10.1	11.9	9.8
glutaminy-peptide cyclotransferase	-	CJA_2408	11.0	11.2	10.5	9.8
short chain dehydrogenase	-	CJA_2409	9.3	10.3	9.0	9.0
enoyl-CoA hydratase/isomerase family protein	-	CJA_2410	11.2	11.2	10.4	9.5
arginyl-tRNA synthetase	argS	CJA_2411	10.2	10.1	9.9	11.3
hypothetical protein	-	CJA_2412	11.0	10.5	10.7	9.1
pectate lyase, putative, pel3B	pel3B	CJA_2413	10.0	9.9	9.6	9.8
BNR/Asp-box repeat domain protein	-	CJA_2414	12.0	13.0	11.4	9.7
pectin acetyltransferase, putative, pae12A	pae12A	CJA_2415	11.1	11.3	10.8	9.7
hypothetical protein	-	CJA_2416	12.1	12.7	10.4	10.0
ATP-dependent DNA helicase DinG	dinG	CJA_2417	11.0	11.6	9.7	10.9
Acyltransferase domain protein	-	CJA_2418	11.4	11.4	10.2	11.6
aspartate carbamoyltransferase	pyrB	CJA_2419	10.6	11.4	10.1	11.2
Response regulator	-	CJA_2420	10.4	10.2	10.5	9.8
NAD binding site:D-amino acid oxidase	eryB	CJA_2421	10.3	10.5	10.2	10.3
tRNA and rRNA cytosine-C5-methylase	-	CJA_2422	11.6	11.4	10.0	10.6
hypothetical protein	-	CJA_2423	10.6	10.3	10.7	10.4
glucose-fructose oxidoreductase	gfo	CJA_2424	12.1	12.2	12.3	10.4
excinuclease ABC subunit B	uvrB	CJA_2425	11.1	10.8	11.1	10.9
transcriptional regulator, LysR family	-	CJA_2426	10.3	10.6	10.5	10.3
PEP-CTERM putative exosortase interaction domain protein	-	CJA_2427	10.6	10.9	10.9	9.8
Flavodoxin-like fold subfamily	-	CJA_2428	10.8	10.7	11.5	13.8
pirin	-	CJA_2429	11.0	11.1	11.2	13.1
NAD(P)H:quinone oxidoreductase	-	CJA_2430	11.1	10.3	11.3	13.0
Dps family protein	-	CJA_2432	10.5	10.4	12.6	12.4
acetyltransferase, GNAT family	-	CJA_2433	10.4	11.0	10.3	10.3
von Willebrand factor type A domain protein	-	CJA_2434	11.3	11.7	11.1	9.4
hypothetical protein	-	CJA_2435	9.7	10.1	9.6	10.0
hypothetical protein	-	CJA_2436	10.1	10.0	10.3	10.9
hypothetical protein	-	CJA_2437	9.9	10.0	9.6	10.7
ribonuclease D	rnd	CJA_2438	9.6	9.8	9.3	11.1
recombination protein RecR	recR	CJA_2439	9.9	10.0	9.8	11.9
conserved hypothetical protein TIGR00103	-	CJA_2440	11.0	10.0	11.3	12.7
DNA polymerase III subunits gamma and tau	dnaX	CJA_2441	11.2	11.3	10.6	11.8
hypothetical protein	-	CJA_2442	9.7	9.9	9.9	8.9
thiol peroxidase	-	CJA_2443	12.5	11.8	11.8	13.0

histidine kinase sensor protein	-	CJA_2444	10.3	10.7	10.9	9.4
two-component response regulator	-	CJA_2445	9.8	10.7	10.0	9.3
transcriptional activator MetR	metR-1	CJA_2446	9.7	10.0	9.5	10.6
MorA	-	CJA_2447	10.6	10.6	10.8	10.2
5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase	metE	CJA_2448	13.6	11.9	11.4	15.0
hypothetical protein	-	CJA_2449	9.0	9.0	9.3	9.5
hypothetical protein	-	CJA_2450	9.2	9.0	10.8	9.9
CRISPR-associated protein Cas2	cas2	CJA_2451	9.1	9.2	9.3	9.4
CRISPR-associated protein Cas1	cas1	CJA_2452	9.6	9.6	10.1	10.0
CRISPR-associated protein Cas4	cas4	CJA_2453	10.8	10.1	11.5	11.4
CRISPR-associated protein, Csd2 family	csd2	CJA_2454	9.9	9.5	10.8	11.6
CRISPR-associated protein, Csd1 family	csd1	CJA_2455	9.3	9.3	9.6	10.7
CRISPR-associated protein Cas5, Dvulg subtype	-	CJA_2456	10.1	10.2	10.3	11.0
CRISPR-associated helicase Cas3 domain protein	cas3	CJA_2457	9.2	9.2	9.4	9.9
hypothetical protein	-	CJA_2458	10.1	10.3	9.9	9.3
putative TonB-dependent receptor	-	CJA_2459	11.2	11.5	11.6	9.2
EAL domain protein	-	CJA_2460	11.2	11.1	12.3	9.5
probable sensor/response hybrid	-	CJA_2461	10.4	11.4	9.9	9.1
hypothetical protein	-	CJA_2462	10.3	9.8	11.1	9.3
hypothetical protein	-	CJA_2463	9.5	9.5	9.6	10.7
hypothetical protein	-	CJA_2464	9.0	8.9	9.2	11.1
DNA-binding protein HU family	-	CJA_2465	10.1	9.4	10.2	11.9
histidine triad family protein	-	CJA_2466	12.5	12.1	12.5	10.7
prolyl-tRNA synthetase	proS	CJA_2467	10.0	10.0	9.7	11.9
hypothetical protein	-	CJA_2468	10.3	10.7	10.8	11.2
carbohydrate binding protein, putative, cbp2F	cbp2F	CJA_2469	10.3	10.3	10.1	9.2
hypothetical protein	-	CJA_2470	8.9	8.9	8.8	8.8
endo-1,4-beta-xylanase, xyn10A	xyn10A	CJA_2471	10.8	10.0	9.8	9.0
endo-1,4-beta glucanase, cel9A	cel9A	CJA_2472	10.0	9.7	9.5	9.0
cellobiohydrolase, putative, cel6A	cel6A	CJA_2473	13.3	10.2	9.4	9.6
hypothetical protein	-	CJA_2474	10.5	8.9	8.9	9.3
endo-1, 4-beta mannanase, man5B	man5B	CJA_2475	9.9	10.2	9.3	9.0
hypothetical protein	-	CJA_2476	9.2	9.1	9.2	8.9
endo-1,4-beta-glucanase/xyloglucanase, putative, gly74A	gly74A	CJA_2477	9.9	10.7	9.3	9.0
lysyl-tRNA synthetase	lysS	CJA_2478	11.0	11.2	10.0	12.6
peptide chain release factor 2	prfB	CJA_2479	9.3	9.8	9.1	11.6
endo-1, 4-beta mannanase, man26B	man26B	CJA_2480	10.3	10.9	9.7	9.7
CobQ/CobB/MinD/ParA nucleotide binding domain protein	-	CJA_2481	11.1	11.4	10.3	11.5
AcrB/AcrD/AcrF family protein	-	CJA_2482	10.5	11.6	9.3	11.9
efflux transporter, RND family, MFP subunit	acrE	CJA_2483	11.2	11.7	10.3	13.1

hydrolase, NUDIX family	-	CJA_2484	11.0	11.5	10.2	10.2
tryptophan halogenase	-	CJA_2485	10.4	10.8	10.0	9.6
hypothetical protein	-	CJA_2486	9.3	9.2	9.1	8.9
nodulation protein	-	CJA_2487	11.7	12.2	10.5	10.3
hypothetical protein	-	CJA_2488	10.4	10.2	10.1	9.6
hypothetical protein	-	CJA_2489	9.9	9.8	10.1	9.7
tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	mnmA	CJA_2490	10.4	10.9	10.1	11.6
hypothetical protein	-	CJA_2491	9.5	9.6	9.3	10.6
adenylosuccinate lyase	purB	CJA_2492	10.5	10.7	10.1	12.9
hypothetical protein	-	CJA_2493	10.5	10.8	9.8	11.6
acetyltransferase, GNAT family	-	CJA_2494	10.3	10.6	10.1	10.4
hypothetical protein	-	CJA_2495	11.1	10.8	11.1	10.7
hypothetical protein	-	CJA_2496	11.0	10.4	12.4	11.1
hypothetical protein	-	CJA_2497	8.9	9.0	9.0	9.5
hypothetical protein	-	CJA_2498	9.7	9.6	10.0	9.9
putative protein encoding reversible inactivation of extracellular polysaccharic	-	CJA_2499	9.2	9.2	9.2	9.2
hypothetical protein	-	CJA_2500	9.3	9.2	9.3	11.2
hypothetical protein	-	CJA_2501	9.5	9.1	10.3	11.9
hypothetical protein	-	CJA_2502	9.3	9.1	9.4	10.8
hypothetical protein	-	CJA_2503	8.9	8.9	8.9	9.0
hypothetical protein	-	CJA_2504	9.4	9.3	9.8	10.2
hypothetical protein	-	CJA_2505	9.3	9.1	9.5	10.1
hypothetical protein	-	CJA_2506	9.7	9.3	9.6	9.7
hypothetical protein	-	CJA_2507	9.9	9.7	10.0	10.1
hypothetical protein	-	CJA_2508	9.1	9.0	9.1	10.4
hypothetical protein	-	CJA_2509	10.0	9.5	10.3	11.3
hypothetical protein	-	CJA_2510	10.2	9.9	9.3	9.7
hypothetical protein	-	CJA_2511	9.3	9.0	9.2	10.0
Integrase core domain protein	-	CJA_2512	10.1	9.5	10.0	10.4
hypothetical protein	-	CJA_2513	9.3	9.0	9.1	9.6
hypothetical protein	-	CJA_2514	9.7	9.2	10.3	12.1
hypothetical protein	-	CJA_2515	9.7	9.3	11.3	12.3
hypothetical protein	-	CJA_2516	10.2	9.9	10.6	11.9
Thrombospondin type 3 repeat family	-	CJA_2517	9.5	9.6	9.3	10.8
putative peptidyl-prolyl cis-trans isomerase D	-	CJA_2518	10.2	10.0	10.1	12.9
peptidyl-prolyl cis-trans isomerase D	-	CJA_2519	11.0	9.5	11.9	13.5
IPT/TIG domain protein	-	CJA_2520	10.1	9.8	10.2	11.5
Putative fatty acid transport system, membrane protein	fadL	CJA_2521	9.6	9.5	10.3	9.7
transcription regulator protein	-	CJA_2523	10.2	10.0	11.1	11.9
integration host factor, alpha subunit	ihfA	CJA_2524	9.6	9.8	11.7	12.5

phenylalanyl-tRNA synthetase, beta subunit	pheT	CJA_2525	11.1	11.5	10.7	13.1
phenylalanyl-tRNA synthetase, alpha subunit	pheS	CJA_2526	9.8	9.5	9.5	12.6
50S ribosomal protein L20	rplT	CJA_2527	9.9	9.0	9.4	13.4
50S ribosomal protein L35	rpml	CJA_2528	11.2	9.1	9.4	14.5
initiation factor 3	infC	CJA_2529	9.9	9.2	9.5	13.9
threonyl-tRNA synthetase	thrS	CJA_2530	11.6	11.4	10.9	13.5
putative sulfite reductase, flavoprotein component	-	CJA_2531	10.4	10.2	10.1	10.2
efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	-	CJA_2532	9.6	9.4	9.4	9.9
macrolide ABC efflux protein	-	CJA_2533	9.6	9.5	9.4	9.8
efflux transporter, RND family, MFP subunit	-	CJA_2534	10.4	10.4	10.5	10.1
sulfite reductase (NADPH) flavoprotein alpha-component	cysJ	CJA_2535	10.4	11.1	9.5	9.6
hypothetical protein	-	CJA_2536	9.2	9.2	9.1	10.0
hypothetical protein	-	CJA_2537	11.5	11.9	11.3	11.6
plasmolipin	-	CJA_2538	9.7	9.6	10.0	10.6
exogenous ferric siderophore TonB-dependent receptor	cirA2	CJA_2539	9.8	9.8	9.5	11.1
hypothetical protein	-	CJA_2540	10.0	10.3	9.8	10.2
yhgl protein	-	CJA_2541	11.2	11.0	11.7	12.9
B12-dependent methionine synthase	metH	CJA_2542	10.2	10.0	9.9	11.3
hypothetical protein	-	CJA_2543	9.3	9.7	9.3	9.6
hypothetical protein	-	CJA_2544	10.0	10.4	9.6	9.8
hypothetical protein	-	CJA_2545	10.4	10.3	10.6	10.7
hypothetical protein	-	CJA_2546	10.0	10.5	9.4	9.8
putative CvpA family protein	-	CJA_2547	11.6	12.0	11.8	10.3
hypothetical protein	-	CJA_2548	10.4	10.8	9.9	9.6
shikimate kinase	-	CJA_2549	11.9	11.3	12.8	10.0
Alx protein	-	CJA_2550	10.8	10.2	10.5	9.7
siroheme synthase	-	CJA_2551	12.1	12.4	11.2	11.7
seryl-tRNA synthetase	serS	CJA_2552	11.0	10.2	11.1	12.5
crcB protein	crcB	CJA_2553	12.9	12.1	12.7	13.4
ATPase, AAA family domain protein	-	CJA_2554	10.6	10.8	10.3	11.6
outer membrane lipoprotein carrier protein LolA	lolA	CJA_2555	10.9	10.9	10.8	11.5
DNA translocase ftsK	ftsK	CJA_2556	11.2	11.9	10.0	10.9
hypothetical protein	-	CJA_2557	11.9	11.1	10.8	9.7
signal-transducing histidine kinase	-	CJA_2558	9.7	9.5	9.6	9.1
two-component response regulator	-	CJA_2559	12.1	11.4	11.1	9.5
response regulator	-	CJA_2560	11.2	10.9	11.2	9.5
thioredoxin-disulfide reductase	trxB	CJA_2561	10.5	10.5	10.4	12.1
SpoVR family protein	-	CJA_2562	10.8	10.2	13.7	9.8
hypothetical protein	-	CJA_2563	10.5	9.9	14.6	10.1
protein kinase	-	CJA_2564	10.1	9.8	14.8	10.0

leucyl/phenylalanyl-tRNA--protein transferase	aat	CJA_2565	10.3	10.2	9.8	10.2
arginyl-tRNA-protein transferase	-	CJA_2566	9.6	9.5	9.4	9.4
translation initiation factor IF-1	infA	CJA_2567	9.3	9.1	9.2	10.6
ATP-binding protease component ClpA	clpA	CJA_2568	10.5	9.9	14.8	12.0
ATP-dependent Clp protease adaptor protein ClpS	clpS	CJA_2569	9.0	8.9	10.1	11.0
cold-shock protein CspD	cspD	CJA_2570	10.0	9.4	9.4	10.1
isocitrate dehydrogenase, NADP-dependent	-	CJA_2571	13.1	12.2	12.5	14.0
pseudouridylate synthase	-	CJA_2572	11.2	11.8	11.2	11.1
HD domain protein	-	CJA_2573	10.9	11.0	10.8	10.2
MazG family protein	-	CJA_2574	10.2	10.8	9.8	10.9
GTP pyrophosphokinase	-	CJA_2575	10.8	11.0	10.8	11.7
23S rRNA (uracil-5-)-methyltransferase RumA	rumA	CJA_2576	9.4	9.4	9.1	10.2
cysteine synthase B	cysM	CJA_2577	10.3	10.4	9.8	12.0
DNA repair protein RecO	recO	CJA_2578	10.2	10.6	10.2	9.5
GacS	gacS	CJA_2579	11.2	11.5	10.9	9.8
GTP-binding protein Era	era	CJA_2580	9.9	9.9	10.0	10.8
ribonuclease III	rnc	CJA_2581	9.7	10.6	9.4	10.3
hypothetical protein	-	CJA_2582	10.1	9.5	11.6	11.9
signal peptidase I	lepB	CJA_2583	11.3	11.1	11.5	12.3
GTP-binding protein LepA	lepA	CJA_2584	10.4	10.4	10.1	12.1
MucD	mucD	CJA_2585	12.7	11.3	14.6	12.6
hypothetical protein	-	CJA_2586	8.9	8.9	9.0	9.7
hypothetical protein	-	CJA_2587	11.7	11.4	13.8	11.5
putative sodium-type flagellar protein MotY	-	CJA_2588	12.1	12.8	13.5	11.0
dihydroorotase	pyrC	CJA_2589	11.2	11.7	11.5	12.1
ribonuclease T	rnt	CJA_2590	9.4	9.3	9.2	10.4
hypothetical protein	-	CJA_2591	11.8	12.2	10.7	10.8
MaoC-like domain protein	-	CJA_2592	9.3	9.6	9.2	9.8
universal stress protein family	-	CJA_2593	10.7	9.9	12.2	13.3
putative lipoprotein	-	CJA_2594	11.1	10.5	14.3	11.2
hypothetical protein	-	CJA_2595	10.0	9.7	10.7	10.9
phosphoribosylformylglycinamide synthase	purL	CJA_2596	10.4	10.5	9.8	12.6
lytic murein transglycosylase, putative, lmt23C	lmt23C	CJA_2597	10.5	10.6	10.7	10.7
ABC-type amino acid transport, signal transduction systems	-	CJA_2598	11.1	11.0	11.0	9.4
putative oxidoreductase, FAD-binding	-	CJA_2599	9.9	10.1	9.7	11.2
hypothetical protein	-	CJA_2600	9.4	9.2	9.5	10.9
transcriptional regulator, GntR family	-	CJA_2601	9.8	9.4	10.8	11.8
hypothetical protein	-	CJA_2602	11.4	10.7	11.8	12.0
hypothetical protein	-	CJA_2603	9.5	9.6	9.8	11.8
ferredoxin-NADP reductase	fpr	CJA_2604	13.1	12.7	12.7	13.9

electron transfer flavoprotein FAD-binding domain	etfA	CJA_2605	10.3	10.5	10.5	13.8
electron transfer flavoprotein beta subunit	-	CJA_2606	10.6	10.8	10.8	13.9
transcriptional regulator, LysR family	-	CJA_2607	10.2	10.4	9.8	11.5
electrotransfer ubiquinone oxidoreductase	etf-QO	CJA_2608	12.1	13.1	12.0	11.9
hypothetical protein	-	CJA_2609	11.3	11.1	11.6	10.1
beta-galactosidase, putative, bgl2C	bgl2C	CJA_2610	10.1	11.8	9.7	9.1
endo-chitinase, putative, chi18D	chi18D	CJA_2611	11.8	12.0	11.5	9.1
Dna-J like membrane chaperone protein	djIA	CJA_2612	11.0	11.1	11.2	10.0
hypothetical protein	-	CJA_2613	10.5	11.8	10.0	9.9
hypothetical protein	-	CJA_2614	10.2	10.0	9.4	8.9
carbohydrate binding protein, putative, cbp2E	cbp2E	CJA_2615	13.1	10.3	9.6	9.0
carbohydrate binding protein, putative, cbp2D	cbp2D	CJA_2616	12.2	10.3	9.7	9.3
hypothetical protein	-	CJA_2617	9.6	9.1	9.0	9.0
alpha amylase, putative, amy13A	amy13A	CJA_2618	10.2	9.8	10.8	9.2
Rhs family protein	wapA	CJA_2619	10.6	11.0	11.5	9.3
hypothetical protein	-	CJA_2620	10.1	10.0	12.1	9.3
IS66 family element, transposase	-	CJA_2622	14.0	13.1	14.1	11.4
Rhs family protein	-	CJA_2623	9.8	10.2	11.1	9.7
lactoylglutathione lyase	gloA	CJA_2624	9.8	9.9	10.0	10.3
hypothetical protein	-	CJA_2625	9.5	9.4	9.6	9.9
TRAP transporter, DctM-like membrane protein	-	CJA_2626	10.7	11.5	10.3	10.4
cytochrome oxidase maturation protein, cbb3-type	ccoS	CJA_2627	10.8	10.4	11.9	11.4
cation-transporting P-type ATPase	-	CJA_2628	10.8	11.9	10.3	10.6
hypothetical protein	-	CJA_2629	10.7	11.1	10.8	11.5
iron-sulfur cluster-binding protein	-	CJA_2630	10.8	10.6	10.6	11.8
cytochrome c oxidase, cbb3-type, subunit III	ccoP	CJA_2631	10.5	10.3	10.3	12.9
cytochrome c oxidase subunit-related protein	-	CJA_2632	10.7	10.1	10.1	13.6
cytochrome c oxidase, cbb3-type, subunit II	ccoO	CJA_2633	11.9	12.0	10.8	13.8
cytochrome c oxidase, cbb3-type, subunit I	ccoN	CJA_2634	12.7	12.0	11.6	14.0
argininosuccinate synthase	argG	CJA_2635	11.9	11.4	10.8	14.1
methyl-accepting chemotaxis protein	-	CJA_2636	10.0	10.4	10.0	9.7
exonuclease I	sbcB	CJA_2637	11.4	11.8	10.9	10.7
carbonic anhydrase	-	CJA_2638	11.7	11.6	11.0	12.4
PAS domain S-box protein	-	CJA_2639	10.9	10.9	10.8	9.3
putative response regulator	-	CJA_2640	11.0	11.4	10.4	10.3
putative SpoIIAA family protein	-	CJA_2641	9.5	9.2	9.4	10.5
fumarate hydratase, class I	-	CJA_2642	11.1	11.5	10.8	12.3
hypothetical protein	-	CJA_2643	12.0	12.0	13.2	12.2
hypothetical protein	-	CJA_2644	11.8	11.6	12.4	11.7
superoxide dismutase	-	CJA_2645	13.2	11.1	12.6	14.7

chaperonin GroEL	groL	CJA_2646	12.8	11.4	11.5	14.9
GroES protein	groES	CJA_2647	10.7	10.6	9.9	14.1
fxsA protein	fxsA	CJA_2648	10.6	11.2	9.7	9.8
hypothetical protein	-	CJA_2649	11.3	11.2	11.0	9.6
AmpG protein	-	CJA_2650	11.8	12.0	10.5	10.2
MGMT family protein	-	CJA_2651	9.0	9.1	9.0	9.1
hypothetical protein	-	CJA_2652	10.1	10.0	10.6	12.0
putative AmpE	-	CJA_2653	12.5	12.0	11.9	13.0
N-acetyl-anhydromuranmyl-L-alanine amidase	ampD	CJA_2654	10.2	10.4	10.0	9.6
probable ATPase	-	CJA_2655	11.3	11.5	10.6	10.8
hypothetical protein	-	CJA_2656	10.6	11.8	9.5	10.4
carbohydrate binding protein, putative, cbp32B	cbp32B	CJA_2657	10.1	11.0	9.3	9.4
OsmC/Ohr family protein	-	CJA_2658	10.5	10.2	10.3	11.6
cAMP-regulatory protein	-	CJA_2659	11.0	10.8	10.6	11.6
indole-3-glycerol phosphate synthase	trpC	CJA_2660	9.9	9.5	9.9	11.2
anthranilate phosphoribosyltransferase	trpD	CJA_2661	11.5	11.3	11.5	12.9
anthranilate synthase component II	trpG	CJA_2662	11.4	11.6	11.6	13.0
anthranilate synthase component I	trpE	CJA_2663	11.4	11.8	11.0	12.3
rRNA methylase	-	CJA_2664	10.0	10.4	9.6	10.5
uncharacterized FAD-dependent dehydrogenase	-	CJA_2665	11.7	12.3	10.7	11.6
ribulose-phosphate 3-epimerase	rpe	CJA_2666	11.9	11.8	11.0	11.5
hypothetical protein	-	CJA_2667	12.7	12.7	13.0	11.2
DTW domain protein	-	CJA_2668	9.5	9.4	9.2	10.2
putative preprotein translocase SecE subunit	-	CJA_2670	9.3	9.3	9.1	11.5
triosephosphate isomerase	-	CJA_2671	10.1	10.0	9.4	13.0
phosphoglucosamine mutase	glmM	CJA_2672	11.7	11.4	11.1	13.0
dihydropteroate synthase	folP	CJA_2673	11.7	11.3	11.6	12.5
cell division protein FtsH	ftsH	CJA_2674	10.9	9.9	10.6	11.6
ribosomal RNA large subunit J	rrmJ	CJA_2675	11.8	12.0	11.9	12.1
hypothetical protein	-	CJA_2676	11.8	11.2	11.6	12.1
kinesin light chain-like protein	-	CJA_2677	10.6	10.6	10.0	9.6
putative lipoprotein	-	CJA_2678	10.4	10.4	10.1	9.4
HasR	hasR	CJA_2679	10.0	9.9	10.0	8.9
sigma factor regulatory protein, FecR/PupR family	-	CJA_2680	9.9	10.9	9.3	9.2
RNA polymerase sigma factor, sigma-70 family	-	CJA_2681	10.7	10.4	10.1	9.6
Heme oxygenase	-	CJA_2682	10.1	10.3	9.6	9.2
hypothetical protein	-	CJA_2683	10.1	10.7	9.4	9.4
possible energy transducer TonB, C-terminal region	-	CJA_2684	11.5	11.2	11.1	9.9
transcription elongation factor	greA	CJA_2685	10.0	9.6	10.2	12.4
carbamoyl phosphate synthase large subunit	carB	CJA_2686	10.0	10.1	9.7	12.6

carbamoyl-phosphate synthase, small subunit	carA	CJA_2687	10.2	10.1	10.2	12.8
dihydrodipicolinate reductase	dapB	CJA_2688	11.0	11.8	10.2	11.5
GTP cyclohydrolase II	ribA	CJA_2689	10.5	10.8	10.6	11.7
putative conserved hypothetical protein TIGR02281	-	CJA_2690	10.9	11.2	10.5	11.4
Phosphatidylglycerophosphatase A	-	CJA_2691	11.0	10.8	11.6	11.4
thiamine-monophosphate kinase	thiL	CJA_2692	11.4	11.6	10.6	12.1
transcription antitermination protein NusB	nusB	CJA_2693	10.2	10.3	10.1	12.8
6,7-dimethyl-8-ribityllumazine synthase	ribH	CJA_2694	11.1	10.8	10.3	13.3
bifunctional protein 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyc	ribB/A	CJA_2695	10.1	10.0	10.2	12.7
riboflavin synthase subunit alpha	ribE	CJA_2696	12.8	14.0	11.8	12.4
RDD family domain protein	-	CJA_2697	11.6	12.3	11.3	11.2
riboflavin biosynthesis protein RibD	ribD	CJA_2698	9.6	9.9	9.3	11.0
conserved hypothetical protein TIGR00244	-	CJA_2699	9.5	9.6	9.2	10.7
putative amino acid ABC transporter, periplasmic amino acid-binding portion	-	CJA_2700	11.2	11.5	11.6	10.4
GGDEF domain protein	-	CJA_2701	10.5	11.0	11.0	10.3
hypothetical protein	-	CJA_2702	10.6	11.1	11.5	10.2
serine hydroxymethyltransferase	glyA	CJA_2703	12.8	11.7	11.2	14.4
hypothetical protein	-	CJA_2704	8.9	8.9	9.0	9.2
hypothetical protein	-	CJA_2705	10.5	10.4	10.0	9.5
alpha-xylosidase, putative, xyl31A	xyl31A	CJA_2706	11.1	11.2	11.2	11.7
beta-galactosidase, putative, bgl35A	bgl35A	CJA_2707	11.3	11.8	10.8	10.4
hypothetical protein	-	CJA_2708	8.8	8.8	8.8	8.9
TonB-dependent receptor	-	CJA_2709	9.6	9.7	9.7	9.8
alpha-L-fucosidase, putative, afc95A	afc95A	CJA_2710	10.0	10.0	10.0	9.1
hypothetical protein	-	CJA_2711	11.3	10.6	12.6	9.4
hypothetical protein	-	CJA_2712	9.4	9.3	10.0	8.9
tryptophan halogenase	-	CJA_2713	10.4	10.3	10.6	9.4
hypothetical protein	-	CJA_2714	11.7	11.5	13.5	9.2
putative outer membrane phospholipase A precursor	-	CJA_2715	11.5	11.3	12.1	10.2
hypothetical protein	-	CJA_2716	11.7	11.7	12.1	10.3
hypothetical protein	-	CJA_2717	10.6	10.6	10.8	10.8
ABC transporter, periplasmic substrate-binding protein	-	CJA_2718	11.4	12.3	14.4	9.1
ABC transporter, permease protein	-	CJA_2719	11.9	11.6	12.7	9.1
ABC transporter, ATP-binding protein	-	CJA_2720	10.3	10.9	10.9	9.0
hypothetical protein	-	CJA_2721	9.6	10.0	10.0	9.0
hypothetical protein	-	CJA_2722	11.1	10.5	11.5	9.4
urea amidolyase homolog	-	CJA_2723	9.7	10.3	10.0	9.0
hypothetical protein	-	CJA_2724	9.2	9.2	9.1	9.1
nicotinate-nucleotide pyrophosphorylase	nadC	CJA_2725	11.2	10.9	11.2	11.5
spermine/spermidine synthase family protein	-	CJA_2726	9.5	9.3	9.9	10.4

type IV pilin accessory protein	tfpZ	CJA_2727	10.2	9.8	10.9	10.5
Fimbrial protein precursor (Pilin)	pilA	CJA_2728	9.8	9.4	10.4	10.9
pilin	-	CJA_2729	13.7	10.8	13.1	13.2
PilB protein	pilB	CJA_2730	9.9	9.8	10.1	10.8
type IV pilus biogenesis protein PilC	pilC	CJA_2731	9.8	9.6	9.9	10.8
type IV pilus prepilin peptidase PilD	pilD	CJA_2732	9.6	9.5	10.2	10.7
dephospho-CoA kinase	coaE	CJA_2733	10.8	10.7	11.0	11.0
Domain of unknown function (DUF329) family	-	CJA_2734	9.4	9.2	9.4	9.7
hypothetical protein	-	CJA_2735	11.8	11.3	13.4	10.6
hypothetical protein	-	CJA_2736	9.6	9.6	9.8	10.4
putative lipoprotein	-	CJA_2737	11.2	11.2	10.9	11.1
c-type cytochrome biogenesis protein	dsbD	CJA_2738	10.6	10.5	10.5	10.1
3-dehydroquinate dehydratase	aroQ	CJA_2739	10.7	10.5	10.8	12.0
acetyl-CoA carboxylase, biotin carboxyl carrier protein	accB	CJA_2740	10.2	9.8	9.7	13.5
acetyl-CoA carboxylase, biotin carboxylase	accC	CJA_2741	10.2	10.2	9.5	12.7
ribosomal protein L11 methyltransferase	prmA	CJA_2742	12.6	13.2	12.2	12.2
MJ0042 family finger-like domain protein	-	CJA_2743	10.8	10.5	11.6	11.3
hypothetical protein	-	CJA_2744	13.6	12.6	13.1	10.0
tRNA-dihydrouridine synthase	-	CJA_2745	10.0	9.9	9.8	12.7
Hin recombinational enhancer binding protein	fis	CJA_2746	11.0	11.0	11.0	13.4
bifunctional purine biosynthesis protein PurH	purH	CJA_2747	11.7	11.0	10.9	13.5
phosphoribosylamine--glycine ligase	purD	CJA_2748	10.9	10.9	10.6	12.9
hypothetical protein	-	CJA_2749	11.0	10.8	11.5	11.8
Zn-dependent protease	-	CJA_2750	12.0	11.8	11.8	11.0
nucleic acid binding protein	-	CJA_2751	11.4	11.3	10.8	11.0
hypothetical protein	-	CJA_2752	11.5	11.1	11.4	10.6
oxidoreductase	-	CJA_2753	11.0	12.9	9.7	9.9
hypothetical protein	-	CJA_2754	10.5	10.3	10.7	11.4
hypothetical protein	-	CJA_2755	10.7	11.1	10.7	9.9
oxaloacetate decarboxylase gamma chain	-	CJA_2756	12.8	12.5	12.0	12.9
oxaloacetate decarboxylase	oadA	CJA_2757	12.6	12.6	11.4	13.1
oxaloacetate decarboxylase beta chain	-	CJA_2758	11.2	11.4	10.6	11.3
beta glucanase, putative, glu16F	glu16F	CJA_2759	11.0	11.2	10.6	9.7
cellulase, putative, cel5G	cel5G	CJA_2760	11.0	10.6	11.0	9.2
hypothetical protein	-	CJA_2761	10.2	10.0	10.9	9.2
transcriptional regulator, AraC family domain protein	-	CJA_2762	10.4	10.0	11.7	9.3
beta glucanase, putative, gly16E	glu16E	CJA_2763	9.5	9.5	9.1	8.9
glutathionylspermidine synthase family protein	-	CJA_2764	10.8	11.2	10.8	11.2
putative lipoprotein	-	CJA_2765	13.4	13.8	12.3	13.0
predicted membrane protein	-	CJA_2766	11.0	11.8	10.3	12.0

PEP-CTERM putative exosortase interaction domain protein	-	CJA_2767	11.9	11.7	11.6	11.8
cysteine synthase A	cysK	CJA_2768	11.4	12.0	10.4	10.6
alpha-L-arabinofuranosidase, abf51A	abf51A	CJA_2769	11.0	10.5	10.8	9.9
endo-1, 4-beta mannanase, man26A	man26A	CJA_2770	10.8	11.0	10.2	9.6
pentapeptide repeat domain protein	-	CJA_2771	12.8	12.4	13.8	9.5
Glucuronate isomerase	uxaC	CJA_2772	12.3	12.4	12.2	11.1
regucalcin	-	CJA_2773	11.0	10.8	10.6	10.6
hypothetical protein	-	CJA_2774	10.2	10.3	9.9	9.3
sodium/glucose cotransport protein	-	CJA_2775	10.9	10.3	10.8	11.5
short chain dehydrogenase/reductase	-	CJA_2776	10.9	10.9	10.5	11.4
transcriptional regulator, GntR family	-	CJA_2777	10.0	9.7	9.3	11.7
phosphate transport system regulatory protein PhoU	phoU	CJA_2778	10.1	10.3	10.0	9.4
phosphate ABC transporter, ATP-binding protein	pstB	CJA_2779	10.3	10.1	10.7	10.0
phosphate ABC transporter, permease protein	pstA	CJA_2780	10.5	10.2	10.8	9.6
phosphate ABC transporter, permease protein	pstC	CJA_2781	11.2	10.9	11.1	9.2
phosphate binding protein	pstS	CJA_2782	10.3	10.3	10.2	9.3
ClpXP protease specificity-enhancing factor	sspB	CJA_2783	12.1	12.5	12.9	12.2
ubiquinol--cytochrome c reductase, cytochrome b	petB	CJA_2784	11.9	12.1	10.7	13.2
ubiquinol-cytochrome c reductase, iron-sulfur subunit	petA	CJA_2785	10.8	10.6	11.2	14.0
ribosomal protein S9	rpsI	CJA_2786	11.2	11.1	9.9	13.6
ribosomal protein L13	rplM	CJA_2787	9.8	9.3	9.3	13.8
Predicted ATPase	-	CJA_2788	11.0	11.3	11.4	11.1
hypothetical protein	-	CJA_2789	11.2	11.4	11.0	10.4
hypothetical protein	-	CJA_2790	11.7	11.8	11.1	10.0
hypothetical protein	-	CJA_2791	12.8	13.2	13.6	11.4
AlgW protein	algW	CJA_2792	11.2	11.1	11.4	11.1
ABC transporter, ATP-binding protein	-	CJA_2793	11.4	11.0	10.9	12.0
histidinol dehydrogenase	hisD	CJA_2794	11.6	11.6	11.0	11.6
ATP phosphoribosyltransferase catalytic subunit	hisG	CJA_2795	11.1	11.3	10.3	12.6
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	murA	CJA_2796	10.1	10.1	9.9	12.3
BoIA/YrbA family protein	-	CJA_2797	11.6	11.4	12.0	13.1
Toluene tolerance, Ttg2 superfamily	-	CJA_2798	11.4	10.8	12.9	12.5
hypothetical protein	-	CJA_2799	11.2	11.4	11.6	10.4
sugar isomerase, KpsF/GutQ family subfamily	-	CJA_2800	11.4	11.8	10.6	12.0
phosphatase, YrbI family	-	CJA_2801	10.5	10.8	10.1	11.4
hypothetical protein	-	CJA_2802	10.7	10.8	10.3	11.3
OstA-like protein superfamily	-	CJA_2803	12.6	13.6	11.1	12.5
ABC transporter, ATP-binding protein	-	CJA_2804	10.6	10.6	10.3	11.3
hypothetical protein	-	CJA_2805	9.3	9.3	9.9	10.5
RNA polymerase factor sigma-54	rpoN	CJA_2806	10.7	10.8	11.0	11.4

ribosomal subunit interface protein	yfiA	CJA_2807	11.6	10.2	14.5	13.6
phosphotransferase enzyme IIA	ptsN	CJA_2808	11.7	11.6	13.6	13.1
hypothetical protein	-	CJA_2809	11.9	11.4	12.9	13.0
Phosphocarrier protein HPr (Histidine-containing protein)	pstH	CJA_2810	10.3	9.9	11.9	11.8
hypothetical protein	-	CJA_2811	10.0	9.9	10.3	10.0
hypothetical protein	-	CJA_2812	11.2	11.0	12.6	12.5
ribonuclease, Rne/Rng family	-	CJA_2813	10.3	10.7	10.3	11.5
septum formation protein Maf	-	CJA_2814	10.6	10.8	10.3	11.3
putative rod shape-determining protein MreD	-	CJA_2815	14.0	13.6	14.0	12.8
rod shape-determining protein MreC	mreC	CJA_2816	12.6	12.8	11.2	12.5
rod shape-determining protein MreB	mreB	CJA_2817	11.7	11.0	11.5	13.4
aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C	gatC	CJA_2818	10.3	10.0	9.9	12.0
aspartyl/glutamyl-tRNA amidotransferase subunit A	gatA	CJA_2819	9.8	10.0	9.6	11.9
aspartyl/glutamyl-tRNA amidotransferase subunit B	gatB	CJA_2820	11.6	11.2	11.0	12.9
hypothetical protein	-	CJA_2821	10.2	9.7	10.9	11.8
OmpA family protein	-	CJA_2823	12.5	10.9	13.8	13.9
internalin E	inIE	CJA_2824	12.7	12.4	13.6	12.5
hypothetical protein	-	CJA_2825	12.4	12.8	13.0	12.3
hypothetical protein	-	CJA_2826	10.7	10.9	10.9	11.6
phosphoribosylaminoimidazole-succinocarboxamidesynthase	purC	CJA_2827	12.4	11.6	11.7	13.1
metallo-beta-lactamase superfamily domain protein	-	CJA_2828	10.6	10.7	11.2	12.2
putative lipoprotein	-	CJA_2829	11.7	11.4	12.1	13.2
dihydrodipicolinate synthase	dapA	CJA_2830	10.8	11.1	10.9	13.0
quinolinate synthetase	nadA	CJA_2831	12.8	12.6	13.0	13.4
sensory box protein	-	CJA_2834	10.9	10.6	10.9	9.5
exsB protein	-	CJA_2835	10.7	10.9	10.7	11.5
radical SAM domain protein	-	CJA_2836	10.8	11.0	10.4	11.0
YaiC/YhcK/ArdA family protein	adrA	CJA_2837	10.9	11.1	11.0	10.0
hypothetical protein	-	CJA_2838	11.8	11.2	12.1	10.6
magnesium and cobalt transport protein CorA	corA	CJA_2839	12.1	11.8	12.4	11.5
lipid A biosynthesis lauroyl acyltransferase	htrB	CJA_2840	10.3	10.4	10.3	10.8
hypothetical protein	-	CJA_2841	10.7	10.4	10.8	10.9
hypothetical protein	-	CJA_2842	9.5	9.5	9.3	10.5
glutaredoxin homolog	-	CJA_2843	9.5	9.2	9.9	11.9
hypothetical protein	-	CJA_2844	9.4	9.4	10.2	9.9
Sensory transduction histidine kinase	baeS	CJA_2845	10.0	10.0	10.0	9.9
DNA-binding response regulator	baeR	CJA_2846	10.2	10.1	10.2	10.3
putative HrpA-like helicase	-	CJA_2847	9.6	9.8	9.3	9.6
protocatechuate dioxygenase	-	CJA_2848	10.4	9.9	10.3	9.3
two-component system sensor histidine kinase/response regulator, hybrid (or	-	CJA_2849	10.9	11.3	10.9	9.1

hypothetical protein	-	CJA_2850	8.9	9.0	9.0	8.8
hypothetical protein	-	CJA_2851	10.7	10.9	9.9	9.1
hypothetical protein	-	CJA_2852	9.3	9.2	9.4	9.0
hypothetical protein	-	CJA_2853	10.0	9.8	10.4	10.1
hypothetical protein	-	CJA_2858	9.7	10.8	9.3	9.4
beta-lactamase	-	CJA_2859	10.0	10.0	10.5	10.3
hypothetical protein	-	CJA_2860	9.2	9.9	9.1	9.1
hypothetical protein	-	CJA_2861	10.7	12.0	10.0	9.7
hypothetical protein	-	CJA_2865	11.0	10.9	12.4	10.4
hypothetical protein	-	CJA_2866	9.3	9.3	9.6	9.0
putative TonB-dependent receptor protein	-	CJA_2867	9.4	9.5	9.2	9.0
Tat (twin-arginine translocation) pathway signal sequence domain protein	-	CJA_2868	9.7	10.3	9.3	9.0
carbohydrate binding protein, putative, cbp26A	cbp26A	CJA_2869	10.1	10.6	9.7	9.0
hypothetical protein	-	CJA_2870	10.7	11.5	10.7	8.9
hypothetical protein	-	CJA_2871	12.3	12.8	11.5	9.0
alpha-glucosidase, putative, adg31A	adg31A	CJA_2872	11.8	11.6	11.6	9.1
iron transporter	-	CJA_2873	10.9	11.3	11.2	9.6
GGDEF domain protein	-	CJA_2874	10.0	9.9	10.2	9.4
hypothetical protein	-	CJA_2875	11.2	11.4	11.5	9.8
putative two-component, response regulator	-	CJA_2876	12.6	13.0	12.8	10.3
argD acetylornithine aminotransferase	-	CJA_2877	10.1	10.5	10.3	12.5
ornithine carbamoyltransferase	argF	CJA_2878	10.8	10.8	10.9	11.9
hypothetical protein	-	CJA_2879	9.8	9.6	10.7	10.2
hypothetical protein	-	CJA_2880	10.9	10.2	12.8	9.9
tryptophan halogenase	-	CJA_2881	9.6	9.5	10.1	10.1
TonB-dependent receptor	-	CJA_2882	11.7	11.1	11.7	12.0
hypothetical protein	-	CJA_2883	10.6	10.0	11.4	11.0
lytic murein transglycosylase, putative, lmt23D	lmt23D	CJA_2884	10.0	9.9	10.5	9.7
hypothetical protein	-	CJA_2885	11.0	11.8	11.0	10.8
DNA polymerase II	-	CJA_2886	11.4	11.2	10.7	9.3
alpha-glucuronidase, gla67A	gla67A	CJA_2887	10.5	10.4	10.3	9.3
endo-1,4-beta-xylanase, xyn10D	xyn10D	CJA_2888	9.9	9.7	10.2	9.5
acetyl xylan esterase, putative, axe2B	axe2B	CJA_2889	10.0	10.0	9.9	9.7
hypothetical protein	-	CJA_2890	12.8	12.4	12.5	9.2
catalase/peroxidase HPI	-	CJA_2891	13.7	12.8	12.6	9.8
Glycerophosphoryl diester phosphodiesterase	ugpQ	CJA_2892	10.0	9.9	10.4	9.8
hypothetical protein	-	CJA_2893	11.2	11.2	12.6	10.7
Small-conductance mechanosensitive channel	-	CJA_2894	11.5	11.3	12.4	11.2
aromatic amino acid aminotransferase	maspC	CJA_2895	10.7	11.7	11.1	10.9
nicotinate-nucleotide--dimethylbenzimidazolephosphoribosyltransferase	cobT	CJA_2896	11.1	10.9	10.4	10.5

cobalamin 5'-phosphate synthase	cobS	CJA_2897	10.1	10.0	9.7	9.7
fructose-2;6-bisphosphatase	-	CJA_2898	12.1	12.1	11.3	10.3
HAD-superfamily subfamily IIA hydrolase, TIGR01458	-	CJA_2899	11.5	11.3	11.3	9.6
MATE efflux family protein	-	CJA_2900	10.3	11.3	10.0	9.5
histidinol-phosphate aminotransferase	hisC	CJA_2901	13.1	13.4	12.3	11.9
putative lipoprotein	-	CJA_2902	10.1	9.9	10.0	9.3
DNA topoisomerase IV subunit B	parE	CJA_2903	11.5	11.4	10.9	11.7
hypothetical protein	-	CJA_2904	11.3	12.3	10.3	10.0
Uvs099	uvs099	CJA_2905	11.2	11.2	11.5	11.4
hypothetical protein	-	CJA_2906	10.7	11.8	11.9	11.0
Uvs098	uvs098	CJA_2907	11.4	11.9	12.3	12.1
conserved hypothetical protein TIGR00052	-	CJA_2908	13.1	12.6	13.6	13.6
thiamine biosynthesis protein ThiC	thiC	CJA_2909	10.0	9.6	9.9	12.3
phosphomethylpyrimidine kinase	thiD	CJA_2910	10.9	10.9	10.1	11.2
putative pH regulated Na(+)/H(+) antiporter	-	CJA_2911	12.0	11.4	11.9	13.3
putative Na+/H+ antiporter NhaD	-	CJA_2912	11.6	11.6	11.1	11.8
outer membrane efflux protein	opmH	CJA_2913	12.1	11.1	13.0	13.4
pectate lyase, putative, pel3C	pel3C	CJA_2914	9.2	9.1	9.1	9.0
BNR/Asp-box repeat domain protein	-	CJA_2915	11.1	11.5	11.3	9.7
KDO transferase, putative, kdt30A	kdt30A	CJA_2916	11.4	11.5	11.2	10.0
putative mutT protein	-	CJA_2917	11.6	12.7	11.4	11.7
arginine biosynthesis bifunctional protein ArgJ	argJ	CJA_2918	11.8	11.6	11.3	12.6
preprotein translocase subunit SecA	secA	CJA_2919	11.0	10.8	10.8	12.2
peptidase	-	CJA_2920	12.8	13.1	12.8	11.3
UDP-3-O-acyl N-acetylglucosamine deacetylase, putative, lpx11A	lpx11A	CJA_2921	10.5	10.0	10.8	11.8
hypothetical protein	-	CJA_2922	8.9	8.9	8.9	9.4
cell division protein FtsZ	ftsZ	CJA_2923	9.9	9.6	12.5	12.6
hypothetical protein	-	CJA_2924	9.3	9.2	9.3	9.9
cell division protein FtsA	ftsA	CJA_2925	10.8	10.6	12.1	12.4
FtsQ	ftsQ	CJA_2926	10.4	10.5	10.5	11.3
D-alanine--D-alanine ligase	-	CJA_2927	10.7	10.5	11.2	12.2
UDP-N-acetylmuramate--L-alanine ligase	murC	CJA_2928	10.4	10.6	10.4	11.6
mur beta-N-acetylglucosaminyltransferase, putative, mur28A	mur28A	CJA_2929	11.3	11.7	11.1	11.1
cell division protein FtsW	ftsW	CJA_2930	11.1	11.1	11.9	10.5
UDP-N-acetylmuramoyl-L-alanyl-D-glutamatesynthetase	murD	CJA_2931	12.4	12.1	12.1	11.5
phospho-N-acetylmuramoyl-pentapeptide-transferase	mraY	CJA_2932	11.1	11.1	11.7	10.9
UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-al	murF	CJA_2933	10.5	10.5	9.8	10.5
UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	murE	CJA_2934	11.4	11.5	10.9	11.4
penicillin-binding protein 3 - Pseudomonas aeruginosa	ftsI	CJA_2935	11.0	11.4	10.3	10.1
cell division protein FtsL	-	CJA_2936	10.8	11.9	10.7	10.9

S-adenosyl-methyltransferase MraW	mraW	CJA_2937	10.1	10.2	10.2	11.6
mraZ protein	mraZ	CJA_2938	9.6	9.6	9.9	11.2
response regulator	-	CJA_2939	10.3	10.6	10.6	9.4
protein-glutamate methyltransferase CheB	cheB-1	CJA_2940	11.4	11.6	11.3	9.8
putative cheB, glutamate methyltransferase	-	CJA_2941	13.1	14.0	11.9	9.7
chemotaxis protein methyltransferase CheR	-	CJA_2942	11.6	11.4	11.6	9.7
methyl-accepting chemotaxis protein	-	CJA_2943	11.4	11.3	11.4	9.1
chemotaxis protein	-	CJA_2944	9.9	10.0	10.4	9.3
chemotaxis sensor histidine kinase CheA	cheA-1	CJA_2945	10.6	10.9	10.8	9.4
STAS domain protein	-	CJA_2946	10.7	11.0	10.4	9.5
chemotaxis protein CheY	cheY-1	CJA_2947	10.6	10.2	11.4	9.9
putative methyl-accepting chemotaxis protein	-	CJA_2948	10.8	11.1	10.6	9.2
hypothetical protein	-	CJA_2949	12.1	11.0	12.0	9.3
phosphoenolpyruvate carboxylase	ppc	CJA_2950	10.8	10.8	10.2	12.6
Molybdopterin oxidoreductase Fe4S4 domain family	-	CJA_2954	10.4	10.2	11.0	9.0
methyl-accepting chemotaxis protein	-	CJA_2955	11.8	11.6	10.9	9.4
hypothetical protein	-	CJA_2956	10.3	10.7	10.3	9.3
EAL domain protein	-	CJA_2957	10.5	9.9	11.5	10.7
hypothetical protein	-	CJA_2958	8.8	8.8	8.9	8.9
cellulase, putative, cel5F	cel5F	CJA_2959	9.9	9.9	9.6	9.4
ACT domain protein/phosphoserine phosphatase SerB	-	CJA_2960	11.2	11.4	10.3	11.3
hypothetical protein	-	CJA_2961	12.3	11.9	13.2	10.8
acyltransferase family protein	-	CJA_2962	11.6	11.5	11.9	9.5
hypothetical protein	-	CJA_2963	13.9	14.1	14.1	11.5
UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl- meso-diaminopimelate I	mpl	CJA_2964	11.8	12.4	11.4	11.0
hypothetical protein	rpiB2	CJA_2965	10.0	9.4	10.3	11.2
3-polyprenyl-4-hydroxybenzoate decarboxylase	-	CJA_2966	13.2	13.8	13.5	12.4
hydroxymethylglutaryl-CoA lyase, (HMG-CoA lyase) (HL) (3-hydroxy-3-methylg	-	CJA_2967	12.9	13.1	12.8	11.5
hypothetical protein	-	CJA_2968	10.9	10.5	10.2	10.6
acetyltransferase, GNAT family	-	CJA_2969	10.9	10.6	10.8	10.7
hypothetical protein	-	CJA_2970	12.1	11.8	12.2	10.1
Smr domain protein	-	CJA_2971	10.4	10.4	11.1	10.2
acetate--CoA ligase	acsA	CJA_2972	11.7	11.9	11.7	11.6
hypothetical protein	-	CJA_2973	10.3	10.0	11.0	10.8
aspartate 1-decarboxylase	panD	CJA_2974	10.7	10.3	11.0	11.9
pantoate--beta-alanine ligase	panC	CJA_2975	10.0	9.8	9.9	11.7
MOSC domain protein	-	CJA_2976	11.6	11.0	11.4	10.5
prevent-host-death family protein	-	CJA_2977	10.7	10.1	11.1	10.9
replicative DNA helicase	dnaB	CJA_2978	11.3	11.3	10.7	12.2
addiction module toxin, Txe/YoeB family	-	CJA_2979	10.7	10.5	10.3	10.7

ribosomal protein L9	rplI	CJA_2980	10.1	9.7	9.7	13.5
ribosomal protein S18	rpsR	CJA_2981	10.0	9.2	9.6	14.2
30S ribosomal protein S6	rpsF	CJA_2982	10.1	9.2	9.1	14.2
endo-1,4-beta glucanase, cel5B	cel5B	CJA_2983	13.9	10.5	9.9	10.0
beta glucanase, putative, glu16D	glu16D	CJA_2984	9.7	10.1	9.2	9.1
glycoside hydrolase, putative, gly16A	gly16A	CJA_2985	10.5	11.1	10.1	9.5
PEP-CTERM putative exosortase interaction domain protein	-	CJA_2986	14.0	14.1	13.1	9.6
hypothetical protein	-	CJA_2988	11.6	11.9	11.5	9.2
hypothetical protein	-	CJA_2989	11.2	10.7	11.5	9.9
putative lipoprotein	-	CJA_2990	11.1	10.4	10.6	9.5
putative DNA binding protein	-	CJA_2991	10.3	10.0	11.0	9.9
hypothetical protein	-	CJA_2992	9.5	9.3	9.4	10.0
endo-chitinase, putative, chi18C	chi18C	CJA_2993	11.6	11.7	11.2	9.2
RNA methyltransferase, TrmH family, group 3	-	CJA_2994	10.5	11.0	10.3	10.4
putative ribonuclease R	-	CJA_2995	10.3	10.5	10.3	11.4
pyochelin biosynthetic protein PchC	pchC	CJA_2997	10.6	10.5	11.1	10.0
involved in polyketide synthesis	pkxE	CJA_2998	11.2	11.1	12.0	10.1
halogenase A	halA	CJA_2999	11.2	11.0	11.2	10.0
MmpIV	-	CJA_3000	9.8	9.6	9.9	9.5
Beta-ketoacyl synthase, N-terminal domain protein	-	CJA_3001	10.7	10.5	10.5	9.2
oxidoreductase, zinc-binding dehydrogenase family	-	CJA_3002	11.0	10.3	10.3	9.1
EpoC	-	CJA_3003	10.4	10.6	10.0	9.0
putative BarE protein	-	CJA_3004	11.1	10.9	11.6	9.3
hypothetical protein	-	CJA_3005	11.2	12.1	11.3	10.0
hypothetical protein	-	CJA_3006	9.5	9.4	10.0	9.8
beta-xylosidase/alpha-L-arabinofuranosidase, putative, gly43H	gly43H	CJA_3007	12.5	12.0	11.4	9.9
beta-xylosidase, putative, xyl39A	xyl39A	CJA_3008	11.1	11.7	10.7	9.4
hypothetical protein	-	CJA_3009	10.8	11.3	11.0	9.7
cellulase, putative, cel5D	cel5D	CJA_3010	11.2	11.2	11.0	9.4
transcriptional regulator, AraC family domain protein	-	CJA_3011	11.6	12.1	11.0	9.8
alpha-L-arabinofuranosidase, putative, abf43K	abf43K	CJA_3012	11.1	11.2	10.5	9.8
YicJ-like protein	-	CJA_3013	11.7	11.8	11.2	9.4
hypothetical protein	-	CJA_3014	9.7	9.7	9.4	9.6
L-arabinose isomerase	-	CJA_3015	10.0	10.0	9.7	9.1
L-ribulose-5-phosphate 4-epimerase	araD	CJA_3016	10.0	10.1	10.2	9.1
ribulokinase	araB	CJA_3017	10.1	10.6	9.8	9.0
beta-xylosidase/alpha-L-arabinofuranosidase, putative, gly43N	gly43N	CJA_3018	9.6	9.6	9.5	9.1
ABC transporter periplasmic binding protein	-	CJA_3019	11.3	11.4	10.6	9.4
sugar ABC transporter ATP-binding protein	-	CJA_3020	12.1	12.6	11.2	9.4
sugar ABC transporter permease protein	-	CJA_3021	11.8	11.9	11.4	9.3

inner membrane ABC transporter permease protein Yjff	-	CJA_3022	12.4	12.6	11.8	9.4
hypothetical protein	-	CJA_3023	11.3	11.0	11.0	9.3
RNA polymerase sigma factor, sigma-70 family	-	CJA_3024	10.8	11.5	10.2	9.3
hypothetical protein	-	CJA_3025	11.6	11.5	11.4	9.5
hypothetical protein	-	CJA_3026	11.6	11.2	13.5	11.2
hypothetical protein	-	CJA_3027	10.6	10.3	12.4	10.9
DGPF domain superfamily	-	CJA_3028	10.8	11.4	12.2	10.7
transcriptional regulatory protein	-	CJA_3029	12.4	12.0	13.0	10.5
hypothetical protein	-	CJA_3030	10.9	10.4	11.8	9.3
cell wall degradation protein	-	CJA_3031	10.4	11.9	9.8	9.3
hypothetical protein	-	CJA_3032	10.0	9.9	10.1	9.5
Peptidase family S41B family	-	CJA_3033	10.7	10.5	10.7	11.2
hypothetical protein	-	CJA_3034	10.5	10.7	12.0	10.3
hypothetical protein	-	CJA_3035	9.8	10.4	10.3	9.9
hypothetical protein	-	CJA_3036	10.9	10.6	11.2	9.4
hypothetical protein	-	CJA_3037	9.5	10.2	9.3	9.0
putative AAA family ATPase	-	CJA_3038	10.1	10.5	9.9	9.0
hypothetical protein	-	CJA_3039	11.1	11.3	10.5	9.4
hypothetical protein	-	CJA_3040	10.2	10.5	9.6	9.1
hypothetical protein	-	CJA_3041	12.1	11.8	10.6	9.5
hypothetical protein	-	CJA_3042	9.5	9.5	9.3	9.0
hypothetical protein	-	CJA_3043	9.3	9.4	9.2	9.1
hypothetical protein	-	CJA_3044	10.1	10.4	9.5	9.1
hypothetical protein	-	CJA_3045	10.3	11.0	9.6	9.0
hypothetical protein	-	CJA_3046	11.8	12.5	10.5	9.2
hypothetical protein	-	CJA_3047	9.2	9.5	9.0	8.9
hypothetical protein	-	CJA_3048	12.8	12.5	11.5	9.4
hypothetical protein	-	CJA_3049	11.4	11.6	10.8	9.1
hypothetical protein	-	CJA_3050	11.4	10.9	11.0	9.1
conserved hypothetical phage tail region protein subfamily	-	CJA_3051	9.5	9.4	9.3	9.0
hypothetical protein	-	CJA_3052	11.6	11.8	10.0	9.0
conserved hypothetical phage tail region protein subfamily	-	CJA_3053	11.7	11.2	10.8	9.2
Phage tail sheath protein	-	CJA_3054	10.6	10.2	9.6	9.0
hypothetical protein	-	CJA_3055	10.6	10.6	10.4	9.1
hypothetical protein	-	CJA_3056	11.4	11.6	10.1	8.9
hypothetical protein	-	CJA_3057	12.3	12.6	11.4	8.9
hypothetical protein	-	CJA_3058	9.4	9.4	9.3	8.9
hypothetical protein	-	CJA_3059	12.0	11.3	12.2	9.0
MopR	mopR	CJA_3060	9.1	9.1	9.1	8.8
xylose isomerase	xylA	CJA_3061	10.8	11.0	10.3	9.7

xylulose kinase (xylulokinase)	-	CJA_3062	10.3	10.1	9.6	9.3
Nudix hydrolase	nuhA	CJA_3063	12.0	11.7	11.4	11.5
MFS transporter	xylE	CJA_3064	13.0	12.3	12.1	11.3
hypothetical protein	-	CJA_3065	12.5	12.7	12.5	9.3
endo-beta-1,4-xylanase, xyn10C	xyn10C	CJA_3066	12.0	11.2	11.7	9.2
beta-xylosidase/alpha-L-arabinofuranosidase, putative, gly43J	gly43J	CJA_3067	10.8	10.8	11.0	9.2
hypothetical protein	-	CJA_3068	10.8	11.7	10.5	9.9
Starvation sensing protein rspA	rspA	CJA_3069	11.0	11.2	10.9	9.7
beta-xylosidase/alpha-L-arabinofuranosidase, putative, gly43G	gly43G	CJA_3070	13.2	12.9	13.6	11.7
putative module of glucan-glucohydrolase	-	CJA_3071	11.4	10.3	11.8	10.6
TonB-dependent receptor	-	CJA_3072	11.4	10.4	11.8	10.1
adenylosuccinate synthetase	purA	CJA_3073	10.6	10.4	10.6	12.9
ATP phosphoribosyltransferase, regulatory subunit	hisZ	CJA_3074	10.0	10.0	9.8	11.8
hypothetical protein	-	CJA_3075	8.9	8.9	8.9	10.6
HflC protein	hflC	CJA_3076	10.3	10.1	10.4	12.6
HflK protein	hflK	CJA_3077	10.1	9.7	10.4	13.3
hypothetical protein	-	CJA_3078	10.8	10.6	10.8	13.0
Hfq protein	hfq	CJA_3079	13.6	11.0	14.6	14.1
tRNA delta(2)-isopentenylpyrophosphate transferase	miaA	CJA_3080	9.9	9.7	12.1	11.7
DNA mismatch repair protein	mutL	CJA_3081	10.7	11.3	10.3	10.8
N-acetylmuramoyl-L-alanine amidase	-	CJA_3082	10.9	11.3	10.5	10.3
hypothetical protein	-	CJA_3083	10.1	10.0	11.4	9.1
hypothetical protein	-	CJA_3084	11.7	12.2	13.1	9.5
putative sensory box protein	-	CJA_3085	11.6	12.4	11.5	9.3
conserved hypothetical protein TIGR00150	-	CJA_3086	11.0	10.9	10.7	10.7
YjeF family protein	-	CJA_3087	9.7	9.9	9.2	10.0
hypothetical protein	-	CJA_3088	9.8	10.4	9.8	9.1
hypothetical protein	-	CJA_3089	10.5	10.1	11.4	9.5
hypothetical protein	-	CJA_3090	10.3	10.2	11.8	10.7
hypothetical protein	-	CJA_3091	8.8	8.8	8.8	8.9
hypothetical protein	-	CJA_3092	9.8	9.6	10.6	9.1
iron-sulfur cluster-binding protein	-	CJA_3093	11.0	11.2	11.4	10.0
hypothetical protein	-	CJA_3094	9.7	10.0	9.9	9.2
hypothetical protein	-	CJA_3095	11.2	12.2	10.7	9.2
hypothetical protein	-	CJA_3096	11.1	12.5	10.3	9.2
hypothetical protein	-	CJA_3097	9.5	9.5	9.8	9.1
dehydrogenase subunit	-	CJA_3098	11.3	11.5	10.5	10.0
6-phosphogluconate dehydrogenase	gnd	CJA_3099	11.3	11.0	10.8	13.2
hypothetical protein	-	CJA_3100	10.1	10.3	10.9	10.2
oxidoreductase, GMC family	-	CJA_3101	12.0	11.5	11.6	10.4

hypothetical protein	-	CJA_3102	11.0	10.3	10.8	10.7
acetyl xylan esterase, putative, axe2A	ce2C	CJA_3103	10.9	10.5	11.0	10.3
pectate lyase, pel10A	pel10A	CJA_3104	10.6	10.8	10.5	9.3
hypothetical protein	-	CJA_3105	9.6	9.9	9.9	8.9
carbohydrate binding protein, putative, cbp2B	cbp2B	CJA_3106	13.5	13.3	13.0	9.3
carbohydrate binding protein, putative, cbp2C	cbp2C	CJA_3107	11.4	11.0	10.9	9.5
lipase family protein	-	CJA_3108	10.1	10.1	11.1	9.6
hypothetical protein	-	CJA_3109	9.4	9.8	11.4	9.6
beta-lactamase	-	CJA_3110	13.0	13.4	13.9	10.5
hypothetical protein	-	CJA_3111	10.4	9.9	12.6	9.6
putative dipeptidyl peptidase IV	-	CJA_3112	10.7	10.5	10.8	9.2
hypothetical protein	-	CJA_3113	9.2	9.2	9.1	8.9
hypothetical protein	-	CJA_3114	11.5	11.0	12.4	9.1
putative lipoprotein	-	CJA_3115	9.7	9.7	9.7	9.1
pectin methylesterase putative, pme8B	pme8B	CJA_3116	10.9	10.5	11.0	9.2
oligoribonuclease	orn	CJA_3117	11.9	11.0	12.4	10.3
ribosome-associated GTPase	-	CJA_3118	10.1	9.8	10.3	10.2
rhodanese	rhda	CJA_3119	9.9	10.2	11.1	10.1
pectate lyase, putative, pel1G	pel1G	CJA_3120	11.2	11.3	11.3	9.2
hypothetical protein	-	CJA_3121	9.5	9.3	9.9	10.3
hypothetical protein	-	CJA_3122	9.2	9.1	9.8	9.8
hypothetical protein	-	CJA_3123	12.5	12.7	12.1	11.5
hypothetical protein	-	CJA_3124	10.8	11.2	10.3	10.7
endo-beta-N-acetylglucosaminidase, putative, acm73A	acm73A	CJA_3125	9.9	10.1	9.7	9.8
alpha-amylase, putative, amy13I	amy13I	CJA_3126	10.7	11.0	9.6	9.3
polysaccharide deacetylase, putative, pda4D	pda4D	CJA_3127	10.3	10.6	9.8	9.4
hypothetical protein	-	CJA_3128	10.7	11.2	10.9	10.0
hypothetical protein	-	CJA_3129	9.5	9.8	9.2	9.5
hypothetical protein	-	CJA_3130	8.9	8.9	9.0	9.3
hypothetical protein	-	CJA_3131	12.1	12.5	11.6	11.7
DNA topoisomerase IV subunit A	parC	CJA_3132	10.6	10.6	10.2	11.7
putative lipoprotein	-	CJA_3133	9.5	9.5	9.5	10.1
hypothetical protein	-	CJA_3134	13.7	13.4	13.1	13.0
hypothetical protein	-	CJA_3135	13.3	13.9	12.5	12.4
hypothetical protein	-	CJA_3136	9.9	9.9	9.7	10.3
metallo-beta-lactamase superfamily protein	glob1	CJA_3137	11.1	11.5	11.0	10.7
hypothetical protein	-	CJA_3138	12.0	12.1	11.4	9.7
chitin binding protein, putative, cbp33/10B	cbp33/10B	CJA_3139	14.4	13.7	13.1	11.1
phosphatidylserine decarboxylase	psd	CJA_3140	9.6	9.6	9.7	10.3
Integral membrane protein TerC family superfamily	-	CJA_3141	10.6	10.8	11.0	10.1

hypothetical protein	-	CJA_3142	10.1	9.9	10.8	9.8
HD domain protein	-	CJA_3143	11.3	11.0	12.0	11.2
uroporphyrinogen decarboxylase	hemE	CJA_3144	13.2	12.9	12.5	12.3
Na/Pi cotransporter family protein	-	CJA_3145	11.6	11.7	10.6	10.5
glutamate synthase subunit beta	gltD	CJA_3146	11.4	12.2	10.6	12.9
glutamate synthase subunit alpha	gltB	CJA_3147	10.9	11.1	10.3	12.9
putative lipoprotein	-	CJA_3148	11.0	11.0	11.4	10.6
hypothetical protein	-	CJA_3149	10.2	11.1	11.5	10.5
tryptophan halogenase	-	CJA_3150	10.9	10.6	11.1	10.8
transcriptional regulator, LysR family	-	CJA_3151	9.8	9.7	9.8	10.4
cation:proton antiporter	-	CJA_3152	9.6	9.7	10.1	9.7
PEP-CTERM putative exosortase interaction domain protein	-	CJA_3153	11.7	11.6	11.9	10.5
hypothetical protein	-	CJA_3154	8.9	8.9	8.9	8.9
hypothetical protein	-	CJA_3155	11.2	11.1	11.3	11.5
glycosyl transferase, putative, gt39A	gt39A	CJA_3156	11.9	12.6	11.7	11.9
putative serine protease	-	CJA_3157	10.9	10.9	10.8	11.2
hypothetical protein	-	CJA_3158	12.2	11.7	12.3	11.0
thiol-disulfide interchange protein DsbD homolog	-	CJA_3159	9.5	9.8	9.6	9.3
tonB dependent receptor-related protein	-	CJA_3160	10.4	10.2	10.2	9.4
pullulanase, putative, pul13B	pul13B	CJA_3161	9.8	10.4	9.9	9.5
hypothetical protein	-	CJA_3162	10.9	11.3	11.1	10.3
NAD(FAD)-utilizing dehydrogenase	-	CJA_3163	10.1	10.4	9.6	10.4
sialic acid-specific 9-O-acetyltransferase	-	CJA_3164	10.3	10.6	9.7	9.5
hypothetical protein	-	CJA_3165	10.4	10.3	10.0	10.6
peptidase, M16 (pitrilysin) family	-	CJA_3166	12.1	11.3	11.9	12.4
hypothetical protein	-	CJA_3167	10.5	10.9	10.4	10.2
hypothetical protein	-	CJA_3168	10.6	10.9	10.6	9.0
S1 RNA binding domain protein	-	CJA_3169	9.8	9.7	9.4	11.9
orotidine 5'-phosphate decarboxylase	-	CJA_3170	9.8	9.9	9.6	11.3
alkylphosphonate utilization operon protein PhnA	phnA	CJA_3171	12.3	11.3	12.0	12.7
hypothetical protein	-	CJA_3172	10.0	10.4	9.8	9.8
putative lipoprotein	-	CJA_3173	11.5	11.8	10.7	9.9
putative arylsulfatase	-	CJA_3174	9.7	10.0	9.3	9.2
hypothetical protein	-	CJA_3175	9.0	8.9	8.9	8.9
tetratricopeptide repeat domain protein	-	CJA_3176	9.0	9.0	8.9	9.0
ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein	-	CJA_3177	9.0	9.1	9.0	9.0
response regulator	-	CJA_3178	9.1	9.2	9.1	9.4
hypothetical protein	-	CJA_3179	11.0	10.7	11.9	9.6
hypothetical protein	-	CJA_3180	9.6	9.6	10.8	9.3
hypothetical protein	-	CJA_3181	10.3	11.6	10.6	9.1

putative PAP2 superfamily	-	CJA_3182	9.1	9.0	9.2	9.1
CcdB antidote CcdA	ccdA	CJA_3183	9.4	9.4	9.7	9.7
Transposase IS4 family	-	CJA_3184	10.5	10.6	11.4	10.7
putative maturase	-	CJA_3185	9.9	9.8	9.9	10.3
integrase	int	CJA_3186	9.8	10.0	10.6	9.4
Outer membrane efflux protein domain protein	-	CJA_3187	9.1	9.3	9.2	9.0
HlyD family secretion protein	-	CJA_3188	9.6	9.4	9.5	9.1
hypothetical protein	-	CJA_3189	8.9	9.0	8.9	8.9
ABC-2 type transporter domain protein	-	CJA_3190	10.1	10.5	9.7	9.1
hypothetical protein	-	CJA_3191	9.2	9.2	9.3	9.5
quaternary ammonium compound resistance protein	qacG	CJA_3192	10.0	9.9	11.1	9.7
hypothetical protein	-	CJA_3193	10.1	10.6	10.7	9.6
ClpB	clpB	CJA_3194	10.0	10.0	10.5	11.3
putative Macrolide-efflux protein	-	CJA_3195	9.9	10.5	10.5	9.1
microcystin synthetase associated thioesterase	-	CJA_3196	10.4	10.3	12.1	9.7
glycosyl transferase, putative, gt1C	gt1C	CJA_3197	10.2	10.1	10.5	9.4
MxaD	mxuD	CJA_3198	9.7	9.6	10.0	9.4
hypothetical protein	-	CJA_3199	9.0	8.9	9.2	8.9
hypothetical protein	-	CJA_3200	9.8	10.0	10.2	9.1
hypothetical protein	-	CJA_3201	10.8	10.6	11.3	9.3
hypothetical protein	-	CJA_3202	10.3	9.9	11.1	9.3
hypothetical protein	-	CJA_3203	9.1	9.1	9.5	9.1
YfiH	-	CJA_3204	10.5	11.3	10.5	10.5
pseudouridine synthase, RluA family subfamily	-	CJA_3205	9.5	10.0	9.9	10.4
competence protein ComL	-	CJA_3206	12.0	11.3	13.2	13.0
glutamine-dependent NAD ⁺ synthetase signal peptide protein	adgA	CJA_3207	10.1	10.1	10.5	12.2
sensor kinase	pilS	CJA_3208	9.7	9.7	10.5	9.9
PilR	pilR	CJA_3209	9.6	9.4	10.8	11.2
type IV pilin	-	CJA_3210	9.3	9.3	10.2	10.4
putative fimbrial protein	-	CJA_3211	10.2	9.6	11.8	11.8
type 4 fimbrial biogenesis protein PilW	pilW	CJA_3212	9.2	9.2	9.8	9.9
pre-pilin like leader sequence	fimT	CJA_3213	10.0	10.3	10.7	10.4
4-hydroxy-3-methylbut-2-enyl diphosphate reductase	ispH	CJA_3214	10.2	10.2	10.7	12.1
peptidyl-prolyl cis-trans isomerase, FKBP-type	-	CJA_3215	10.9	10.7	11.5	12.7
signal peptidase II	lspA	CJA_3216	10.3	10.2	11.6	12.3
isoleucyl-tRNA synthetase	ileS	CJA_3217	10.5	10.5	10.6	12.4
riboflavin biosynthesis protein RibF	ribF	CJA_3218	9.2	9.1	9.2	10.6
integral membrane protein MviN	mviN	CJA_3219	11.0	11.9	10.0	9.5
hypothetical protein	-	CJA_3220	10.1	9.9	12.1	12.1
hypothetical protein	-	CJA_3221	11.1	10.9	11.7	9.6

hypothetical protein	-	CJA_3222	10.2	10.8	11.1	9.3
Phytanoyl-CoA dioxygenase (PhyH) family	-	CJA_3223	9.7	9.8	10.4	9.5
Glycerophosphoryl diester phosphodiesterase family	-	CJA_3224	10.2	10.8	10.6	9.6
probable transcriptional regulator arsR family	-	CJA_3225	9.3	9.5	10.0	10.3
quinol oxidase, subunit I	qxtA	CJA_3226	11.6	12.3	13.3	11.2
cytochrome oxidase subunit II superfamily	-	CJA_3227	10.8	11.4	11.6	11.0
hypothetical protein	-	CJA_3228	9.5	9.6	10.2	10.0
hypothetical protein	-	CJA_3229	9.8	9.6	11.1	10.3
hypothetical protein	-	CJA_3230	9.1	9.3	9.2	9.4
PepSY-associated TM helix family	-	CJA_3231	9.9	9.8	9.7	9.0
hypothetical protein	-	CJA_3232	9.9	10.9	10.9	9.5
TonB-dependent receptor protein	-	CJA_3233	9.5	9.5	9.3	9.0
transporter, solute:sodium symporter (SSS) family	-	CJA_3234	9.4	9.8	9.8	9.5
hypothetical protein	-	CJA_3235	9.6	9.8	10.1	10.2
L-ectoine synthase	ectC	CJA_3236	10.6	10.6	10.6	12.2
diaminobutyrate--2-oxoglutarate aminotransferase	ectB	CJA_3237	9.7	9.6	10.3	12.2
L-2,4-diaminobutyric acid acetyltransferase	-	CJA_3238	10.9	11.1	12.2	12.8
hypothetical protein	-	CJA_3239	8.8	8.8	9.0	10.1
transcriptional regulator, MarR family	-	CJA_3240	11.0	10.4	12.1	10.3
hypothetical protein	-	CJA_3241	9.2	9.1	9.6	9.1
mannosidase-like protein	-	CJA_3243	10.0	9.9	10.4	9.5
TonB-dependent receptor	-	CJA_3244	10.4	10.2	10.5	9.4
hypothetical protein	-	CJA_3245	9.4	9.2	9.7	8.9
TonB-dependent receptor	-	CJA_3246	10.4	10.1	10.3	10.7
alpha-amylase, putative, amy13H	amy13H	CJA_3247	11.2	11.8	9.6	9.4
alpha-glucosidase, putative, adg31B	agd31B	CJA_3248	10.3	9.6	9.7	9.0
cyclomaltodextrin glucoamylase, putative, cgt13A	cgl13A	CJA_3249	10.0	9.5	9.9	9.7
3-dehydroquinate synthase	-	CJA_3250	10.6	10.6	10.4	9.5
Phytanoyl-CoA dioxygenase (PhyH) superfamily	-	CJA_3251	9.3	9.3	9.4	9.1
6-phospho-beta-glucosidase, putative, pbg4A	pbg4A	CJA_3252	10.7	10.5	10.6	9.2
putative glucokinase	-	CJA_3253	11.8	11.5	12.2	9.6
Glucose-1-phosphate adenylyltransferase	glgC	CJA_3254	10.3	10.1	10.3	9.2
glycosyl transferase, putative, gt5B	gt5B	CJA_3255	10.2	10.2	10.1	9.0
hypothetical protein	-	CJA_3256	9.8	10.3	9.7	9.0
homolog of 4-aminobutyrate aminotransferase GabT	-	CJA_3257	11.1	10.7	10.9	9.2
hypothetical protein	-	CJA_3258	9.5	9.4	9.6	8.9
hypothetical protein	-	CJA_3259	10.2	10.7	9.9	9.0
ABC transporter, ATP-binding protein	-	CJA_3260	10.0	10.2	10.3	9.0
ABC transporter domain protein	-	CJA_3261	10.5	11.0	10.1	8.9
kinase, pfkB family	-	CJA_3262	11.2	12.1	11.6	9.0

cyclomalto-dextrin glucanotransferase, putative, cgt13B	cgt13B	CJA_3263	11.8	12.1	10.7	9.2
putative glutathione peroxidase	-	CJA_3264	10.3	10.7	10.1	9.5
hypothetical protein	-	CJA_3265	11.2	10.9	10.7	10.5
putative lipoprotein	-	CJA_3266	9.4	9.3	9.3	10.2
putative thiol:disulfide interchange protein DsbE	-	CJA_3267	10.9	11.3	11.0	11.3
hypothetical protein	-	CJA_3268	9.2	9.3	9.3	10.0
hypothetical protein	-	CJA_3269	9.4	9.7	9.5	9.7
hypothetical protein	-	CJA_3270	12.4	13.3	11.0	10.1
hypothetical protein	-	CJA_3271	10.0	9.9	9.7	9.8
hypothetical protein	-	CJA_3272	10.2	10.9	9.8	9.5
hypothetical protein	-	CJA_3273	9.5	9.4	9.7	9.0
hypothetical protein	-	CJA_3274	10.4	10.1	10.2	9.5
putative lipoprotein	-	CJA_3275	9.5	9.8	9.1	9.1
hypothetical protein	-	CJA_3276	10.4	10.7	10.1	9.6
hypothetical protein	-	CJA_3277	10.8	11.4	11.1	9.7
transcriptional regulator, AraC family domain protein	-	CJA_3278	10.5	10.1	11.4	9.1
endo-1,4-beta-xylanase, putative, xyn5A	xyn5A	CJA_3279	11.4	12.1	11.6	9.1
endo-1,4-beta-xylanase, xyn10B	xyn10B	CJA_3280	10.0	10.2	9.9	9.2
alpha-L-arabinofuranosidase, abf62A	abf62A	CJA_3281	11.2	11.4	11.3	9.6
ferruloyl esterase, putative, fee1B	fee1B	CJA_3282	13.8	14.5	12.3	9.4
hypothetical protein	-	CJA_3283	9.9	9.8	10.6	9.2
transcriptional regulator, AraC family	-	CJA_3284	9.9	9.8	11.0	9.3
hypothetical protein	-	CJA_3285	11.3	11.1	11.3	9.0
endo-beta-galactosidase, putative, ebg98A	ebg98	CJA_3286	11.5	11.5	11.8	9.3
ferruloyl esterase, fee1A	fee1A	CJA_3287	10.7	10.5	10.6	9.3
tyrosine recombinase XerC	xerC	CJA_3288	9.9	10.2	10.0	9.9
hypothetical protein	-	CJA_3289	9.6	9.9	9.8	10.9
diaminopimelate epimerase	dapF	CJA_3290	9.5	9.5	9.3	11.3
diaminopimelate decarboxylase	lysA	CJA_3291	10.5	10.9	10.1	12.5
hypothetical protein	-	CJA_3292	12.3	12.5	12.2	13.2
Sigma-54 interaction domain protein	-	CJA_3293	9.8	10.2	9.6	9.2
FHA domain protein	-	CJA_3294	12.0	12.7	12.1	11.7
putative serine/threonine protein kinase	-	CJA_3295	11.5	11.4	13.3	11.4
hypothetical protein	-	CJA_3296	10.5	10.5	12.6	11.3
hypothetical protein	-	CJA_3297	10.3	9.9	13.4	12.0
putative TonB-dependent receptor	-	CJA_3298	10.2	10.4	10.8	11.7
putative transcriptional regulator	-	CJA_3299	10.7	10.7	11.7	9.3
carbohydrate binding protein, putative, cbp6C	cbp6C	CJA_3300	12.5	13.2	12.1	9.1
hypothetical protein	-	CJA_3301	9.7	9.8	10.9	9.0
hypothetical protein	-	CJA_3302	12.7	12.4	13.1	10.4

hypothetical protein	-	CJA_3303	10.4	10.0	11.4	10.4
TonB-dependent receptor	-	CJA_3304	11.6	12.4	11.9	9.4
glucan exo-1,3-beta glucosidase, putative, glu5A	glu5A	CJA_3305	12.0	11.8	10.7	9.9
glycoside hydrolase family 30, gly30A	gly30A	CJA_3306	10.3	10.5	11.1	10.4
Mannose-6-phosphate isomerase-like protein	manC	CJA_3307	9.8	9.9	9.5	10.5
hypothetical protein	-	CJA_3308	9.1	9.0	9.1	9.5
MATE efflux family protein	-	CJA_3309	10.4	10.8	10.9	10.2
RHS Repeat family	-	CJA_3310	9.6	9.4	9.7	11.2
FG-GAP repeat domain protein	-	CJA_3311	9.2	9.1	9.7	11.7
TonB family C-terminal domain protein	-	CJA_3312	11.0	11.0	11.5	11.3
putative adventurous gliding motility protein S	-	CJA_3313	10.4	11.4	10.0	11.0
hypothetical protein	-	CJA_3314	10.6	10.4	10.4	11.4
adventurous gliding motility protein R	aglR	CJA_3315	11.0	11.8	10.8	11.5
hypothetical protein	-	CJA_3316	11.1	11.2	10.8	10.3
putative TPR domain protein	-	CJA_3317	9.8	10.4	9.6	9.4
tetratricopeptide repeat domain protein	-	CJA_3318	9.6	9.7	9.4	9.5
hypothetical protein	-	CJA_3319	11.0	11.1	10.7	10.3
hypothetical protein	-	CJA_3320	11.3	11.8	11.2	11.0
hypothetical protein	-	CJA_3321	10.1	10.0	10.8	10.4
hypothetical protein	-	CJA_3322	11.5	12.7	11.2	11.3
General secretion pathway protein M	gspM	CJA_3323	10.7	10.3	10.8	10.2
General secretion pathway protein L	gspL	CJA_3324	10.3	10.4	10.3	10.7
General secretion pathway protein K	gspK	CJA_3325	9.3	9.3	9.5	10.1
General secretion pathway protein J	gspJ	CJA_3326	10.1	10.0	10.1	10.9
General secretion pathway protein I	gspI	CJA_3327	12.6	12.2	13.1	12.3
General secretion pathway protein H	gspH	CJA_3328	9.4	9.8	9.5	11.2
General secretion pathway protein G	gspG	CJA_3329	9.8	9.5	10.8	11.9
General secretion pathway protein F	gspF	CJA_3330	10.9	10.9	10.6	11.2
General secretion pathway protein E	gspE	CJA_3331	10.7	10.7	10.9	12.0
General secretion pathway protein D	gspD	CJA_3332	11.1	11.4	11.6	11.5
General secretion pathway protein C	gspC	CJA_3333	12.2	12.7	11.8	10.6
exodeoxyribonuclease VII, small subunit	xseB	CJA_3334	9.5	9.5	9.7	10.9
geranyltranstransferase	ispA	CJA_3335	10.5	11.8	9.9	10.9
1-deoxy-D-xylulose-5-phosphate synthase	dxs	CJA_3336	11.2	11.7	10.4	11.2
cellulase, putative, cel5E	cel5E	CJA_3337	9.4	9.4	9.3	9.0
endo- 1,4-beta-mannanase man5A	man5A	CJA_3338	11.0	10.9	11.0	9.0
carbohydrate esterase, putative, cae1C	cae1C	CJA_3339	10.3	10.3	9.7	9.9
alcohol dehydrogenase C	adhC	CJA_3340	11.8	12.3	11.3	10.8
transcriptional regulator, LysR family	-	CJA_3341	10.5	10.9	9.8	9.6
nucleoside-transport system protein	nupG	CJA_3342	13.1	13.1	12.5	11.1

Oxidoreductase family, NAD-binding Rossmann fold domain protein	-	CJA_3343	10.9	10.2	10.6	10.4
AP endonuclease family 2 C terminus family	-	CJA_3344	11.1	10.3	11.6	10.7
CAAX amino terminal protease family protein	-	CJA_3345	12.1	11.7	12.9	11.4
chaperone protein DnaJ	dnaJ	CJA_3346	10.8	10.5	10.5	13.3
molecular chaperone DnaK	dnaK	CJA_3347	11.9	10.9	12.3	14.3
co-chaperone GrpE	grpE	CJA_3348	11.3	11.5	10.8	13.8
hypothetical protein	-	CJA_3349	9.0	9.1	9.5	8.8
methyl-accepting chemotaxis protein	-	CJA_3350	11.7	11.5	12.0	9.2
DNA repair protein RecN	recN	CJA_3351	9.6	10.6	9.5	9.7
transcriptional regulator Fur	fur	CJA_3352	11.3	10.3	13.5	12.9
Outer membrane lipoprotein omlA precursor	-	CJA_3353	12.5	11.8	14.4	13.0
GGDEF domain protein	-	CJA_3354	11.5	12.4	11.4	9.6
sensory box/GGDEF family protein	-	CJA_3355	10.9	11.3	10.0	9.0
response regulator	-	CJA_3356	12.0	12.0	11.8	10.1
HD domain protein	-	CJA_3357	12.5	12.3	12.2	9.7
two-component hybrid sensor and regulator	-	CJA_3358	10.4	10.3	10.2	9.7
two-component hybrid sensor and regulator	-	CJA_3359	11.9	12.5	10.9	9.7
Protein yfjF	-	CJA_3360	9.3	9.2	9.2	9.6
hypothetical protein	-	CJA_3361	10.6	10.8	9.9	10.7
SsrA-binding protein	smpB	CJA_3362	9.8	10.1	9.5	11.2
transcriptional regulator, LuxR family	-	CJA_3363	10.8	11.0	9.6	10.1
hypothetical protein	-	CJA_3364	11.2	11.2	12.4	10.0
hydrolase, alpha/beta fold family	-	CJA_3365	14.3	14.5	13.1	11.9
transcriptional regulator, LuxR family	-	CJA_3366	11.9	11.7	11.7	11.1
putative lipoprotein	-	CJA_3367	10.7	10.8	10.4	9.7
hypothetical protein	-	CJA_3368	11.1	11.6	10.3	9.9
cellulase, putative, cel5C	cel5C	CJA_3369	11.9	11.6	11.1	10.7
hypothetical protein	-	CJA_3370	11.4	11.9	10.8	9.8
outer membrane protein, OMP85 family	-	CJA_3371	12.0	12.0	10.9	10.0
hypothetical protein	-	CJA_3372	11.0	11.1	10.6	11.4
hypothetical protein	-	CJA_3373	9.4	9.6	9.2	9.9
hypothetical protein	-	CJA_3374	11.3	11.4	11.1	10.6
sensory box/GGDEF family protein	-	CJA_3375	12.3	12.2	11.6	11.5
hypothetical protein	-	CJA_3376	12.1	12.5	11.8	12.0
regulator of nucleoside diphosphate kinase	rnk	CJA_3377	10.7	11.1	11.0	12.6
hypothetical protein	-	CJA_3378	8.9	8.9	9.1	9.3
MATE efflux family protein subfamily	-	CJA_3379	9.9	10.0	9.6	9.4
excitatory amino acid transporter	-	CJA_3380	10.8	11.4	10.8	10.3
hypothetical protein	-	CJA_3381	9.7	9.9	9.7	10.0
murein polymerase, putative, gt51B	gt51B	CJA_3382	10.9	11.5	9.7	9.7

hemY protein	-	CJA_3383	9.7	9.9	9.5	10.4
putative uroporphyrinogen III methylase	-	CJA_3384	9.8	9.4	10.1	10.9
uroporphyrinogen-III synthase	hemD	CJA_3385	11.1	10.7	10.6	11.6
porphobilinogen deaminase	hemC	CJA_3386	9.3	9.4	9.2	10.9
high affinity choline transporter	-	CJA_3387	13.4	13.7	12.8	12.7
hypothetical protein	-	CJA_3388	9.8	10.3	9.8	9.5
PA5285-like protein	-	CJA_3389	12.2	11.9	12.9	12.4
Nitrogen regulatory protein P-II	-	CJA_3390	10.6	9.8	14.8	11.7
ammonium transporter	-	CJA_3391	12.4	12.1	15.5	11.5
Nitrogen regulatory protein P-II	-	CJA_3392	9.8	9.7	15.5	9.4
hypothetical protein	-	CJA_3393	9.7	9.3	9.9	9.8
Mg chelatase homolog	-	CJA_3394	10.2	10.8	9.8	9.7
EAL domain protein	-	CJA_3395	10.6	11.1	10.2	9.8
ATP-dependent DNA helicase Rep	rep	CJA_3396	10.0	10.1	10.1	10.6
Cytochrome c5	-	CJA_3397	10.6	10.3	10.0	12.0
putative PEP-CTERM system histidine kinase	prsK	CJA_3398	11.5	11.8	11.2	10.3
putative PEP-CTERM system response regulator	prsR	CJA_3399	10.1	10.5	10.2	10.8
hypothetical protein	-	CJA_3400	11.0	10.9	12.3	10.6
hypothetical protein	-	CJA_3401	10.7	10.9	11.1	9.8
putative lipoprotein	-	CJA_3402	10.4	10.4	11.0	9.7
PEP-CTERM putative exosortase interaction domain protein	-	CJA_3403	9.8	9.4	9.6	12.6
eight transmembrane protein EpsH (proposed exosortase)	-	CJA_3404	10.3	11.0	10.4	9.7
glycosyl transferase, putative, gt2M	gt2M	CJA_3405	11.0	11.3	10.9	10.6
capK related-protein	cAPK	CJA_3406	10.0	9.9	9.9	10.5
glycosyl transferase, putative, gt2I	gt2I	CJA_3407	10.0	9.9	10.5	10.8
polysaccharide deacetylase protein, putative, pda4E	pda4E	CJA_3408	11.0	11.6	11.7	11.2
hypothetical protein	-	CJA_3409	9.4	9.4	9.4	9.9
glycosyl transferase, putative, gt4B	gt4B	CJA_3410	10.0	9.7	10.0	10.3
glycosyl transferase, putative, gt4A	gt4A	CJA_3411	9.9	9.6	9.5	10.0
O-antigen polymerase family protein	-	CJA_3412	9.1	9.0	9.3	9.2
glycosyl transferase, group 1 family protein domain protein	-	CJA_3413	9.1	9.2	9.2	9.7
hypothetical protein	-	CJA_3414	9.5	9.5	10.5	10.8
hypothetical protein	-	CJA_3415	9.3	9.1	9.8	11.8
glycosyl transferase, putative, gt2L	gt2L	CJA_3416	8.9	8.8	9.0	10.5
polysaccharide biosynthesis family protein	-	CJA_3417	9.1	9.0	9.2	9.6
hypothetical protein	-	CJA_3418	9.5	9.3	10.2	10.9
TPR domain protein	-	CJA_3419	9.3	9.2	9.6	10.5
hypothetical protein	-	CJA_3420	9.4	9.2	9.8	11.1
hypothetical protein	-	CJA_3421	9.3	9.1	9.5	10.9
putative polysaccharide biosynthesis protein	-	CJA_3422	9.6	9.3	10.6	11.8

polysaccharide chain length determinant protein	-	CJA_3423	9.1	8.9	9.3	10.1
Polysaccharide biosynthesis/export protein	-	CJA_3424	9.8	9.9	9.4	10.5
Bacterial sugar transferase	lthA	CJA_3425	10.7	10.1	11.5	11.7
polysaccharide biosynthesis protein	-	CJA_3426	10.0	9.7	9.8	11.7
NAD dependent epimerase/dehydratase family superfamily	-	CJA_3427	10.0	9.9	10.1	12.5
polysaccharide deacetylase, putative, pda4C	pda4C	CJA_3428	10.2	10.2	10.6	11.6
putative lipoprotein	-	CJA_3430	9.2	9.0	9.2	9.5
antirepressor protein	-	CJA_3431	9.6	9.9	9.6	9.6
hypothetical protein	-	CJA_3432	9.4	9.4	10.8	11.2
transcriptional regulator, Cro/Ci family	-	CJA_3433	8.8	8.9	8.9	9.3
UDP-glucose dehydrogenase	-	CJA_3434	9.3	9.4	9.6	12.3
dTDP-glucose 4,6-dehydratase	rfbB	CJA_3435	9.5	9.2	9.8	13.2
glucose-1-phosphate thymidyltransferase	rfbA	CJA_3436	9.9	9.5	10.9	13.8
dTDP-4-dehydrorhamnose reductase	rfbD	CJA_3437	9.5	9.0	10.2	13.5
dTDP-4-dehydrorhamnose 3,5-epimerase	rfbC	CJA_3438	9.0	8.9	9.4	12.6
Wzm	wzm	CJA_3439	8.9	8.8	9.0	10.7
Wzt	wzt	CJA_3440	9.2	9.0	9.4	11.7
glycosyl transferase, putative, gt2G	gt2G	CJA_3441	9.4	9.2	9.9	12.8
glycosyl transferase, putative, gt4C	gt4C	CJA_3442	9.5	9.1	9.8	13.0
hypothetical protein	-	CJA_3443	9.5	9.2	9.7	13.3
hypothetical protein	-	CJA_3444	9.8	9.3	10.6	13.7
Capsule polysaccharide biosynthesis protein family	-	CJA_3445	10.5	9.8	11.0	13.5
hypothetical protein	-	CJA_3446	9.2	9.2	10.0	11.9
hypothetical protein	-	CJA_3447	9.7	9.6	10.6	12.3
glycosyl transferase, group 2 family protein	-	CJA_3448	8.9	8.8	9.1	11.1
putative GtrC	-	CJA_3449	8.9	8.8	8.9	10.8
glycosyl transferase, putative, gt2E	gt2E	CJA_3450	9.4	8.9	9.8	11.6
glycosyl transferase, putative, gt2D	gt2D	CJA_3451	9.1	9.0	9.7	11.2
glycosyl transferase, putative, gt2C	gt2C	CJA_3452	8.9	8.8	9.0	10.2
hypothetical protein	-	CJA_3453	9.1	9.0	9.2	9.9
glycosyl transferase, putative, gt2B	gt2B	CJA_3454	9.4	9.4	9.4	10.1
WbgZ	-	CJA_3455	9.5	9.3	9.9	10.4
NAD dependent epimerase/dehydratase-like protein	wbjF	CJA_3456	9.3	9.4	9.3	10.4
Glycosyl transferase group 4-like protein	wbpL	CJA_3457	10.7	11.3	11.0	11.0
hypothetical protein	-	CJA_3458	9.3	9.2	10.2	10.4
GGDEF domain protein	-	CJA_3459	10.3	10.6	10.6	10.2
acyl-CoA dehydrogenase	-	CJA_3460	10.4	9.6	10.7	10.3
efflux ABC transporter, permease protein	-	CJA_3461	11.2	11.8	11.7	10.5
ABC transporter, ATP-binding protein	-	CJA_3462	9.2	9.1	9.1	9.4
hypothetical protein	-	CJA_3463	9.8	9.6	10.4	10.9

putative cobalamin synthesis protein	-	CJA_3464	10.6	10.2	12.0	10.8
predicted GTPase	-	CJA_3465	10.6	10.5	14.3	9.8
putative TonB-dependent receptor	-	CJA_3466	10.0	10.2	9.9	9.7
tryptophan halogenase	-	CJA_3467	10.0	10.0	10.2	9.3
Bacterial extracellular solute-binding protein	-	CJA_3468	10.7	10.5	11.1	9.3
product exhibits features of a methyl-accepting chemotaxis protein	-	CJA_3469	9.5	9.4	10.0	9.1
endo-1, 4-beta mannanase, man5C	man5C	CJA_3470	9.9	9.9	10.2	9.1
hypothetical protein	-	CJA_3471	8.8	8.8	8.8	8.8
GGDEF domain protein	-	CJA_3472	9.6	9.9	9.6	9.5
hypothetical protein	-	CJA_3473	9.0	9.0	9.1	9.5
DsbA	dsbA	CJA_3474	12.3	11.8	13.8	13.0
hypothetical protein	-	CJA_3475	9.0	9.0	9.0	9.8
cytochrome c4	-	CJA_3476	9.4	9.2	9.2	12.2
putative GTPase, involved in coordination of cell cycle (EngB)	-	CJA_3477	10.3	10.9	10.2	11.2
DNA polymerase I	-	CJA_3478	9.8	9.8	9.8	10.9
hypothetical protein	-	CJA_3479	9.6	9.7	14.1	12.5
high-affinity zinc uptake system protein ZnuA	-	CJA_3480	10.4	10.8	10.7	10.7
hypothetical protein	-	CJA_3481	10.1	10.2	10.3	10.5
transcriptional regulator np20	np20	CJA_3482	9.9	9.8	10.1	10.5
zinc ABC transporter, ATP-binding protein ZnuC	znuC	CJA_3483	9.7	9.8	9.6	10.4
permease of ABC zinc transporter ZnuB	znuB	CJA_3484	10.4	10.8	10.4	10.1
hypothetical protein	-	CJA_3485	9.1	9.1	9.5	9.9
Metallo-phosphoesterase	-	CJA_3486	11.8	12.7	11.1	9.2
putative integral membrane protein	-	CJA_3487	11.7	11.8	11.2	10.3
thioesterase family protein domain protein	-	CJA_3488	11.8	12.0	12.2	10.9
hydratase/decarboxylase family protein	-	CJA_3489	12.4	13.2	11.9	11.1
PA5346-like protein	-	CJA_3490	12.1	12.2	12.3	11.5
ATP-dependent DNA helicase RecG	-	CJA_3491	10.4	11.1	10.2	10.3
transcriptional regulator, LysR family	-	CJA_3492	10.4	10.5	11.2	11.4
hypothetical protein	-	CJA_3493	10.4	10.7	10.3	10.9
OmpA domain protein	oprF	CJA_3494	12.5	11.7	13.6	14.3
tRNA (guanine-N(7)-)-methyltransferase	trmB	CJA_3495	11.5	10.2	13.0	13.7
hypothetical protein	-	CJA_3496	11.1	11.3	10.6	10.5
RNA polymerase factor sigma-32	rpoH	CJA_3497	12.5	11.4	14.1	12.4
cell division protein FtsX	ftsX	CJA_3498	9.1	9.1	9.0	9.5
cell division ABC transporter, ATP-binding protein FtsE	ftsE	CJA_3499	10.8	10.8	11.1	11.8
signal recognition particle receptor FtsY	ftsY	CJA_3500	10.5	11.1	9.8	10.7
putative methyltransferase	-	CJA_3501	9.4	9.5	9.7	9.8
hypothetical protein	-	CJA_3502	10.1	10.5	10.4	9.4
pantetheine-phosphate adenylyltransferase	coaD	CJA_3503	12.8	12.4	13.5	12.0

transglycosylase associated gene	-	CJA_3504	9.9	9.9	11.0	9.9
formamidopyrimidine-DNA glycosylase	mutM	CJA_3505	11.9	12.0	11.5	10.4
hypothetical protein	-	CJA_3506	10.4	9.4	10.2	10.5
PEP-CTERM putative exosortase interaction domain protein	-	CJA_3507	11.3	10.2	11.1	10.5
hypothetical protein	-	CJA_3508	12.5	12.3	13.6	9.7
hypothetical protein	-	CJA_3509	9.6	9.5	10.3	9.2
probable two-component sensor	-	CJA_3510	11.5	13.0	10.6	9.4
Response regulator receiver domain protein	-	CJA_3511	9.9	10.0	10.5	9.3
hypothetical protein	-	CJA_3512	9.3	9.5	9.5	9.2
glutathione-regulated potassium-efflux system protein	kefB	CJA_3513	10.6	10.3	11.2	10.2
ribosomal protein L33	rpmG	CJA_3514	11.6	10.0	11.2	13.7
ribosomal protein L28-related protein	rpmB	CJA_3515	11.8	9.7	10.9	14.0
hypothetical protein	-	CJA_3516	11.1	11.7	11.2	9.2
putative lipoprotein	-	CJA_3517	9.2	9.0	11.0	11.3
hypothetical protein	-	CJA_3518	11.1	11.0	11.8	9.8
putative adenylate cyclase	-	CJA_3519	10.4	10.3	11.3	9.8
hypothetical protein	-	CJA_3520	10.1	10.0	10.9	9.0
cyclic AMP receptor protein	-	CJA_3521	11.5	11.2	11.7	10.4
DNA repair protein RadC	-	CJA_3522	9.7	9.4	9.3	9.1
phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine	coaBC	CJA_3523	11.1	11.5	10.6	10.4
phosphomannomutase AlgC	algC	CJA_3524	12.3	12.3	11.2	10.6
acetylglutamate kinase	argB	CJA_3525	10.3	10.4	10.3	11.5
nucleoid occlusion protein	slmA	CJA_3526	9.9	10.4	9.3	9.7
hypothetical protein	-	CJA_3527	9.3	9.3	9.5	10.5
orotate phosphoribosyltransferase	pyrE	CJA_3528	11.3	11.8	11.1	12.2
catabolite repression control protein	crc	CJA_3529	10.6	10.2	12.8	12.7
Tat (twin-arginine translocation) pathway signal sequence domain protein	-	CJA_3530	10.0	9.5	9.7	9.6
thiamine biosynthesis protein Thil	thil	CJA_3531	10.8	10.7	10.3	10.7
transporter, monovalent cation:proton antiporter family	-	CJA_3532	11.1	11.3	11.5	10.1
hypothetical protein	-	CJA_3533	10.6	10.3	10.4	9.1
glutamine synthetase, type I	glnA	CJA_3534	12.2	10.1	15.4	13.5
hypothetical protein	-	CJA_3535	10.4	10.2	11.3	9.6
hypothetical protein	-	CJA_3536	12.1	12.5	14.2	9.9
nitrogen regulation protein NR(I)	ntrC	CJA_3537	10.9	11.1	14.8	10.5
Methyl-accepting chemotaxis protein	-	CJA_3538	12.6	11.8	12.2	10.6
hypothetical protein	-	CJA_3539	11.4	12.6	10.8	9.5
ExoD	exoD	CJA_3540	12.8	12.9	11.9	10.7
CBS domain protein	-	CJA_3541	11.0	10.8	10.5	10.5
hypothetical protein	-	CJA_3542	9.7	9.7	9.9	9.6
hypothetical protein	-	CJA_3543	10.4	10.2	9.9	11.7

hypothetical protein	-	CJA_3544	11.2	11.2	10.8	9.8
hypothetical protein	-	CJA_3545	12.6	13.3	11.9	10.1
Phytanoyl-CoA dioxygenase (PhyH) family	-	CJA_3546	12.6	12.6	12.5	11.7
ABC transporter, ATP-binding protein	-	CJA_3547	10.6	10.8	10.0	10.3
putative conserved hypothetical protein TIGR02444	-	CJA_3548	11.4	11.5	10.5	9.5
hypothetical protein	-	CJA_3549	10.6	10.1	11.5	9.9
Divergent polysaccharide deacetylase family	-	CJA_3550	10.3	10.6	10.2	9.2
carboxyl-terminal protease	-	CJA_3551	10.0	9.8	10.0	10.3
peptidase, M23/M37 family	-	CJA_3552	10.4	10.5	9.9	10.6
phosphoglyceromutase	gpmI	CJA_3553	13.6	13.4	12.7	13.1
hypothetical protein	-	CJA_3554	10.2	10.3	9.8	10.2
rhodanese-like domain protein	-	CJA_3555	10.3	10.6	9.4	11.7
glutaredoxin 3	grxC	CJA_3556	10.3	10.2	10.0	12.0
protein-export protein SecB	secB	CJA_3557	10.4	9.8	9.8	12.1
exopolyphosphatase	-	CJA_3558	11.1	10.8	10.4	10.4
rhamnogalacturonan lyase, rgl11A	rgl11A	CJA_3559	11.6	12.2	10.4	9.2
polyphosphate kinase	ppk	CJA_3560	9.8	9.5	9.5	9.5
putative lipoprotein	-	CJA_3561	9.8	9.5	10.8	11.1
hypothetical protein	-	CJA_3562	11.0	10.4	12.8	9.4
hypothetical protein	-	CJA_3563	14.3	14.4	13.5	9.8
beta-lactamase	bla	CJA_3564	12.4	12.5	11.7	10.1
CAAX amino terminal protease family	-	CJA_3565	10.4	11.0	10.1	9.5
DNA-dependent helicase II	uvrD	CJA_3566	9.8	10.1	9.8	10.4
extracellular solute-binding protein, family 7	-	CJA_3567	10.0	10.0	9.9	9.9
hypothetical protein	-	CJA_3568	9.0	8.9	9.0	9.2
guanylate kinase (GMP kinase)	-	CJA_3569	11.0	11.0	11.1	10.4
DNA-directed RNA polymerase, omega chain	rpoZ	CJA_3570	11.3	10.7	11.8	13.0
guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	spoT	CJA_3571	10.8	11.0	10.7	10.9
putative endoribonuclease L-PSP	-	CJA_3572	11.3	11.3	11.7	11.4
dihydrolipoamide dehydrogenase	-	CJA_3573	10.6	11.0	11.0	11.9
hypothetical protein	-	CJA_3574	9.1	9.1	9.8	9.3
hypothetical protein	-	CJA_3575	10.2	10.0	11.6	9.9
hypothetical protein	-	CJA_3576	9.2	9.2	9.4	9.4
hypothetical protein	-	CJA_3577	9.4	9.3	10.4	9.6
hypothetical protein	-	CJA_3578	10.1	9.7	11.2	9.8
potassium transporter peripheral membrane component	trkA	CJA_3579	9.9	10.7	9.6	10.2
ribosomal RNA small subunit methyltransferase B	sun	CJA_3580	9.2	9.4	9.1	9.9
methionyl-tRNA formyltransferase	fmt	CJA_3581	9.7	9.8	9.3	10.5
peptide deformylase	def	CJA_3582	10.7	12.0	10.9	11.2
LysM domain protein	-	CJA_3583	11.8	11.8	11.8	10.9

putative methyl-accepting chemotaxis protein	-	CJA_3584	10.3	10.2	12.0	9.5
smf protein	smf	CJA_3585	10.9	11.9	11.0	9.5
Sua5/YciO/YrdC/YwIC family protein	-	CJA_3586	12.9	12.7	12.9	11.5
coproporphyrinogen III oxidase	hemF	CJA_3587	9.8	10.2	9.7	10.5
shikimate 5-dehydrogenase	aroE	CJA_3588	13.3	12.9	12.6	11.9
hypothetical protein	-	CJA_3589	9.0	9.1	9.0	9.0
hypothetical protein	-	CJA_3590	10.4	11.0	10.5	9.5
hypothetical protein	pldB3	CJA_3591	10.7	10.3	10.9	9.6
hypothetical protein	-	CJA_3592	11.8	12.8	11.0	10.1
alpha-L-fucosidase, putative, afc95B	afc95B	CJA_3593	10.6	10.3	10.1	9.7
xylosidase/arabinosidase, putative, gly43B	gly43B	CJA_3594	10.3	10.7	10.0	9.9
putative Fructose repressor	-	CJA_3595	9.1	9.1	9.1	9.4
TonB-dependent receptor	-	CJA_3596	9.9	11.0	9.6	9.4
hypothetical protein	-	CJA_3597	8.8	8.9	8.9	9.0
carboxylesterase type B	estA1	CJA_3598	9.2	9.3	9.3	9.3
putative lipoprotein	-	CJA_3599	9.6	9.5	10.7	9.5
hypothetical protein	-	CJA_3600	9.9	9.8	10.0	9.3
beta-xylosidase/alpha-L-arabinofuranosidase, putative, gly43I	gly43I	CJA_3601	9.3	9.2	9.7	9.5
peptidase, M16 (pitrilysin) family	-	CJA_3602	9.1	8.9	9.9	10.7
hypothetical protein	-	CJA_3603	9.3	9.0	9.7	10.4
putative toxin transporter	-	CJA_3604	9.2	9.1	9.5	9.7
putative toxin secretion, membrane fusion protein	-	CJA_3605	9.6	9.2	10.4	10.0
hypothetical protein	-	CJA_3606	9.0	8.9	9.3	10.0
PIN (PiIT N terminus) domain	-	CJA_3607	10.3	10.4	11.6	10.7
possible virulence-associated protein	-	CJA_3608	10.2	10.0	11.8	10.7
transcriptional regulator, LysR family	-	CJA_3609	9.6	10.1	10.1	9.3
DoxD-like family protein	-	CJA_3610	10.7	11.2	12.3	13.8
Protein yhhW	-	CJA_3611	9.5	9.5	9.7	12.2
Plasmid maintenance system killer protein	-	CJA_3612	9.4	9.3	9.9	11.5
helix-turn-helix domain protein	-	CJA_3613	9.0	8.9	9.2	10.3
ABC-type multidrug transport system, permease component	-	CJA_3614	9.2	9.5	9.3	9.0
ABC-type multidrug transport system, ATPase component	-	CJA_3615	10.6	10.3	11.0	9.3
membrane-fusion protein	-	CJA_3616	9.5	9.4	9.9	9.3
Transcriptional regulator	-	CJA_3617	10.6	10.6	11.1	9.7
ABC transporter, ATP-binding protein	-	CJA_3618	9.7	10.4	9.6	9.8
Binding-protein-dependent transport systems inner membrane component dc	-	CJA_3619	9.9	10.0	10.1	10.0
putative Bacterial extracellular solute-binding protein	-	CJA_3620	11.0	12.7	10.5	11.0
putative lipoprotein	-	CJA_3621	10.6	10.3	11.2	10.4
fumarylacetoacetate hydrolase family protein	-	CJA_3622	10.3	10.3	10.7	10.4
sensory box protein	-	CJA_3623	10.0	10.1	10.1	10.4

anhydrase, family 3 protein	-	CJA_3624	11.3	11.1	11.3	11.3
oligopeptidase A	prlC	CJA_3625	9.5	9.6	10.2	10.9
hypothetical protein	-	CJA_3626	9.1	9.1	9.2	9.8
TonB-dependent receptor	-	CJA_3627	9.5	9.3	9.5	9.0
hypothetical protein	-	CJA_3628	9.6	9.7	10.0	9.4
hypothetical protein	-	CJA_3629	10.2	10.3	11.9	9.5
tryptophan halogenase	-	CJA_3630	9.9	10.0	10.1	9.4
Alpha-2-macroglobulin family N-terminal region family	-	CJA_3631	9.9	10.3	10.1	9.6
HsdR	-	CJA_3632	10.5	10.3	11.9	10.4
hypothetical protein	-	CJA_3633	10.9	11.3	11.4	10.2
hypothetical protein	-	CJA_3634	10.0	9.9	10.8	10.3
hypothetical protein	-	CJA_3635	10.0	10.0	10.4	10.2
hypothetical protein	-	CJA_3636	9.6	9.4	10.9	11.3
hypothetical protein	-	CJA_3637	9.9	9.7	12.2	12.0
type I restriction system specificity protein	hsdS-1	CJA_3638	9.3	9.2	10.8	11.3
ATP-dependent DNA helicase	-	CJA_3639	10.4	11.3	11.6	11.6
type I restriction-modification system specificity subunit	-	CJA_3640	10.3	10.2	11.8	11.7
probable orn/arg/lys decarboxylase	-	CJA_3641	10.2	10.2	12.0	12.5
putative helicase	-	CJA_3642	9.2	9.6	9.2	9.4
ubiquinone/menaquinone biosynthesis methyltransferase UbiE	-	CJA_3643	12.1	12.4	11.3	11.8
hypothetical protein	-	CJA_3644	9.3	10.0	9.1	9.9
2-polyprenylphenol 6-hydroxylase	ubiB	CJA_3645	9.7	10.0	9.7	10.1
hypothetical protein	-	CJA_3646	11.6	11.8	12.9	11.5
putative DNA helicase	-	CJA_3647	10.5	10.3	11.0	10.5
hypothetical protein	-	CJA_3648	9.2	9.1	9.6	9.6
possible DNA methylase	-	CJA_3649	10.1	10.5	11.0	10.2
hypothetical protein	-	CJA_3650	9.7	9.9	9.7	9.8
putative restriction endonuclease	-	CJA_3651	11.1	12.2	11.0	9.5
hypothetical sensory box/GGDEF family protein	-	CJA_3653	9.3	9.3	9.4	9.2
ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein prot	-	CJA_3654	10.8	10.7	10.1	10.1
D-tyrosyl-tRNA(Tyr) deacylase	dtd	CJA_3655	11.0	11.6	11.1	11.3
proline iminopeptidase	pip	CJA_3656	10.0	10.8	9.9	10.6
predicted transcriptional regulator	-	CJA_3657	9.8	10.2	10.4	9.8
DNA-3-methyladenine glycosylase I	tag	CJA_3658	10.7	10.8	11.2	10.3
hydrophobic compound transport factor	-	CJA_3659	10.3	10.4	10.4	10.4
Uncharacterised protein family (UPF0131) superfamily	-	CJA_3660	11.2	11.3	12.1	10.3
ferrochelataase	hemH	CJA_3661	10.7	10.5	10.9	10.3
OmpA-like transmembrane domain protein	-	CJA_3662	11.9	11.9	13.3	12.6
hypothetical protein	-	CJA_3663	10.1	10.1	10.0	10.2
GTP-binding protein TypA	typA	CJA_3664	10.5	10.6	10.2	12.8

sensory box/GGDEF family protein	-	CJA_3665	9.8	10.3	10.3	9.1
Thrombospondin type 3 repeat family	-	CJA_3666	10.9	11.1	10.3	11.2
hypothetical protein	-	CJA_3667	9.2	9.1	9.5	9.2
hypothetical protein	-	CJA_3668	10.6	10.4	10.2	10.8
hypothetical protein	-	CJA_3669	10.2	10.0	10.6	10.7
hypothetical protein	-	CJA_3670	10.3	9.8	9.9	11.4
conserved hypothetical phage tail region protein	-	CJA_3671	9.6	9.4	9.7	11.2
conserved hypothetical phage tail region protein	-	CJA_3672	10.7	10.9	10.5	11.3
hypothetical protein	-	CJA_3673	9.9	9.5	11.6	10.8
hypothetical protein	-	CJA_3674	9.4	9.4	9.4	9.6
Rhs element Vgr protein	-	CJA_3675	11.2	11.4	10.8	9.8
PAAR motif family	-	CJA_3676	9.5	10.7	9.1	9.1
GPW / gp25 family protein	-	CJA_3677	10.5	11.2	9.8	9.4
hypothetical protein	-	CJA_3678	9.4	9.6	9.2	9.1
hypothetical protein	-	CJA_3679	10.0	9.9	9.5	9.4
hypothetical protein	-	CJA_3680	10.0	10.4	9.7	9.3
hypothetical protein	-	CJA_3681	9.9	9.8	9.7	9.3
hypothetical protein	-	CJA_3682	10.6	10.7	10.7	9.5
hypothetical protein	-	CJA_3683	8.9	9.0	8.9	8.9
hypothetical protein	-	CJA_3684	10.1	10.6	9.8	9.1
AAA superfamily ATPase	-	CJA_3685	9.4	9.4	9.1	9.1
hypothetical protein	-	CJA_3686	11.4	11.3	12.6	9.8
hypothetical protein	-	CJA_3688	10.7	11.1	11.3	9.7
hypothetical protein	-	CJA_3689	9.9	9.9	11.0	9.7
hypothetical protein	-	CJA_3690	9.5	9.3	10.8	9.7
hypothetical protein	-	CJA_3691	9.6	9.8	9.9	9.5
hypothetical protein	-	CJA_3692	10.3	10.8	10.7	9.7
trypsin domain/PDZ domain protein	-	CJA_3693	10.5	11.3	10.6	10.8
hypothetical protein	-	CJA_3694	10.2	10.5	10.2	10.5
heavy metal efflux pump, CzcA family	-	CJA_3695	10.9	11.3	10.3	9.2
cation efflux system protein	-	CJA_3696	9.9	10.3	9.4	9.1
putative cation efflux system protein	-	CJA_3697	9.0	9.1	9.0	8.9
hypothetical protein	-	CJA_3698	11.8	12.8	10.7	9.9
Permease of the major facilitator superfamily	-	CJA_3699	11.1	11.0	11.5	9.6
arsenic resistance operon regulator	arsR	CJA_3700	11.2	11.1	11.1	9.7
hypothetical protein	-	CJA_3701	11.5	11.2	11.7	11.2
Predicted transcriptional regulator	-	CJA_3702	9.9	9.5	10.8	10.1
hypothetical protein	-	CJA_3703	9.9	10.0	9.9	9.8
beta glucanase, putative, glu16C	glu16C	CJA_3704	11.1	11.8	11.0	9.7
transcriptional regulator, AraC family	-	CJA_3705	10.4	10.9	10.6	9.5

beta glucanase, putative, glu16G	glu16G	CJA_3706	10.4	10.8	10.7	9.1
alkaline phosphatase-like protein	-	CJA_3707	11.6	12.6	10.7	9.2
radical SAM domain protein protein	-	CJA_3708	10.9	11.2	11.6	9.4
hypothetical protein	-	CJA_3709	10.2	10.3	10.5	10.0
plasmid stabilization system protein, RelE/ParE family	-	CJA_3710	9.7	9.8	10.1	9.8
transcriptional regulator, GntR family	-	CJA_3711	10.8	10.6	10.2	10.0
iron-sulfur cluster-binding protein	-	CJA_3712	10.2	10.3	10.4	10.0
hypothetical protein	-	CJA_3713	9.4	9.4	9.7	9.2
sensory box protein	-	CJA_3714	9.6	9.9	9.6	9.7
Bacterial Transmembrane Pair family	-	CJA_3715	9.7	9.5	10.4	10.4
transcriptional regulator, LysR family	-	CJA_3716	9.1	9.2	9.1	9.9
adenine-specific DNA methyltransferase	dam	CJA_3717	9.0	9.0	9.2	10.2
hypothetical protein	-	CJA_3718	9.7	9.3	11.6	9.6
hypothetical protein	-	CJA_3719	10.1	10.3	11.0	10.4
MrfJ protein	mrfJ	CJA_3720	10.7	10.7	11.4	11.4
methylated-DNA-[protein]-cysteine S-methyltransferase	-	CJA_3721	10.1	10.3	10.7	10.9
TonB-dependent ferric achromobactin receptor	-	CJA_3722	10.6	11.0	10.7	11.2
hypothetical protein	-	CJA_3723	9.9	10.2	11.6	9.6
hypothetical protein	-	CJA_3724	10.0	9.8	11.5	10.1
Plasmid stabilization system protein	-	CJA_3725	9.3	9.2	10.3	11.0
Antitoxin of toxin-antitoxin stability system	-	CJA_3726	9.1	9.2	9.4	9.9
hypothetical protein	-	CJA_3727	10.2	10.0	11.5	10.2
hypothetical protein	-	CJA_3728	9.0	8.9	9.2	9.2
UvrD/REP helicase	-	CJA_3729	8.9	8.9	9.0	9.0
hypothetical protein	-	CJA_3730	8.9	8.9	9.1	9.1
hypothetical protein	-	CJA_3731	10.0	9.7	11.3	10.4
hypothetical protein	-	CJA_3732	9.4	9.6	9.9	11.6
hypothetical protein	-	CJA_3733	9.8	9.7	11.7	12.5
hypothetical protein	-	CJA_3736	9.7	9.4	11.8	10.1
putative pyridine nucleotide-disulphide oxidoreductase	-	CJA_3737	10.7	11.9	11.9	9.9
Transcriptional regulator family	-	CJA_3738	9.1	9.1	9.5	9.4
Transcriptional regulator	-	CJA_3739	8.9	8.8	8.9	9.0
hypothetical protein	-	CJA_3740	9.5	9.6	9.7	9.8
hypothetical protein	-	CJA_3741	9.5	10.6	9.4	9.2
transcriptional regulatory protein	-	CJA_3742	9.1	9.6	9.1	9.3
lipase	lipP	CJA_3743	9.9	10.1	10.0	9.6
transcriptional regulator	-	CJA_3744	9.3	9.4	9.2	9.3
reductase	-	CJA_3745	9.0	9.1	9.0	9.1
transcriptional regulator, LuxR family	-	CJA_3746	10.1	10.5	10.6	9.3
Chitinase Csn46F	-	CJA_3747	11.3	12.1	12.5	9.1

hypothetical protein	-	CJA_3748	8.9	8.9	9.1	8.8
hypothetical protein	-	CJA_3749	9.4	9.7	9.6	8.9
aminotransferase	-	CJA_3750	9.6	9.4	9.7	9.1
hypothetical protein	-	CJA_3751	10.0	10.0	10.9	9.0
FAD binding domain protein	-	CJA_3752	9.7	9.8	9.5	9.2
putative transporter	-	CJA_3753	11.9	13.0	11.5	9.5
Choline/Carnitine o-acyltransferase superfamily	-	CJA_3754	9.7	9.7	9.4	9.1
probable FMN oxidoreductase	-	CJA_3755	10.2	10.3	10.0	9.3
hypothetical protein	-	CJA_3756	10.5	11.1	10.2	9.1
short-chain dehydrogenase	-	CJA_3757	10.3	11.1	9.9	9.5
hypothetical protein	-	CJA_3758	10.4	10.5	10.9	10.0
hypothetical protein	-	CJA_3759	9.4	9.3	9.6	9.5
putative arylamine N-acetyltransferase	-	CJA_3760	9.5	9.4	9.5	9.1
hypothetical protein	-	CJA_3761	9.6	9.7	9.8	8.9
endo-1,4-beta-xylanase, xyn11B	xyn11B	CJA_3762	10.4	10.2	10.2	9.0
endo-1,4-beta-xylanase, esterase, xyn11A	xyn11A	CJA_3763	10.5	10.4	9.8	9.5
hypothetical protein	-	CJA_3764	8.8	8.8	8.8	9.1
hypothetical protein	-	CJA_3765	8.8	8.8	8.8	8.8
integral membrane protein	-	CJA_3766	9.8	9.7	10.8	10.2
Periplasmic binding protein	-	CJA_3767	10.4	11.2	10.4	11.2
cobalamin biosynthetic protein	cobC	CJA_3768	9.7	10.0	9.9	11.1
cobalamin biosynthesis protein CobD	cobD	CJA_3769	9.1	9.0	9.1	10.3
cobinamide kinase	cobP	CJA_3770	8.9	8.9	8.9	9.6
heme/hemin ABC transporter, ATP-binding protein	-	CJA_3771	9.5	9.4	9.2	10.9
probable permease of ABC transporter	-	CJA_3772	9.2	9.4	9.5	10.4
cobyric acid synthase CobQ	cobQ	CJA_3773	10.4	11.1	10.0	11.7
cob(I)alamin adenosyltransferase	cobO	CJA_3774	10.7	10.4	10.6	13.5
putative TonB-dependent receptor	-	CJA_3775	10.7	10.5	10.6	14.3
hypothetical protein	-	CJA_3776	10.2	9.9	10.0	12.0
hypothetical protein	-	CJA_3777	8.9	9.0	8.9	8.9
hypothetical protein	-	CJA_3778	10.9	12.1	10.3	9.5
putative lipoprotein	-	CJA_3779	9.1	9.2	9.2	9.0
hypothetical protein	-	CJA_3780	9.9	10.1	10.4	9.1
endo-beta-mannanase, putative, man5E	man5E	CJA_3784	9.1	9.1	9.4	10.1
putative hypoxanthine phosphoribosyltransferase	-	CJA_3787	9.0	8.9	10.0	10.3
hypothetical protein	-	CJA_3788	8.9	8.9	9.5	9.5
putative phosphoribosylglycinamide synthetase	-	CJA_3789	9.1	9.0	9.5	9.9
putative methylthioadenosine/S-adenosyl homocysteine nucleosidase	-	CJA_3790	8.9	8.9	9.3	9.9
hypothetical protein	-	CJA_3791	8.9	8.9	9.2	9.7
DEAD/DEAH box helicase	-	CJA_3794	9.0	9.0	9.8	10.2

hypothetical protein	-	CJA_3795	9.3	9.2	10.8	11.2
hypothetical protein	-	CJA_3796	8.9	8.8	9.0	9.4
Tn7-Cj, transposition protein TnsE	tnsE	CJA_3797	9.1	9.0	9.7	9.2
Tn7-Cj, transposition protein TnsD	tnsD	CJA_3798	9.0	9.0	9.2	8.9
Tn7-Cj, transposition protein TnsC	tnsC	CJA_3799	9.0	9.0	9.4	9.1
Tn7-Cj, transposase protein TnsB	tnsB	CJA_3800	9.7	9.6	11.4	9.5
Tn7-Cj, transposase protein TnsA	tnsA	CJA_3801	9.1	9.1	9.9	9.3
glucosamine--fructose-6-phosphate aminotransferase, isomerizing	glmS	CJA_3802	9.4	9.5	10.2	11.0
Putative transcriptional regulator, DeoR family	srlR	CJA_3803	10.0	10.0	10.7	10.5
cellulase, putative, cel9C	cel9C	CJA_3804	9.2	9.2	9.4	9.5
Helix-turn-helix domain protein	-	CJA_3805	9.5	9.4	10.9	10.2
UDP-N-acetylglucosamine pyrophosphorylase	glmU	CJA_3806	9.8	9.8	9.9	11.2
SEC-C motif domain protein	-	CJA_3807	9.6	9.7	9.6	9.6
ATP synthase F1, epsilon subunit	atpC	CJA_3808	9.9	9.3	9.7	13.4
F0F1 ATP synthase subunit beta	atpD	CJA_3809	9.8	9.3	9.8	14.1
ATP synthase F1, gamma subunit	atpG	CJA_3810	10.0	9.4	9.8	14.5
ATP synthase F1, alpha subunit	atpA	CJA_3811	10.5	10.0	10.0	14.5
ATP synthase F1, delta subunit	atpH	CJA_3812	10.1	9.6	9.5	14.6
ATP synthase F0, B subunit	atpF	CJA_3813	9.7	9.2	9.4	14.4
ATP synthase F0, C subunit	atpE	CJA_3814	10.3	9.7	10.4	14.4
F0F1 ATP synthase subunit A	atpB	CJA_3815	11.3	10.5	11.6	13.4
hypothetical protein	-	CJA_3816	9.8	10.1	9.8	10.9
hypothetical protein	-	CJA_3817	9.7	10.1	9.4	10.9
chromosome partitioning protein Soj	soj	CJA_3818	9.9	10.5	9.6	11.6
methyltransferase GidB	gidB	CJA_3819	9.7	9.7	9.7	11.2
tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	gidA	CJA_3820	9.2	9.2	9.2	10.9
hypothetical protein	-	CJA_3821	8.9	9.0	8.9	8.8
tRNA modification GTPase TrmE	trmE	CJA_3822	9.3	9.3	9.4	10.2
inner membrane protein, 60 kDa	-	CJA_3823	11.0	11.0	11.2	13.3
conserved hypothetical protein TIGR00278	-	CJA_3824	10.2	10.4	10.2	12.6
ribonuclease P protein component	rnpA	CJA_3825	9.9	9.9	10.3	12.7
ribosomal protein L34	rpmH	CJA_3826	8.9	8.9	9.0	12.1