

## DNA Microarray and Gene Ontology Enrichment Analysis Reveals That a Mutation in *opsX* Affects Virulence and Chemotaxis in *Xanthomonas oryzae* pv. *oryzae*

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***Xanthomonas oryzae* pv. *oryzae* (*Xoo*) causes bacterial leaf blight (BLB) in rice (*Oryza sativa* L.). In this study, we investigated the effect of a mutation in *opsX* (XOO1056), which encodes a saccharide biosynthesis regulatory protein, on the virulence and bacterial chemotaxis of *Xoo*. We performed DNA microarray analysis, which showed that 63 of 2,678 genes, including genes related to bacterial motility (flagellar and chemotaxis proteins) were significantly down-regulated (< -2 log<sub>2</sub> fold changes) by the mutation in *opsX*. Indeed, motility assays showed that the mutant strain was nonmotile on semisolid agar swarm plates. In addition, a mutant strain (*opsX*::Tn5) showed decreased virulence against the susceptible rice cultivar, IR24. Quantitative real-time RT-PCR reaction was performed to confirm the expression levels of these genes, including those related to flagella and chemotaxis, in the *opsX* mutant. Our findings revealed that mutation of *opsX* affects both virulence and bacterial motility. These results will help to improve our understanding of *Xoo* and provide insight into *Xoo*-rice interactions.**

**Keywords :** chemotaxis, DNA microarray, *opsX*, virulence, *Xanthomonas oryzae* pv. *oryzae*

Bacterial leaf blight (BLB), caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), is a major disease affecting rice grown in Asian countries. The *opsX* gene, which encodes a saccharide biosynthesis regulatory protein required for the assembly of lipopolysaccharide (LPS), has been cloned from *Xanthomonas campestris* pv. *citrumelo* (Kingsley et al., 1993). LPS from several plant pathogens have been shown to activate a number of defense-related responses in plants. LPS from *X. campestris* can induce generation of transcripts for a defense-related β-1,3-glucanase in turnip (Newman et al., 1995), purified LPS from *Pseudomonas syringae* pv. *syringae* is a weak elicitor of phytoalexins in soybean (Barton-Willis et al., 1984), and LPS from *Ralstonia solanacearum* can induce the synthesis of new polypeptides in tobacco (Leach et al., 1983). Mutation of *opsX* resulted in a loss of virulence on the citrus host, marked by rapid cell death, although the hypersensitive response (HR), host range, and virulence to beans remained unaffected (Kingsley et al., 1993). Although it is tempting to conclude that LPS is responsible for protection from plant inhibitors, mutations in *opsX* also have pleiotropic effects on growth rate, capsular slime, and extracellular polysaccharide (EPS). Indeed, Kingsley et al. (1993) reported that *opsX* of *X. oryzae* pv. *citrumelo* affects biosynthesis of LPS and EPS. In the M28 mutant ( $\Delta$ *opsX*), derived from wild-type *X. oryzae* pv. *citrumelo* strain 3048, loss of LPS decreased EPS production to one-third that of the wild type. Motility is an important virulence factor in many pathogenic species and in some cases is inversely regulated with the expression of other virulence traits (Ottemann and Miller, 1997). Although the chemotactic properties of xanthomonads have not been extensively studied, Feng and Kuo (1975) reported that the rice pathogen *Xoo* showed chemotaxis toward a synthetic medium and water exudates of susceptible rice plants, whereas chemotaxis

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toward hydathode exudates of resistant plants was not observed. In addition, *X. campestris* pv. *campestris* is nonmotile and nonflagellated in the xylem fluid of infected cabbage leaves, which suggests that bacterial movement in the xylem is due to diffusion rather than to motility (Kamoun and Kado, 1990). This suggests that chemotaxis may play a role before the bacteria penetrate the host leaf. However, the role of chemotaxis in bacterial movement inside the plant remains unknown (Kamoun and Kado, 1990).

This study investigated the effect of *opsX* mutation on virulence and xanthan and LPS production in *Xoo*, as well as on the expression of other genes that are known to play roles in chemotaxis.

## Materials and Methods

**Bacterial strains and culture conditions.** The *Xoo* KACC10859 strain was obtained from the Korean Agricultural Culture Collection (KACC) in Jeonju, Korea, and was cultured on yeast dextrose carbonate (YDC) medium (2.0% D-glucose, 2.0% CaCO<sub>3</sub>, 1.0% yeast extract, and 1.5% agar) or in nutrient broth (3% beef extract, 5% peptone, and 1.5% agar, Difco; DB, Seoul, Korea) at 28°C until 2.0 OD<sub>600</sub>. *Xoo* strains were washed twice and immediately transferred into XOM2 medium (0.18% xylose sugar, 670 mM D-, L-methionine, 10 mM sodium L(+)-glutamate, 14.7 mM KH<sub>2</sub>PO<sub>4</sub>, 40 mM MnSO<sub>4</sub>, 240 mM Fe (III) ethylenediaminetetraacetic acid (EDTA), and 5 mM MgCl<sub>2</sub>, pH 6.5).

**Transposon mutagenesis and molecular analysis of the *opsX* mutant.** Insertional mutagenesis was performed using transposome™ (20 ng/ml; Epicentre, Seoul, Korea) and the insertion site was analyzed by polymerase chain reaction (PCR) according to a previously described method (Park et al., 2007). Sequencing and subsequent data analysis were performed using an ABI Prism 3100 automatic DNA sequencer (Thermo Scientific, Seoul, Korea) and sequences were analyzed for similarities using the BLASTN and BLASTX algorithms available at the National Center for Biotechnology Information (NCBI). The *opsX* mutant was analyzed by PCR with the primers *OPSXF* (5'-ATGGCTGTAACGCCGCATC-3') and *OPSXR* (5'-TCAGCGGGTGGTCGGCGC-3'), corresponding to the *opsX* (XOO1056) open reading frame (ORF). The PCR was carried out in a PTC-225 thermocycler (Bio-Rad, Seoul, Korea) with the following conditions: initial denaturation at 95°C for 5 minutes followed by 30 cycles at 95°C for 30 seconds, 65°C for 30 seconds, and 72°C for 2 minutes, and a final extension for 5 minutes at 72°C. For Southern hybridization,

genomic DNA was digested with *EcoRI* (Toyobo, Seoul, Korea), electrophoresed, and transferred to a Hybond-N<sup>+</sup> membrane (GE Healthcare, Seoul, Korea). The kanamycin gene in the transposon was amplified by PCR with the primers KANF (5'-CAATCAGGTGCGACAATC-3') and KANR (5'-TCACCGAGGCAGTTCCAT-3'), and labeled as a probe with [ $\alpha$ -32<sup>P</sup>] dCTP (Ladderman Labeling Kit; TaKaRa, Seoul, Korea). Prehybridization and hybridization were conducted as described by Sambrook and Russell (2001). For complementation, a DNA fragment containing *opsX* was amplified from wild-type genomic DNA by PCR using the primers *OPSXFC* (5'-CTGCAGGAATTGGCAAAACTGCG CG-3'; *PstI* restriction site is underlined) and *OPSXRC* (5'-CTAGCGCGATAGCTTGAGC-3'), and the PCR product was cloned into the pGEM-T easy vector (Promega, Seoul, Korea). The resulting plasmid was digested with *PstI*, ligated into the corresponding sites of the broad host-range vector pHMI, and introduced into the *opsX* mutant strain to obtain the complemented strain (MT/C).

**Oligonucleotide and target preparation.** DNA microarrays with 50-bp oligo spots representing 3382 ORFs, approximately 3/4 of the *Xoo* KACC10331 genome, were synthesized and spotted on addressable electrodes of CustomArray™ 12K microarrays. Microarray™ analysis was performed according to the CustomArray™ 12K microarray protocol provided by CombiMatrix (CombiMatrix Corp.; <http://www.combimatrix.com>).

RNA was isolated from a stationary phase culture (OD<sub>600</sub> = 0.8) using an RNeasy mini kit in accordance with the manufacturer's instructions (Qiagen, Seoul, Korea). Total RNA was eluted with 50 µl of RNase-free water and quantified using an ultraviolet spectrophotometer (ND-1000). Each sample was run on a 1.2% agarose gel to verify the purity and integrity of the RNA. cDNA was synthesized using the MessageAmp™ II-Bacteria Kit (Thermo Scientific). Polyadenylation of the bacterial RNA was performed using *Escherichia coli* poly(A) polymerase and tailed RNA reverse-transcribed in a reaction mixture primed with an oligo (dT) primer and ArrayScript™ (Thermo Scientific) reverse transcriptase. Second-strand cDNA was synthesized and purified for *in vitro* transcription in a reaction mixture containing biotin-modified UTP and T7 RNA polymerase.

**Microarray hybridization.** Hybridization was performed using 5 µg of labeled target sample per CustomArray™ 12K microarray for 16 hours at 45°C with gentle rotation. The arrays were then washed with: (i) 6 × SSPE, 0.05% Tween-20 for 5 minutes, (ii) 3 × SSPE, 0.05% Tween-20

for 1 minute, (iii)  $0.5 \times$  SSPE, 0.05% Tween-20 for 1 minute, and (iv)  $2 \times$  phosphate-buffered saline, 0.1% Tween-20 for 1 minute.

**Data acquisition and analysis.** Hybridized microarrays were scanned (photomultiplier tube, 500–700; pixel size, 5; focus position, 130) using a GenePix 4000B microarray scanner (Axon Instruments, Union City, CA, USA). After data extraction (<https://webapps.combimatrix.com>), the background was calculated for individual samples using factory-built controls with low intensities (lowest intensity, 5–30%) and the median signal intensities were calculated for subtraction. Microarray data of individual samples were normalized by global normalization using probes with signal values greater than zero, < 60,000 (the saturation value), and greater than the lowest 5% of the signal value of each sample. In total, 3,382 probes were used for the final analysis. The local-pooled-error (LPE) test (<http://bioinformatics.oxfordjournals.org/cgi/reprint/19/15/1945>) and fold-change analysis were applied to determine differentially expressed sets of genes using the Avadis Prophetic software version 3.3 (Strand Genomics Ltd., Bangalore, India). For further analysis of the upregulated and downregulated genes, gene ontology (GO) term annotation (biological process, molecular function, and cellular component) and enrichment analysis were performed using the Blast2GO software with default parameters (Conesa et al., 2005).

**Virulence assay.** Leaves of 50-day-old susceptible rice (cultivar IR24) were inoculated with the pathogen by clipping the leaf tips with sterile scissors dipped in a saturated culture ( $10^9$  cells/ml). The rice plants were then grown in a greenhouse at 25–30°C with a relative humidity of 60%. Leaves clipped with scissors dipped in distilled water were used as the control. Lesion length was measured 21 days after inoculation. The virulence

assay was performed in triplicate for both wild-type and mutant strains, and means and standard deviations (SDs) of lesion lengths were calculated for each experiment.

**Determination of EPS and LPS production.** The amount of xanthan in the supernatant was determined by a modified version of the phenol-sulfuric acid method (DuBois et al., 1956). Culture supernatant without bacterial cells (filtered through a 0.45-mm filter; Sigma-Aldrich, Yongin, Korea) was tested to estimate the amount of xanthan. Culture supernatant (0.3 ml) was mixed with 1.65 ml of distilled water and 0.05 ml of 80% (v/v) phenol. Then, 5 ml of 100% sulfuric acid was added to the phenol mixture, suspended, and placed at room temperature for 30 minutes. The concentration of xanthan was spectrophotometrically determined by measuring the absorbance at 490 nm. LPS was extracted using the hot phenol-water method described by Westphal and Jann (1965), subjected to 12% sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE), and visualized via silver staining (Tsai and Frasch, 1982). Nucleic acids were removed by incubation with DNase (Qiagen) and RNase (Qiagen) for 1 hour at 37°C. Proteins were removed by incubation with protease (Qiagen) for 1 hour at 37°C.

**Quantitative real-time RT-PCR assay.** An independent set of cell cultures and total RNA of the two *Xoo* strains were prepared following the same protocol as for the microarray analysis. The sequence of each gene was obtained from the *Xoo* KACC10331 database (<http://www.ncbi.nlm.nih.gov>), and used for primer design by IDT (Integrated DNA Technologies, <https://eu.idtdna.com/Primerquest/Home/Index>). RNA samples from three independent replicates were treated with DNase before cDNA synthesis. Quantitative real-time PCR analysis was performed using a RotorGene 6000 (Qiagen) in 25-

**Table 1.** Primers used in quantitative real-time PCR

ORF ID*	Locus tag	Product	Forward (5'-3')	Reverse (5'-3')
16S			CCTACGGGAGGCAGCAG	ATTACCGCGGCTGCTGGCA
XOO2568	<i>cheV</i>	Chemotaxis protein	CTATACGCTGACGACGAAATC	TTGAACACGCCGACAAA
XOO2558	<i>mcp</i>	Chemotaxis protein	TTGAATGGCAAGAGGATCTG	CGGATGAGTGGACGTGAATAC
XOO2848	<i>tsr</i>	Chemotaxis protein	CGCCGAAAGTACGTGAAATG	GCTGCCTGGTCAGTAGTAA
XOO2577	<i>flgI</i>	Flagellar basal body P-ring biosynthesis protein FlgA	TGTCGGTCGTATTCCAATG	GGTGGTGAAGTCGTTCTGAT
XOO2572	<i>flgE</i>	Flagellar hook protein FlgE	AATACCTTTGTCCGGCATC	CTTGAACCCAGTCGTGTTGA

ORF, open reading frame.

\*All gene sequences were attained from the *Xoo* KACC10331 genomic sequence in the National Center for Biotechnology Information GenBank database (accession no. AE013598).

$\mu\text{l}$  reactions containing 12.5  $\mu\text{l}$  of 2X SensiFAST SYBR No-ROX kit (Bioline, Sydney, Australia), 10 pmol of each primer (Table 1), and 25 ng of cDNA template. The following reaction conditions were used: 3 minutes at 95°C followed by 40 cycles of 95°C for 5 seconds, 60°C for 10 seconds, and 72°C for 15 seconds.

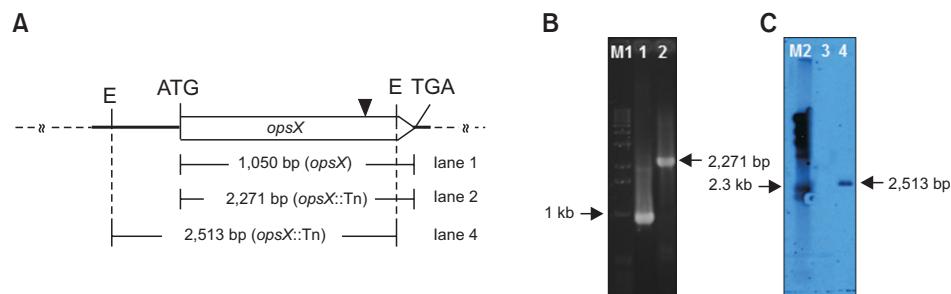
**Swarming and growth rate assays.** Bacterial motility was assayed using a previously described method (Kim et al., 2015). Cultures were grown in nutrient broth (NB) medium for 24 hours, washed 3 times with 1 ml of PME buffer (10 mM potassium phosphate [pH 7.2], 1 mM MgCl<sub>2</sub>, and 0.1 mM EDTA), and then stabbed into swarm agar plates (0.7% NaCl, 0.115% K<sub>2</sub>HPO<sub>4</sub>, 0.02% KH<sub>2</sub>PO<sub>4</sub>, 0.02% KCl, 0.01% yeast extract, and 0.3% agar). For the growth rate assay, fifty microliters of each culture ( $\text{OD}_{600} = 1$ ), prepared from 5 ml of seed culture in NB medium, was inoculated in 5 ml of swarming medium without agar and incubated for 72 hours at 28°C in a shaking incubator. The ODs of each strain were measured using a GENESYS™ 20 Visible Spectrophotometer (Thermo Scientific). The averages and SDs of swarming and growth rates were calculated for each repetition of the experiment.

## Results

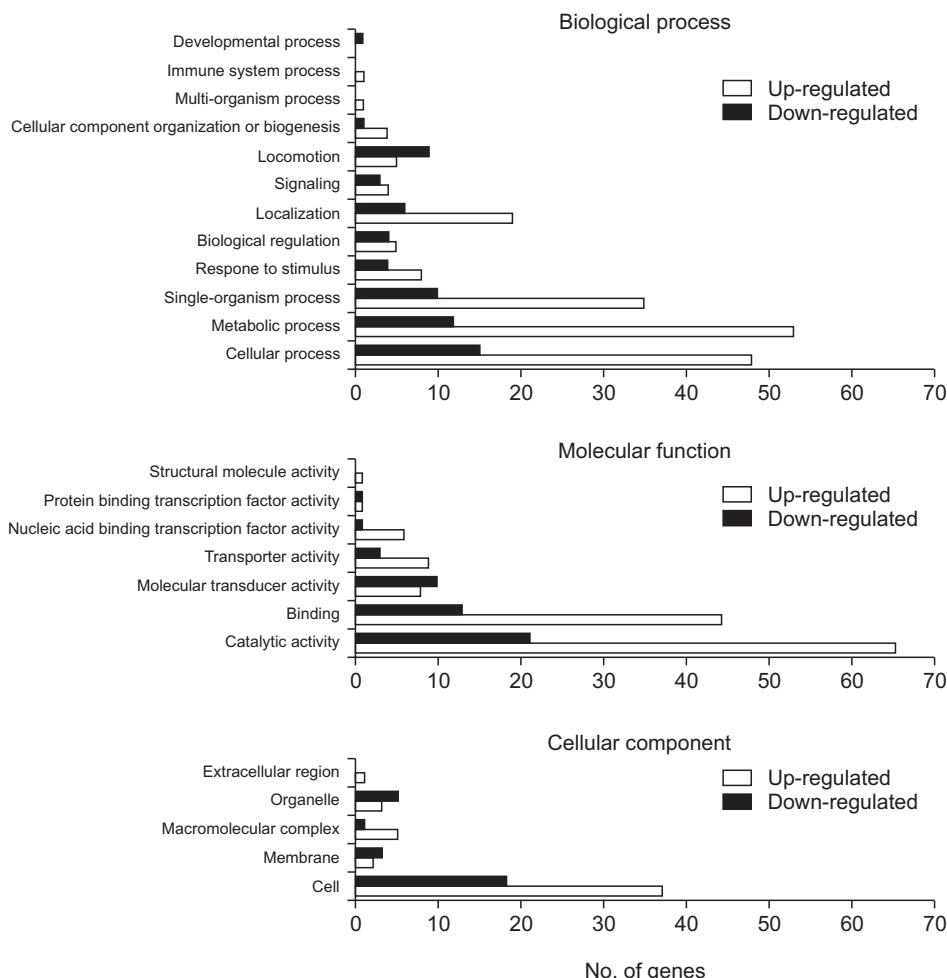
**Molecular characterization of the *opsX* mutant.** Sequencing analysis revealed that the transposon was inserted at nucleotide 838 of *opsX* (Fig. 1A). This gene harbors a 1,050-bp ORF encoding a 349-amino acid saccharide biosynthesis regulatory protein. Transposon insertion into *opsX* was confirmed by PCR amplification of a 2,271-bp fragment from the mutant using the OPSXF and OPSXR primers (Fig. 1B). In the Southern hybridization analysis, a single positive signal (2,513-bp) was detected in the mutant by using the PCR product of the kanamycin-

resistant gene as a probe (Fig. 1C). These results indicate that a single transposon was inserted into *opsX*.

**Expression profiles and quantitative real-time RT-PCR.** The *Xoo* DNA-chip was used to compare the expression profile of the *opsX* mutant with that of the wild-type strain. The resultant expression profile was refined using a false discovery rate of 5% ( $P < 0.05$ ; LPE test) and a log<sub>2</sub> fold change (FC) minimum of  $\pm 2$ ; 259 genes were found to be upregulated or downregulated in the *opsX* mutant (Table S1). The transcripts of these upregulated and downregulated genes were categorized according to their annotated function with respect to biological processes, molecular functions, and cellular components, on the basis of blast and GO term annotation using the Blast2GO software (Conesa et al., 2005). The biological processes mediated by these genes were primarily associated with metabolic processes, cellular processes, single organism processes, localization, signaling, and others (Fig. 2). Only upregulated genes were found to belong to the multi-organism process and immune system process categories. In contrast, only downregulated genes were found to belong to the developmental process category. Molecular functions were primarily related to catalytic and binding activity. Only upregulated genes belonged to the structural molecule activity category. The cellular component categories included cell, membrane, macromolecular complex, organelle, and extracellular region. Only upregulated genes belonged to the extracellular region category. Most of these categories, such as locomotion, molecular transducer activity, membrane, and organelle, contained more downregulated genes than upregulated genes, whereas the cellular process, metabolic process, single-organism process, localization, catalytic activity, binding, and cell categories contained more upregulated than downregulated genes (Fig. 2, Table S2). In GO term enrichment



**Fig. 1.** Genetic mapping and molecular analysis of the *opsX* mutant strain. (A) The solid triangle indicates the site of the Tn5 transposon insertion. Restriction sites for *Eco*RI (E) are also indicated. (B, C) PCR and Southern hybridization analysis for confirmation of transposon insertion in *opsX*: M1, 1-kb ladder; M2, lambda DNA/*Hind*III; lane 1, wild type; lanes 2 and 4, *opsX* mutant. The arrowhead indicates a single positive signal from the transposon (2,513-bp).



**Fig. 2.** Functional categorization of up- and down-regulated genes in the *Xanthomonas oryzae* pv. *oryzae* *opsX* mutant based on GO annotation.

**Table 2.** GO terms enriched in downregulated genes in the *Xanthomonas oryzae* pv. *oryzae* *opsX* mutant

GO-ID	Term	Category	FDR (q-value)	P-value*	TestSeqs
GO:0007165	Signal transduction	P	6.29E-07	2.56E-08	XOO1207, XOO2836, XOO2859, XOO2787, XOO2568, XOO2833, XOO2558, XOO2860, XOO3763, XOO2228, XOO2850, XOO3147, XOO1721
GO:0004871	Signal transducer activity	F	4.97E-06	2.48E-07	XOO1207, XOO2836, XOO2859, XOO2568, XOO2833, XOO2558, XOO2860, XOO2228, XOO2850, XOO3147
GO:0016301	Kinase activity	F	3.29E-02	2.09E-03	XOO1207, XOO2836, XOO2860, XOO2228, XOO3147, XOO3611
GO:0048870	Cell motility	P	3.67E-02	2.99E-03	XOO2572, XOO2849, XOO2607

FDR, false discovery rate.

\*P < 0.05.

analysis, four remarkably enriched GO terms, cell motility (GO:0048870), signal transducer activity (GO:0004871), signal transduction (GO:0007165), and kinase activity (GO:0016301), were identified in the downregulated

genes (Table 2). Among them, six chemotaxis-related genes (XOO2558, XOO2568, XOO2833, XOO2836, XOO2850, and XOO2859) and two flagellar-related genes (XOO2572 and XOO2607) were downregulated

**Table 3.** List of GO terms enriched in downregulated genes in the *Xanthomonas oryzae* pv. *oryzae opsX* mutant

Locus tag	Gene	Product	log <sub>2</sub> FC_mean	log <sub>2</sub> FC_1	log <sub>2</sub> FC_2	log <sub>2</sub> FC_3
XOO1207	<i>colS</i>	Two-component system sensor protein	-2.23	-3.33	-1.63	-1.71
XOO1721	-	Response regulator	-2.18	-2.01	-2.23	-2.31
XOO2228	<i>regS</i>	Two-component system sensor protein	-2.31	-3.26	-1.77	-1.90
XOO2558	<i>mcp</i>	Chemotaxis protein	-2.90	NA	-3.45	-2.34
XOO2568	<i>cheV</i>	Chemotaxis protein	-2.50	NA	-1.90	-3.10
XOO2572	<i>flgE</i>	Flagellar hook protein FlgE	-3.82	-4.02	-3.97	-3.47
XOO2607	<i>fliL</i>	Flagellar protein	-2.37	-2.60	-2.67	-1.84
XOO2787	<i>rrpX</i>	Transcriptional regulator	-2.03	NA	-5.62	1.57
XOO2833	<i>cheW</i>	Chemotaxis protein	-2.44	-2.47	-2.24	-2.61
XOO2836	<i>cheA</i>	Chemotaxis protein	-2.13	-1.98	-2.25	-2.15
XOO2849	-	Hypothetical protein	-3.55	-4.00	-3.29	-3.36
XOO2850	<i>cheW</i>	Chemotaxis protein	-2.54	-3.18	-1.69	-2.74
XOO2859	<i>cheB</i>	Chemotaxis-specific methylesterase	-2.51	-2.28	-2.74	-2.50
XOO2860	<i>pdeA</i>	c-di-GMP phosphodiesterase A	-2.27	-1.99	-2.28	-2.54
XOO3147	<i>fixL</i>	Sensor histidine kinase	-2.64	-2.57	-2.59	-2.75
XOO3611	-	Transcriptional regulator	-2.87	-2.25	-3.44	-2.91
XOO3763	<i>colR</i>	Two-component system regulatory protein	-2.70	-2.71	-2.63	-2.76

NA, not available.

by *opsX* mutation. The log<sub>2</sub> FC levels of these eight genes ranged from -2.13 to -3.82. Among the eight genes, *flgE* (XOO2572) and *cheW* (XOO2850) were most strongly downregulated, by -3.82 FC and -2.54 FC, respectively, by mutation of *opsX* (Table 3). Consistent with the microarray analysis, five genes (*cheV*, XOO2568; *mcp*, XOO2558; *tsr*, XOO2848; *flgI*, XOO2577; and *flgE*, XOO2572) involved in bacterial motility showed relatively lower expression in the *opsX* mutant than in the wild-type strain (Fig. 3).

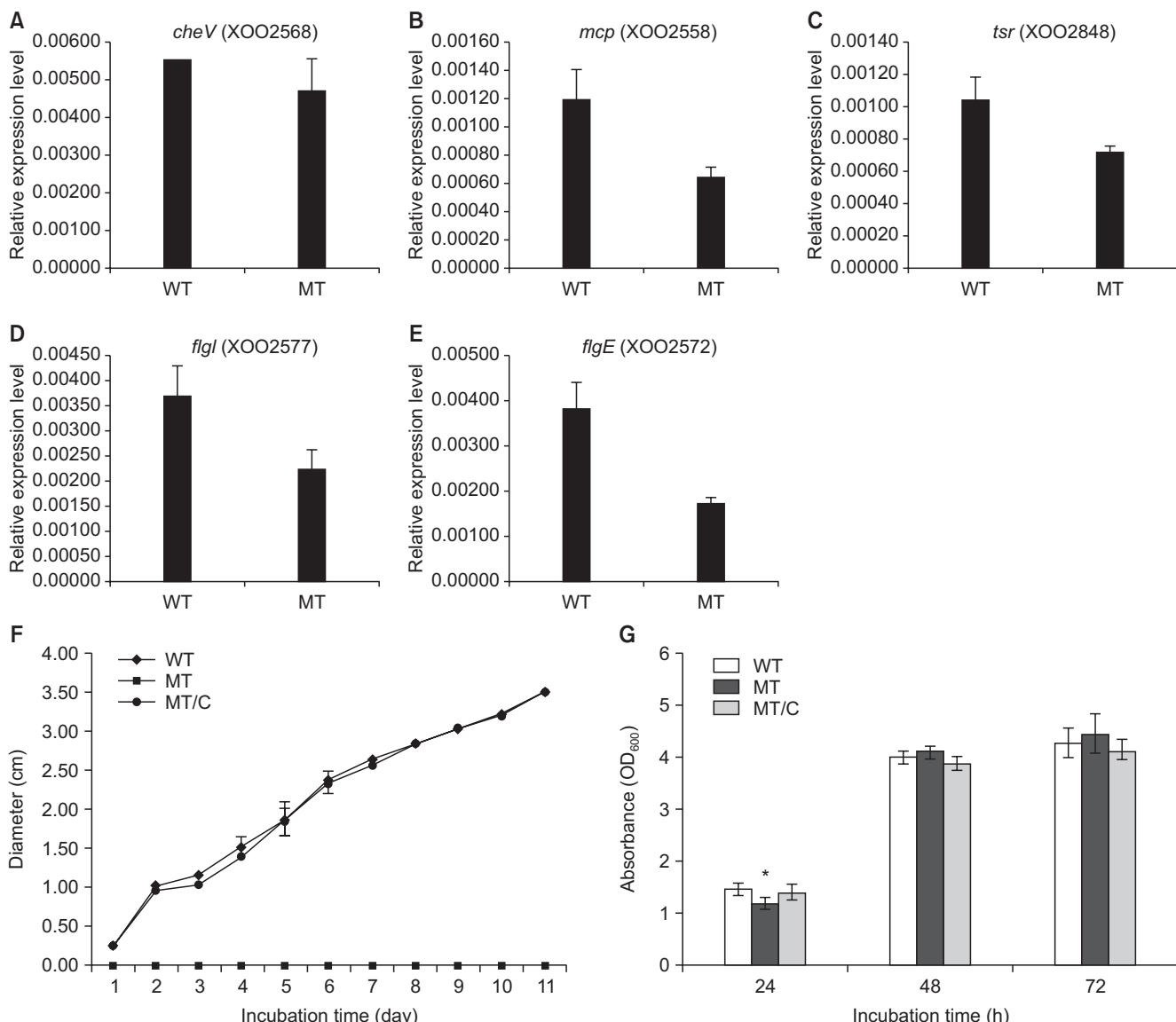
The microarray analysis showed that mutation of *opsX* in *Xoo* affected expression of other genes crucial for virulence, including HR and pathogenicity (*hrp*) genes. According to the genome sequence of *Xoo* KACC10331, the *hrp* gene cluster is composed of nine *hrp* (*hrpF*, *hrpE*, *hrpD6*, *hrpD5*, *hrpB1*, *hrpB2*, *hrpB4*, *hrpB5*, and *hrpB7*), nine *hrc* (*hrc* conserved; *hrcS*, *hrcR*, *hrcQ*, *hrcV*, *hrcU*, *hrcJ* [*hrcB3*], *hrcN*, *hrcT* [*hrcB8*], and *hrcC*) and eight *hpa* (*hpa*-associated; *hpaF*, *hpaB*, *hpaA*, *hpaP*, *hpa1*, *hpa2*, *hpa3*, and *hpa4*) genes (Cho et al., 2008; Lee et al., 2005). Interestingly, six *hrp* genes were slightly downregulated, including *hrcU* (-0.72 log<sub>2</sub> FC), *hpa1* (-0.47 log<sub>2</sub> FC), *hrcR* (-0.30 log<sub>2</sub> FC), *hrpD5* (-0.26 log<sub>2</sub> FC), *hpaB* (-0.10 log<sub>2</sub> FC), and *hrcN* (-0.09 log<sub>2</sub> FC) (Table 4), which are known to be crucial for the HR and virulence in *Xoo* (Cho et al., 2008).

*Xanthomonas* spp. produce a characteristic EPS, xanthan, a polymer composed of repeating pentasaccharide units that protects bacteria from environmental stresses,

including dehydration and toxic compounds (Denny, 1995). The production of xanthan is directed by the gum gene cluster, which consists of 12 genes (*gumB* to *gumM*) and is highly conserved among *Xanthomonas* spp. (Katzen et al., 1998; Vojnov et al., 1998). In addition, the complete genome sequence of *Xoo* KACC10331 revealed a cluster of ORFs in the genome that consisted of a tandem array of 14 ORFs, *gumB*, -C, -D, -E, -F, -G, -H, -I, -J, -K, -L, -M, XOO3167, and -N, similar to the gum operon of *X. campestris* (Lee et al., 2005; Yoon and Cho, 2007). In this study, 9 gum genes (XOO3166, XOO3168, XOO3169, XOO3170, XOO3171, XOO3175, XOO3177, XOO3178, and XOO3179) were downregulated by *opsX* mutation. The log<sub>2</sub> FC levels of the 9 genes ranged from -0.16 to -1.34 (Table 5). However, no GO term enrichment was observed for these downregulated gum genes (Table 3).

**Virulence assay, xanthan, and LPS production.** In the virulence assay, the *opsX* mutant showed a severe decrease in virulence against susceptible rice. Twenty-one days after inoculation, the average length of lesions caused by the *opsX* mutant was 1.67 cm, whereas that of lesions caused by the wild-type strain was 17.67 cm (Fig. 4). In the complementation test, lesions caused by the MT/C strain averaged 15.33 cm, similar to those caused by the wild-type strain (Fig. 4).

Although transcriptome analysis revealed that genes related to xanthan biosynthesis were downregulated in the *opsX* mutant strain, the wild-type and *opsX* mutant



**Fig. 3.** The expression patterns of genes associated with bacterial chemotaxis (*cheV*, A; *mcp*, B; *tsr*, C; *flgI*, D; and *flgE*, E) and effect of *opsX* mutation on swarming (F) and growth rate (G) of *Xanthomonas oryzae* pv. *oryzae* wild-type and *opsX* mutant strains. The gene expression levels (arbitrary units) were normalized using 16S RNA as an internal reference. Gene expression levels were quantified by real-time RT-PCR. WT, wild-type strain; MT, *opsX* mutant strain; MT/C, complemented strains. The asterisk represents statistically significant differences relative to the wild-type strain (paired, two-tailed Student's t-test,  $*P < 0.05$ ).

strains did not differ significantly in xanthan production. Mutation of *opsX* induced an approximately 7% decrease in xanthan production. The average amount of xanthan in the supernatant of the *opsX* mutant and wild-type cultures, measured at  $OD_{490}$ , was 2.33 and 2.51, respectively (Fig. 4). In addition to their similar xanthan production, *opsX* mutant and wild-type strains showed similar growth patterns in YDC medium.

Because Kingsley et al. (1993) reported that mutation of *opsX* affects biosynthesis of LPS in *X. campestris*, we examined LPS in the wild-type and *opsX* mutant strains of

*Xoo*. LPS extracts from the wild-type and mutant strains were prepared from whole-cell lysates and analyzed by SDS-PAGE. The silver-stained LPS gel is shown in Fig. 4. The ladder-like structure of *E. coli* LPS (Sigma-Aldrich) was used as a comparative sample. In these comparisons, the wild-type and mutant strains exhibited similar LPS banding patterns (labeled I and II; Fig. 4).

**Motility and growth rate.** The motility of the wild-type and *opsX* mutant strains was investigated using semisolid swarm plates. In the swarm plate assay, we found that

**Table 4.** Expression profiles of *hrp* genes in the *Xanthomonas oryzae* pv. *oryzae opsX* mutant

Locus tag	Gene	Product	log <sub>2</sub> FC_mean	log <sub>2</sub> FC_1	log <sub>2</sub> FC_2	log <sub>2</sub> FC_3
XOO0095	<i>hpa1</i>	Protein Hpa1	-0.47	-0.40	-0.51	-0.51
XOO0096	<i>hpa2</i>	Protein Hpa2	0.48	0.47	0.27	0.70
XOO0074	<i>hpa4</i>	Hypothetical protein	0.93	2.93	0.43	-0.56
XOO0079	<i>hpaA</i>	Protein HpaA	3.02	NA	2.86	3.19
XOO0075	<i>hpaB</i>	Protein HpaB	-0.10	-0.25	0.00	-0.04
XOO0083	<i>hpaP</i>	HrpC3	2.15	0.04	3.41	2.98
XOO2029	<i>hrcA</i>	Heat-inducible transcription repressor	2.55	4.99	-0.08	2.73
XOO0094	<i>hrcC</i>	Hypothetical protein	0.42	0.65	0.35	0.27
XOO0091	<i>hrcN</i>	Type III secretion system ATPase	-0.09	-0.07	0.03	-0.24
XOO0082	<i>hrcQ</i>	Hypothetical protein	0.94	1.18	0.70	NA
XOO0081	<i>hrcR</i>	Type III secretion system protein	-0.30	-0.39	-0.23	-0.29
XOO0085	<i>hrcU</i>	Type III secretion system protein HrcU	-0.72	-0.59	-0.76	-0.82
XOO0084	<i>hrcV</i>	Protein HrcV	1.58	-0.13	3.28	NA
XOO1725	<i>hrpA</i>	ATP-dependent RNA helicase	1.19	4.45	-0.85	-0.04
XOO0086	<i>hrpB1</i>	Protein HrpB1	1.28	2.47	0.81	0.56
XOO0087	<i>hrpB2</i>	Protein HrpB2	0.47	2.17	-0.06	-0.68
XOO0088	<i>hrpB3</i>	Protein HrpB3	1.51	0.68	0.82	3.03
XOO0089	<i>hrpB4</i>	Protein HrpB4	3.49	NA	3.60	3.39
XOO0090	<i>hrpB5</i>	Type III secretion system protein HrpB	0.27	0.65	-0.11	0.27
XOO0092	<i>hrpB7</i>	Protein HrpB7	NA	NA	NA	NA
XOO0093	<i>hrpB8</i>	Protein HrpB8	1.06	0.29	2.79	0.11
XOO0078	<i>hrpD5</i>	Protein HrpD5	-0.26	-0.26	-0.41	-0.10
XOO0076	<i>hrpE</i>	Hypothetical protein	0.97	0.84	1.25	0.83
XOO0066	<i>hrpF</i>	HrpF protein	0.60	2.64	-0.42	-0.41
XOO1379	<i>hrpG</i>	HrpG protein	0.82	0.25	1.13	1.09
XOO1380	<i>hrpXct</i>	HrpX protein	2.20	NA	2.38	2.02

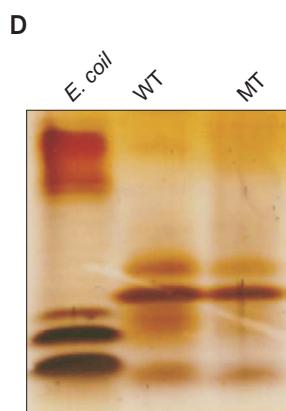
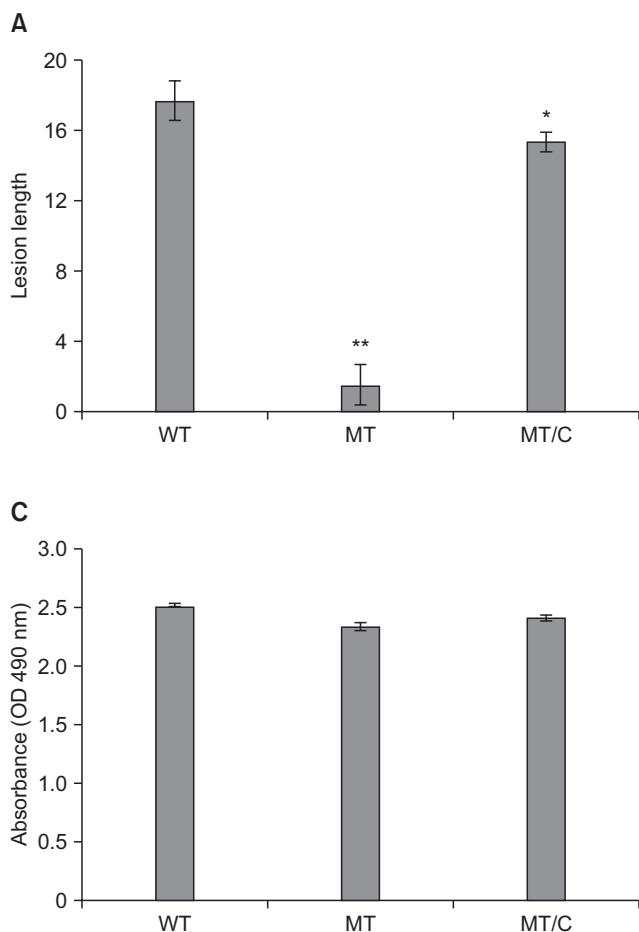
ATPase, adenylylpyrophopatase; ATP, adenosine triphosphate; NA, not available.

**Table 5.** Expression profiles of *gum* genes in the *Xanthomonas oryzae* pv. *oryzae opsX* mutant

Locus tag	Gene	Product	log <sub>2</sub> FC_mean	log <sub>2</sub> FC_1	log <sub>2</sub> FC_2	log <sub>2</sub> FC_3
XOO3179	<i>gumB</i>	Protein GumB	-1.22	-1.31	-0.98	-1.36
XOO3178	<i>gumC</i>	Protein GumC	-0.92	-0.82	-0.94	-1.01
XOO3177	<i>gumD</i>	Protein GumD	-0.62	-0.75	-0.47	-0.65
XOO3176	<i>gumE</i>	Protein GumE	0.12	0.17	0.06	0.14
XOO3175	<i>gumF</i>	Protein GumF	-0.16	-0.37	-0.15	0.03
XOO3173	<i>gumH</i>	Protein GumH	0.89	2.78	-0.34	0.22
XOO3172	<i>gumI</i>	Protein GumI	0.26	0.25	0.28	0.24
XOO3171	<i>gumJ</i>	Protein GumJ	-0.17	0.12	-2.76	2.14
XOO3170	<i>gumK</i>	Glucuronosyltransferase GumK	-0.83	-0.37	-1.51	-0.61
XOO3169	<i>gumL</i>	GumL protein	-0.26	-0.07	-0.13	-0.57
XOO3168	<i>gumM</i>	Protein GumM	-1.34	-1.20	-0.86	-1.95
XOO3166	<i>gumN</i>	GumN protein	-0.35	-0.90	0.09	-0.25

the *opsX* mutant strain was nonmotile compared with the wild-type strain. Following 11 days of incubation, the average diameter of *opsX* mutant colonies was zero cm, whereas that of wild-type colonies was 3.46 cm (Fig. 3F).

These results supported the expression analysis showing downregulation of genes involved in Xoo chemotaxis due to mutation of *opsX*; consequently, the *opsX* mutant strain cannot maintain chemotaxis. We also compared



**Fig. 4.** Virulence (A, B), xanthan (C), and lipopolysaccharide (LPS) production assays (D) of wild-type (WT), mutant (MT), and complemented strains (MT/C). Assays were performed in triplicate, and the means and standard deviation for lesion length and xanthan production were calculated for each experiment. The ladder-like structure of LPS from *Escherichia coli* was used as a comparative sample. The asterisks represent statistically significant differences relative to the WT strain (paired, two-tailed Student's t-test, \* $P < 0.05$ , \*\* $P < 0.01$ ).

the growth rates of the wild-type and *opsX* mutant strains (Fig. 3G). However, the growth rate of the *opsX* mutant was similar to that of the wild-type strain, indicating that mutation of *opsX* did not severely affect bacterial growth, although the growth rate of the *opsX* mutant was slightly increased (Fig. 3G).

## Discussion

The *opsX* gene of *Xoo* showed a strong similarity (89.7% similarity at the amino acid level) to that of *X. campestris* pv. *citrumelo* strain 3048 and > 93% identity with genes from other xanthomonads (data not shown). In addition, the *opsX* gene showed strong conserved-domain homology with adenosine diphosphate (ADP)-heptose-LPS heptosyltransferase, which is involved in the biogenesis of the cell envelope of the bacterial outer membrane. Although Kingsley et al. (1993) reported that *opsX* is required for LPS assembly, virulence, and biosynthesis of EPS in *X. campestris* pv. *citrumelo* strain 3048, understanding the pleiotropic effects of this gene on the physiology of this bacterium remains a major

challenge.

In the present study, the effects of mutation of *opsX* on xanthan, LPS production, and virulence, as well as on the expression of other genes, were evaluated in *Xoo*. Concordant with an earlier study by Kingsley et al. (1993), the *opsX* gene of *X. campestris* pv. *citrumelo* was found to affect biosynthesis of LPS and EPS. The M28 mutant ( $\Delta$ *opsX*), derived from wild-type *X. campestris* pv. *citrumelo* strain 3048, lacked LPS and produced only 33% of the EPS produced by the wild type. However, the xanthan and LPS production changes observed in this study support the hypothesis that *opsX* is not required for xanthan and LPS production in *Xoo* (Fig. 4).

DNA microarray analysis revealed that several genes that play crucial roles in *Xoo* chemotaxis are downregulated by mutation of *opsX* (Fig. 3, Table S1). DNA microarray and enrichment analysis revealed that two other genes, *flgE* (encoding flagellar hook protein, XOO2572) and *fliL* (encoding flagellar protein, XOO2607), were also downregulated (Table 3). Consistent with the DNA microarray and quantitative RT-PCR analyses, the *opsX* mutant strain was nonmotile compared

with the wild-type strain. No GO terms were found to be enriched among the upregulated genes, which indicates that genes that are typically downregulated played essential roles in virulence and bacterial chemotaxis.

LPS is a major component of the outer membrane of Gram-negative bacteria and is composed of three domains: 1) a hydrophobic anchor, known as lipid A; 2) a non-repeating oligosaccharide, known as the core region (an oligosaccharide consisting of an inner and outer region); and 3) a distinct repeating oligosaccharide, known as the O-antigen (Rick, 1987). In enteric bacteria, such as *E. coli* and *Salmonella typhimurium*, the inner core is composed of two ketodeoxyoctonate (KDO) units and two heptose units. The outer core region and the O-antigen are attached to one of the heptose units. In addition, several genes for synthesis of the inner core region have been identified from various enteric bacteria (Heinrichs et al., 1998; Schnaitman and Klena, 1993) and two genes including *rfaC* (*waaC*) and *rfaF* (*waaF*) were identified as heptosyl transferases for transfer of heptose from ADP-heptose to the inner core (Sirisena et al., 1992, 1994). Furthermore, Inoue et al. (2007) reported that all the genes that were involved in core oligosaccharide synthesis, but not those involved in O-antigen synthesis, were required for swarming and the inner core might be necessary for flagellar assembly and function of *E. coli* K-12 strain. As described above, BLASTP searches against the NCBI non-redundant database revealed that the *opsX* gene shared strong sequence similarity to ADP-heptose-LPS heptosyltransferase. This result indicates that the product of the *opsX* gene may also be responsible for the construction of the inner core of LPS as well as for flagellar assembly and function in *Xoo*.

Although further investigation is required to provide a better understanding of *opsX* and its role in bacterial chemotaxis, our findings are the first to suggest that mutation of *opsX* affects chemotaxis and bacterial motility, as well as virulence, in *Xoo*.

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Table S1. Expression profiles of wild-type and the opsX mutant strains of *Xanthomonas oryzae* pv. *oryzae*

Locus tag	Gene	Product	log2	log2	log2	log2	normalized signal (log2 based)						
			FC_mean	FC_1	FC_2	FC_3	opsX Mutant_1	XOO10859 _1	opsX Mutant_2	XOO10859 _2	opsX Mutant_3	XOO10859 _3	pval
XOO0001	<i>dnaA</i>	chromosome replication initiator DnaA	-1.43	-1.30	-1.32	-1.67	7.57	8.87	9.60	10.92	8.86	10.53	0.00
XOO0002	<i>dnaN</i>	DNA polymerase III subunit beta	1.43	3.59	0.55	0.14	6.38	2.79	7.95	7.40	7.07	6.93	0.00
XOO0003	<i>recF</i>	recombination protein F	-0.21	2.97	-3.00	-0.60	5.61	2.65	3.62	6.62	3.45	4.05	0.00
XOO0004	<i>gyrB</i>	DNA gyrase subunit B	-1.05	-0.87	-1.04	-1.23	8.70	9.57	9.49	10.53	8.82	10.05	0.00
XOO0005	-	hypothetical protein	0.46	-1.25	3.46	-0.84	7.98	9.23	8.57	5.11	7.13	7.97	0.00
XOO0006	-	hypothetical protein	-1.69	-1.55	-1.73	-1.78	8.71	10.26	8.88	10.61	7.64	9.42	0.00
XOO0007	-	hypothetical protein	0.42	0.51	0.43	0.31	11.83	11.32	13.23	12.80	12.99	12.68	0.00
XOO0008	<i>tonB</i>	TonB protein	0.83	0.91	0.80	0.79	12.57	11.66	13.94	13.13	13.53	12.74	0.00
XOO0009	<i>exbB</i>	biopolymer transport ExbB protein	-0.02	-0.11	-0.05	0.12	11.67	11.78	12.45	12.50	12.05	11.94	0.00
XOO0010	<i>exbD1</i>	biopolymer transport ExbD1 protein	0.59	0.68	0.70	0.38	12.00	11.32	13.09	12.38	13.26	12.88	0.00
XOO0011	<i>exbD2</i>	biopolymer transport ExbD2 protein	0.82	1.01	0.74	0.70	11.49	10.48	12.88	12.14	12.61	11.91	0.00
XOO0012	<i>pdxJ</i>	pyridoxine 5'-phosphate synthase	0.33	-0.12	0.76	0.34	6.64	6.76	7.26	6.51	7.43	7.09	0.00
XOO0013	-	hypothetical protein	-0.21	-0.21	-0.22	-0.20	11.27	11.48	12.37	12.59	9.98	10.18	0.00
XOO0014	<i>cls</i>	cardiolipin synthetase	0.32	0.28	0.12	0.54	4.60	4.32	7.47	7.35	6.74	6.20	0.00
XOO0019	-	hypothetical protein	0.17	-0.02	1.74	-1.21	6.79	6.81	5.22	3.48	2.20	3.41	0.00
XOO0022	<i>lldD</i>	L-lactate dehydrogenase	0.09	0.03	-0.06	0.30	10.16	10.13	10.66	10.72	9.75	9.45	0.00
XOO0023	-	hypothetical protein	2.47				2.47	4.63	NA	2.54	NA	5.74	3.27
XOO0026	-	transcriptional regulator	-0.01	-3.26			3.24	3.51	6.77	5.72	NA	4.27	1.04
XOO0027	-	trans-2-enoyl-CoA reductase	0.67	0.62	0.63	0.76	4.67	4.05	11.04	10.40	10.63	9.88	0.00
XOO0028	<i>kdgK</i>	2-keto-3-deoxygluconate kinase	-0.14	-0.17	-0.09	-0.14	8.82	8.99	9.70	9.79	9.75	9.90	0.00
XOO0029	<i>iroN</i>	TonB-dependent receptor	-1.09	-1.81	-0.41	-1.06	5.24	7.05	7.70	8.11	7.62	8.68	0.00
XOO0031	-	hypothetical protein	#DIV/0!				1.29	NA	NA	NA	NA	NA	0.26
XOO0035	-	hypothetical protein	#DIV/0!				1.00	NA	1.73	NA	4.80	NA	0.03
XOO0036	-	hypothetical protein	0.43	0.99	-0.08	0.38	7.74	6.75	7.94	8.02	7.46	7.08	0.00
XOO0038	<i>proP</i>	proline/betaine transporter	#DIV/0!				NA	NA	NA	NA	4.17	NA	0.02
XOO0040	<i>trxA</i>	thioredoxin	-1.86		-1.86		NA	NA	3.08	4.94	NA	NA	0.00
XOO0041	<i>atsE</i>	AtsE	-1.13	-0.74	-1.14	-1.51	7.09	7.84	8.59	9.73	7.55	9.06	0.00
XOO0042	-	hypothetical protein	2.37		2.65	2.08	1.95	NA	4.76	2.11	3.38	1.30	0.00
XOO0043	-	MutT-nudix family protein	1.12	0.87	1.09	1.41	3.65	2.78	9.24	8.16	8.65	7.25	0.00
XOO0051	-	hypothetical protein	-1.81	-1.71	-1.83	-1.89	8.94	10.65	10.06	11.89	9.63	11.52	0.00
XOO0055	-	hypothetical protein	-1.11	-1.15	-1.02	-1.17	7.50	8.64	8.21	9.23	7.58	8.76	0.00
XOO0056	<i>sulA</i>	cell division inhibitor	0.02	1.26	-0.78	-0.42	3.52	2.26	6.56	7.34	3.25	3.67	0.00
XOO0057	<i>ygiY</i>	two-component system sensor protein	3.41		3.41		4.65	NA	5.11	1.70	5.28	NA	0.00
XOO0058	<i>bph1</i>	histone H1-like protein	0.85	0.55	0.79	1.23	7.66	7.12	9.38	8.60	9.23	8.00	0.00
XOO0059	<i>htrA</i>	protease Do	-0.70	-0.69	-0.89	-0.52	7.79	8.48	8.86	9.75	7.73	8.25	0.00
XOO0060	-	hypothetical protein	-2.02	-1.89	-2.11	-2.07	10.82	12.72	11.29	13.40	10.93	13.00	0.00
XOO0061	-	hypothetical protein	-2.18	-2.26	-2.16	-2.11	8.61	10.87	9.26	11.42	8.47	10.58	0.00
XOO0062	-	hypothetical protein	-3.21	-4.15	-2.67	-2.81	4.73	8.88	6.92	9.59	6.60	9.41	0.00
XOO0066	<i>hrpF</i>	HrpF protein	0.60	2.64	-0.42	-0.41	6.24	3.60	8.13	8.55	7.75	8.16	0.00
XOO0074	<i>hpa4</i>	hypothetical protein	0.93	2.93	0.43	-0.56	5.90	2.97	5.36	4.92	3.02	3.58	0.00
XOO0075	<i>hpaB</i>	protein HpaB	-0.10	-0.25	0.00	-0.04	7.56	7.81	8.55	8.55	8.00	8.03	0.00
XOO0076	<i>hrpE</i>	hypothetical protein	0.97	0.84	1.25	0.83	9.99	9.16	10.53	9.28	10.87	10.04	0.00
XOO0078	<i>hrpD5</i>	protein HrpD5	-0.26	-0.26	-0.41	-0.10	6.41	6.67	8.01	8.43	7.51	7.61	0.00
XOO0079	<i>hpaA</i>	protein HpaA	3.02		2.86	3.19	2.29	NA	6.28	3.42	6.08	2.89	0.00
XOO0081	<i>hrcR</i>	type III secretion system protein	-0.30	-0.39	-0.23	-0.29	8.00	8.39	4.13	4.36	8.45	8.74	0.00
XOO0082	<i>hrcQ</i>	hypothetical protein	0.94	1.18	0.70		5.20	4.02	4.09	3.39	1.90	NA	0.00
XOO0083	<i>hpaP</i>	hrcP3	2.15	0.04	3.41	2.98	6.28	6.24	7.09	3.69	6.35	3.36	0.00
XOO0084	<i>hrcV</i>	protein HrcV	1.58	-0.13	3.28		2.12	2.25	3.05	-0.23	2.26	NA	0.01
XOO0085	<i>hrcU</i>	type III secretion system protein HrcU	-0.72	-0.59	-0.76	-0.82	11.21	11.80	12.30	13.06	11.01	11.83	0.00
XOO0086	<i>hrpB1</i>	protein HrpB1	1.28	2.47	0.81	0.56	6.14	3.67	8.62	7.81	7.88	7.33	0.00
XOO0087	<i>hrpB2</i>	protein HrpB2	0.47	2.17	-0.06	-0.68	5.39	3.23	6.73	6.79	6.09	6.78	0.00
XOO0088	<i>hrpB3</i>	protein HrpB3	1.51	0.68	0.82	3.03	3.02	2.34	7.03	6.21	6.04	3.01	0.00
XOO0089	<i>hrpB4</i>	protein HrpB4	3.49		3.60	3.39	NA	NA	6.51	2.92	5.90	2.51	0.00
XOO0090	<i>hrpB5</i>	type III secretion system protein HrpB	0.27	0.65	-0.11	0.27	6.19	5.55	6.34	6.46	3.00	2.73	0.00
XOO0091	<i>hrcN</i>	type III secretion system ATPase	-0.09	-0.07	0.03	-0.24	8.11	8.19	8.85	8.83	7.68	7.92	0.00
XOO0092	<i>hrpB7</i>	protein HrpB7	#DIV/0!				2.16	NA	4.28	NA	2.12	NA	0.00
XOO0093	<i>hrpB8</i>	protein HrpB8	1.06	0.29	2.79	0.11	5.63	5.34	6.66	3.87	8.55	8.44	0.00
XOO0094	<i>hrcC</i>	hypothetical protein	0.42	0.65	0.35	0.27	9.70	9.05	10.33	9.98	10.12	9.85	0.00
XOO0095	<i>hpa1</i>	protein Hpa1	-0.47	-0.40	-0.51	-0.51	10.70	11.11	11.18	11.69	9.64	10.14	0.00
XOO0096	<i>hpa2</i>	protein Hpa2	0.48	0.47	0.27	0.70	6.29	5.82	7.72	7.45	6.70	6.00	0.00
XOO0097	-	hypothetical protein	-1.52		-1.07	-1.96	2.95	NA	6.64	7.71	5.63	7.59	0.00
XOO0104	-	hypothetical protein	0.41	-0.56	-0.28	-0.40	6.55	7.11	8.83	9.11	8.30	8.70	0.00
XOO0105	-	hypothetical protein	-0.10	0.09	-0.06	-0.31	7.54	7.45	8.82	8.88	7.87	8.19	0.00
XOO0108	-	ABC transporter substrate binding protein	-0.58	-0.53	-0.53	-0.67	14.02	14.55	14.62	15.15	13.52	14.19	0.00
XOO0109	-	hypothetical protein	-2.20	-2.43	-2.00	-2.15	7.04	9.47	9.04	11.04	7.57	9.72	0.00
XOO0110	-	hypothetical protein	-0.18	1.52	-0.45	-1.60	3.35	1.83	6.67	7.11	4.70	6.30	0.00
XOO0111	-	hypothetical protein	0.10	0.69	-0.03	-0.36	7.40	6.71	4.51	4.54	7.96	8.32	0.00
XOO0112	<i>glaA</i>	glycogen synthase	-1.82	-2.35	-1.76	-1.35	4.85	7.20	7.81	9.58	8.13	9.48	0.00
XOO0113	<i>glaB2</i>	glycogen branching protein	-1.02	-1.01	-0.89	-1.15	8.61	9.61	9.52	10.41	9.12	10.27	0.00
XOO0114	-	malto-oligosyltrehalose trehalohydrolase	-0.71	-0.69	-0.81	-0.65	3.45	4.13	7.47	8.28	3.72	4.36	0.00
XOO0115	<i>malQ</i>	4-alpha-glucanotransferase	-0.47	-0.52	-0.42	-0.47	10.06	10.58	10.15	10.57	9.43	9.90	0.00
XOO0116	<i>glaY</i>	malto-oligosyltrehalose synthase	-0.02	-0.10	0.10	-0.07	9.13	9.23	9.17	9.08	8.57	8.64	0.00
XOO0117	<i>glaX</i>	glycogen debranching protein	-0.52	-0.54	-0.27	-0.76	7.78	8.31	7.47	7.74	6.87	7.63	0.00
XOO0118	-	hypothetical protein	-0.25	2.58	-0.72	-2.62	5.58	2.99	7.13	7.85	5.00	7.62	0.00
XOO0119	<i>mauG</i>	methylamine utilization protein	-0.10	0.00	-0.26	-0.04	7.82	7.82	9.07	9.33	8.80	8.84	0.00
XOO0123	-	Rhs family protein	0.00	-0.23	0.04	0.20	8.65	8.88	8.88	8.83	9.39	9.19	0.00
XOO0130	-	hypothetical protein	#DIV/0!				5.24	NA	5.69	NA	3.67	NA	0.00
XOO0131	<i>virK</i>	VirK protein	1.26		0.11	2.40	4.66	NA	3.34	3.22	4.76	2.36	0.00
XOO0132	-	hypothetical protein	0.76	0.88	0.40	1.00	8.18	7.30	8.47	8.08	9.24	8.23	0.00
XOO0133	<i>rhlE</i>	ATP-dependent RNA helicase	0.84	1.29	0.73	0.51	8.56	7.27	9.08	8.35</td			

XOO0159	-	hypothetical protein	-0.20	-0.10	-0.23	-0.25	9.28	9.38	10.77	11.01	10.18	10.43	0.00
XOO0162	-	hypothetical protein	0.80	2.50	-0.13	0.04	4.98	2.48	7.07	7.20	3.50	3.46	0.00
XOO0163	-	hypothetical protein	-0.52	-0.44	-0.95	-0.17	6.28	6.72	7.23	8.18	6.72	6.89	0.00
XOO0164	-	hypothetical protein	-1.28	-0.60	-1.55	-1.69	6.26	6.86	7.03	8.59	6.37	8.06	0.00
XOO0167	-	hypothetical protein	-0.70	-0.46	0.00	-1.65	2.00	2.46	6.14	6.13	5.88	7.53	0.00
XOO0168	<i>avrBs2</i>	avirulence protein	1.78	0.61	0.90	3.83	3.65	3.03	7.69	6.78	7.49	3.66	0.00
XOO0169	<i>xylR</i>	xylose repressor-like protein	2.33	2.67	3.10	1.22	4.55	1.88	6.56	3.47	3.81	2.59	0.00
XOO0172	-	hypothetical protein	1.09	1.07	1.18	1.03	8.65	7.58	8.99	7.81	8.44	7.42	0.00
XOO0173	-	hypothetical protein	0.19	0.22	0.03	0.32	7.72	7.50	8.95	8.91	8.10	7.78	0.00
XOO0174	-	hypothetical protein	-1.16	-1.76	-0.78	-0.93	5.12	6.87	8.21	8.99	7.65	8.58	0.00
XOO0175	-	hypothetical protein	-0.16			-0.16	NA	NA	NA	NA	5.31	5.47	0.00
XOO0176	-	hypothetical protein	1.59	1.42	1.75	1.59	10.05	8.62	11.03	9.28	10.86	9.27	0.00
XOO0177	<i>gltB</i>	glutamate synthase subunit alpha	-0.57	-0.79	-0.52	-0.39	7.98	8.77	9.50	10.02	9.14	9.54	0.00
XOO0178	<i>gltD</i>	glutamate synthase subunit beta	-0.69	-1.45	-0.06	-0.57	5.73	7.18	7.60	7.66	7.31	7.87	0.00
XOO0189	<i>kdul</i>	5-keto-4-deoxyuronate isomerase	-0.15	-0.25	-0.11	-0.10	7.80	8.05	9.54	9.65	9.16	9.26	0.00
XOO0190	-	LacI family transcriptional regulator	-0.30	-0.52	-0.22	-0.14	6.73	7.25	8.20	8.42	7.74	7.89	0.00
XOO0197	-	alpha-amylase	-1.21	-1.00	-1.26	-1.36	6.94	7.94	8.19	9.46	7.56	8.92	0.00
XOO0212	<i>comM</i>	competence-like protein	1.68		2.90	0.46	4.52	NA	5.07	2.17	6.25	5.80	0.00
XOO0215	-	hypothetical protein	-0.23	-0.05		-0.42	3.49	3.53	4.01	NA	6.44	6.86	0.00
XOO0217	-	hypothetical protein	0.58	0.54	0.58	0.60	7.46	6.91	8.68	8.10	8.57	7.97	0.00
XOO0218	-	hypothetical protein	-0.08	0.04	-0.13	-0.16	3.59	3.56	8.80	8.93	8.50	8.66	0.00
XOO0219	<i>speE</i>	spermidine synthase	0.04	-0.07	-0.12	0.30	8.64	8.71	9.85	9.97	9.17	8.87	0.00
XOO0220	<i>speA</i>	arginine decarboxylase	0.21	0.61	0.33	-0.32	7.20	6.60	8.41	8.08	7.38	7.70	0.00
XOO0223	-	hypothetical protein	0.61	1.09	0.61	0.14	6.29	5.20	3.79	3.18	6.64	6.50	0.00
XOO0224	-	hypothetical protein	1.03	1.26	0.80	1.03	9.90	8.64	11.02	10.23	10.22	9.19	0.00
XOO0225	-	hypothetical protein	0.91	0.58	0.79	1.37	9.58	9.00	10.20	9.40	9.40	8.03	0.00
XOO0226	-	hypothetical protein	0.72	0.72	0.70	0.75	9.67	8.95	11.47	10.78	11.01	10.26	0.00
XOO0227	<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl modification protein Gi	0.22	0.38	0.13	0.16	10.13	9.75	11.74	11.61	11.25	11.09	0.00
XOO0228	<i>ilvA</i>	threonine dehydratase	0.79	0.82	0.56	0.98	7.94	7.12	9.35	8.78	9.22	8.24	0.00
XOO0233	<i>bioC</i>	biotin synthesis protein	0.67	0.77	0.67	0.56	9.70	8.94	10.61	9.94	10.34	9.78	0.00
XOO0234	-	oxidoreductase	1.58	1.31	1.76	1.68	4.28	2.97	8.65	6.89	8.51	6.83	0.00
XOO0235	<i>bioH</i>	biotin biosynthesis protein	1.22	1.19	1.31	1.16	6.80	5.62	8.79	7.49	8.46	7.29	0.00
XOO0238	-	hypothetical protein	1.43	1.57	1.10	1.62	9.58	8.01	10.96	9.86	9.95	8.33	0.00
XOO0239	<i>mdoD</i>	glucan biosynthesis protein D	1.24	1.20	1.14	1.38	9.05	7.85	10.60	9.45	10.30	8.92	0.00
XOO0240	-	sensor histidine kinase	1.98	1.01	1.42	3.50	6.39	5.38	6.91	5.49	7.03	3.53	0.00
XOO0241	<i>tdk</i>	thymidine kinase	0.45	0.55	0.43	0.37	8.31	7.76	9.33	8.90	9.21	8.84	0.00
XOO0242	<i>rep</i>	ATP-dependent DNA helicase	0.64	0.15	0.32	1.45	9.29	9.14	9.97	9.65	8.65	7.20	0.00
XOO0245	-	hypothetical protein	0.38	0.32	0.30	0.50	8.85	8.53	10.63	10.33	9.95	9.45	0.00
XOO0246	<i>lppC</i>	acid phosphatase	0.60	0.34	0.71	0.76	7.73	7.39	8.99	8.28	8.61	7.85	0.00
XOO0247	<i>pyrF</i>	orotidine 5'-phosphate decarboxylase	0.32	0.24	1.00	-0.28	7.45	7.21	7.11	6.11	7.00	7.27	0.00
XOO0248	<i>pmrA</i>	tryptophan halogenase	-0.16	0.01	-0.05	-0.44	8.18	8.17	9.54	9.59	7.38	7.82	0.00
XOO0249	-	OmpA-like protein	0.75	0.83	0.72	0.69	10.49	9.66	11.59	10.87	11.47	10.78	0.00
XOO0250	-	OmpA-like protein	0.04	0.05	0.05	0.03	10.20	10.15	11.59	11.54	11.47	11.44	0.00
XOO0253	-	hypothetical protein	1.73	3.46	0.91	0.83	7.40	3.95	9.95	9.03	9.79	8.96	0.00
XOO0254	<i>p/sB</i>	glycerol-3-phosphate acyltransferase	-0.16	-0.17	-0.22	-0.10	9.49	9.66	11.02	11.23	10.37	10.47	0.00
XOO0264	-	hypothetical protein	-0.27	-0.15	-0.27	-0.39	7.59	7.74	8.81	9.08	8.59	8.97	0.00
XOO0265	-	rhamnogalacturonan acetyl esterase	1.44	0.50	1.75	2.07	6.57	6.07	5.86	4.10	4.38	2.31	0.00
XOO0266	-	hypothetical protein	1.44	1.91	1.16	1.24	9.67	7.77	11.86	10.70	11.37	10.13	0.00
XOO0267	<i>phhA</i>	phenylalanine 4-monooxygenase	1.48	1.51	1.43	1.51	10.25	8.74	11.68	10.25	11.19	9.68	0.00
XOO0268	-	AsnC family transcriptional regulator	2.49	3.07	0.66	3.75	8.15	5.08	7.95	7.30	7.13	3.38	0.00
XOO0280	<i>yahK</i>	alcohol dehydrogenase	0.43	0.34	0.46	0.50	10.30	9.96	11.31	10.85	10.94	10.45	0.00
XOO0281	<i>egl</i>	cellulase	0.40	0.55	0.29	0.34	10.17	9.62	11.53	11.24	11.20	10.86	0.00
XOO0282	<i>egl</i>	cellulase	0.23	0.53	0.05	0.12	5.49	4.96	7.11	7.06	7.16	7.04	0.00
XOO0283	<i>egl</i>	cellulase	0.51	0.25	0.59	0.68	4.31	4.06	9.29	8.70	8.63	7.94	0.00
XOO0288	-	transglycosylase	0.43	0.57	0.49	0.24	8.17	7.60	9.26	8.77	9.02	8.78	0.00
XOO0292	<i>aphB</i>	phytochrome-like protein	0.96	1.09	0.75	1.05	8.11	7.02	8.99	8.25	8.69	7.64	0.00
XOO0299	<i>mutM</i>	formamidopyrimidine-DNA glycosylase	-1.20	-0.92	-1.48	-2.08	NA	7.81	8.73	6.56	8.04	0.00	
XOO0305	<i>vacJ</i>	lipoprotein	-0.30	-0.29	-0.32	-0.29	9.95	10.24	11.65	11.98	11.31	11.60	0.00
XOO0307	<i>yrbC</i>	toluene tolerance protein	-0.07	-0.07	-0.12	-0.02	9.79	9.87	11.24	11.36	10.85	10.87	0.00
XOO0308	<i>yrbD</i>	toluene tolerance protein	-0.57	-0.43	-0.69	-0.61	11.26	11.69	12.06	12.75	11.85	12.45	0.00
XOO0309	<i>yrbE</i>	toluene tolerance protein	-0.48	-0.37	-0.46	-0.63	9.18	9.55	10.14	10.60	9.74	10.36	0.00
XOO0310	<i>yrbF</i>	toluene tolerance protein	-0.59	-0.63	-0.68	-0.47	9.33	9.96	10.50	11.19	10.14	10.60	0.00
XOO0311	-	hypothetical protein	0.11	-0.05	0.25	0.13	8.67	8.72	9.51	9.26	9.04	8.91	0.00
XOO0312	-	acetyltransferase	1.71	1.03	1.65	2.44	8.29	7.26	8.41	6.76	8.32	5.88	0.00
XOO0327	-	hypothetical protein	0.82	-0.37	2.85	-0.03	5.17	5.54	6.40	3.55	3.28	3.31	0.00
XOO0328	<i>aroD</i>	3-dehydroquinate dehydratase	0.07		0.55	-0.41	3.86	NA	7.05	6.50	6.47	6.87	0.00
XOO0329	-	polyvinylalcohol dehydrogenase	1.29	1.89	1.14	0.83	5.12	3.23	7.10	5.97	6.56	5.73	0.00
XOO0332	<i>idnK</i>	glucuronokinase	0.68	0.63	0.62	0.79	9.49	8.86	10.27	9.65	10.17	9.38	0.00
XOO0333	<i>ynaJ</i>	cation symporter	0.69	0.92	0.77	0.38	7.98	7.06	9.69	8.92	8.44	8.06	0.00
XOO0334	<i>ndvB</i>	NdvB protein	0.08	0.12	0.11	0.02	13.42	13.30	14.15	14.04	13.09	13.07	0.00
XOO0335	-	hypothetical protein	0.83	1.13	0.63	0.73	7.82	6.69	8.90	8.27	8.80	8.06	0.00
XOO0336	-	two-component system sensor protein	2.50	2.89	0.64	3.97	6.63	3.73	4.53	3.89	6.87	2.89	0.00
XOO0337	-	hypothetical protein	-0.32	0.10	-0.68	-0.38	7.91	7.81	6.19	6.87	7.27	7.65	0.00
XOO0338	<i>kdgR</i>	transcriptional regulator	1.10		1.38	0.82	4.75	NA	7.62	6.24	6.21	5.39	0.00
XOO0339	<i>fucP</i>	fucose permease	0.51	0.70	0.39	0.43	9.02	8.32	9.49	9.10	10.12	9.68	0.00
XOO0340	-	hypothetical protein	1.03	1.07	0.88	1.13	8.76	7.68	9.94	9.06	9.64	8.51	0.00
XOO0343	-	hypothetical protein	0.43	-0.78	0.08	2.00	5.27	6.05	6.44	6.36	5.65	3.65	0.00
XOO0344	<i>dcp</i>	peptidyl-dipeptidase	0.42	0.53	0.35	0.39	9.73	9.20	10.27	9.92	10.33	9.94	0.00
XOO0345	-	acyltransferase	0.35	0.48	0.38	0.18	11.25	10.76	12.53	12.15	12.34	12.16	0.00
XOO0347	-	hypothetical protein	0.39	0.30	0.50	0.38	9.95	9.65	10.42	9.91	10.24	9.86	0.00
XOO0348	-	pseudouridylate synthase	1.62	3.02	0.73	1.13	8.31	5.29	8.83	8.10	8.38	7.26	0.00
XOO0349	-	hypothetical protein	-0.60	-0.20	-0.74	-0.88	6.73	6.93	8.97	9.71	8.45	9.33	0.00
XOO0350	<i>ubiB</i>	ubiquinone											

XOO0383	<i>czcD</i>	heavy metal transporter	0.10	-0.61	0.80	3.30	3.91	NA	NA	4.18	3.38	0.00	
XOO0385	-	hypothetical protein	0.84	0.56	0.91	1.06	7.86	7.31	9.58	8.67	9.51	8.45	0.00
XOO0387	-	cysteine proteinase	1.53	1.75	1.25	1.59	8.76	7.01	10.44	9.19	9.85	8.26	0.00
XOO0388	<i>natA</i>	sodium ABC transporter ATP-binding protein	2.00	2.74	1.45	1.82	6.52	3.79	8.94	7.49	8.60	6.78	0.00
XOO0389	<i>natB</i>	sodium ABC transporter permease	1.31	1.47	1.46	1.01	8.87	7.40	9.96	8.50	10.05	9.05	0.00
XOO0390	-	TonB-like protein	0.59	0.69	0.58	0.51	11.46	10.77	12.95	12.36	12.76	12.25	0.00
XOO0391	<i>prmA</i>	tryptophan halogenase	2.17	2.20	2.19	2.11	10.32	8.12	11.06	8.87	10.91	8.80	0.00
XOO0392	-	Pass1-like protein	5.13	5.18	5.44	4.76	6.26	1.07	8.19	2.75	7.87	3.11	0.00
XOO0393	<i>sapC</i>	protein SapC protein	3.24	1.47	1.58	6.68	6.83	5.36	7.74	6.16	9.12	2.44	0.00
XOO0394	<i>iroN</i>	TonB-dependent receptor	3.06	3.14	3.10	2.95	9.86	6.72	10.96	7.87	10.35	7.40	0.00
XOO0397	<i>gst</i>	glutathione S-transferase	1.64	1.59	1.42	1.92	9.56	7.97	10.24	8.81	9.75	7.83	0.00
XOO0398	-	dipeptidyl peptidase IV	1.70	2.66	1.78	0.67	8.27	5.61	5.31	3.54	4.26	3.59	0.00
XOO0399	-	hypothetical protein	3.20	2.12	4.29	7.69	5.57	7.60	3.31	6.66	NA	0.00	
XOO0402	<i>hemB</i>	delta-aminolevulinic acid dehydratase	1.28	2.22	0.88	0.75	8.33	6.11	9.85	8.97	9.26	8.51	0.00
XOO0405	-	LysR family transcriptional regulator	-0.72	-0.72			5.22	5.94	5.52	NA	5.28	NA	0.00
XOO0406	-	endonuclease	0.54	0.46	1.13	0.03	7.20	6.74	7.74	6.62	7.70	7.67	0.00
XOO0407	<i>piuB</i>	iron-uptake factor	1.04	1.12	1.04	0.95	9.24	8.12	10.40	9.36	10.31	9.36	0.00
XOO0408	-	hypothetical protein	-0.06	-0.17	0.11	-0.11	9.21	9.39	10.07	9.96	10.15	10.26	0.00
XOO0409	-	hypothetical protein	3.14		1.66	4.63	1.85	NA	7.65	5.99	7.47	2.84	0.00
XOO0410	-	hypothetical protein	2.28	2.91	0.42	3.52	6.11	3.20	8.07	7.65	8.87	5.35	0.00
XOO0412	<i>dinG</i>	ATP-dependent DNA helicase DinG	0.17	0.31	0.20	0.00	9.17	8.87	9.78	9.58	9.31	9.31	0.00
XOO0413	-	membrane-fusion protein	1.58	0.11	2.44	2.17	6.75	6.64	6.51	4.06	6.36	4.19	0.00
XOO0416	-	membrane-fusion protein	0.27	1.01	-0.08	-0.11	7.61	6.60	6.79	6.87	3.64	3.75	0.00
XOO0417	<i>catB</i>	catalase	-0.26	-0.04	-0.23	-0.51	7.24	7.28	7.93	8.16	6.45	6.96	0.00
XOO0418	<i>ankB</i>	ankyrin-like protein	1.27	0.16	1.66	2.00	2.86	2.71	4.16	2.50	5.37	3.37	0.00
XOO0421	-	tRNA-dihydrouridine synthase A	0.68	0.70	0.67	0.65	7.44	6.74	8.71	8.03	8.16	7.51	0.00
XOO0422	-	hypothetical protein	0.25	0.49	-0.03	0.29	11.24	10.75	13.01	13.04	12.13	11.84	0.00
XOO0423	<i>phoP</i>	two-component system regulatory protein	0.74	0.73	0.79	0.70	10.64	9.91	11.44	10.65	11.33	10.63	0.00
XOO0424	<i>phoQ</i>	two-component system sensor protein	0.66	0.60	0.65	0.72	9.48	8.88	10.77	10.11	10.05	9.33	0.00
XOO0425	-	hypothetical protein	1.23	1.33	1.28	1.09	8.30	6.97	9.20	7.92	8.84	7.76	0.00
XOO0426	-	hypothetical protein	2.26	3.56	1.47	1.77	6.49	2.94	8.32	6.85	7.97	6.21	0.00
XOO0427	-	hypothetical protein	-0.96	-0.34	-1.57		2.08	2.43	5.28	6.86	4.65	NA	0.00
XOO0428	<i>birA</i>	biotin-protein ligase	1.34	0.53	0.21	3.29	8.74	8.20	9.48	9.28	8.25	4.96	0.00
XOO0429	<i>baf</i>	pantothenate kinase	0.12	0.51	-0.40	0.26	7.82	7.31	8.37	8.77	8.16	7.90	0.00
XOO0430	-	hypothetical protein	0.40	0.45	0.28	0.45	10.12	9.66	10.77	10.49	9.66	9.20	0.00
XOO0431	<i>tmk</i>	thymidylate kinase	0.39	0.20	0.33	0.64	9.72	9.52	10.50	10.17	9.15	8.50	0.00
XOO0434	-	hypothetical protein	0.98	0.17	1.19	1.57	7.17	7.00	8.78	7.59	8.15	6.58	0.00
XOO0435	<i>argI</i>	arginase	2.23	3.02	2.02	1.65	7.81	4.79	9.39	7.36	8.91	7.26	0.00
XOO0436	-	hypothetical protein	-0.61	-0.59	-0.75	-0.50	7.00	7.59	9.12	9.87	8.69	9.19	0.00
XOO0437	<i>trpS</i>	tryptophanyl-tRNA synthetase	0.45	0.36	0.37	0.61	10.26	9.90	11.21	10.84	10.58	9.97	0.00
XOO0438	-	beta-lactamase-like protein	0.72	0.69	0.72	0.75	8.90	8.21	10.07	9.35	9.85	9.10	0.00
XOO0439	-	peptidase	1.12	1.22	1.13	1.01	11.72	10.50	12.47	11.34	12.62	11.61	0.00
XOO0443	-	hypothetical protein	0.53	1.71	-0.28	0.17	4.84	3.14	7.62	7.90	7.28	7.11	0.00
XOO0444	-	hypothetical protein	2.16		0.41	3.91	6.59	NA	7.80	7.39	7.05	3.14	0.00
XOO0446	<i>yodB</i>	cytochrome B561	0.86	0.88	0.46	1.22	9.51	8.63	5.45	4.99	9.99	8.76	0.00
XOO0447	<i>srpA</i>	catalase	1.01	0.39	2.08	0.55	9.49	9.10	9.89	7.81	9.92	9.37	0.00
XOO0448	<i>prtI</i>	ECF sigma factor	2.75	2.35	3.61	2.28	4.25	1.90	6.40	2.79	3.89	1.61	0.00
XOO0449	<i>prtR</i>	transmembrane regulator protein prtR	3.27	4.13	2.40	7.49	3.36	4.35	NA	6.21	3.81	0.00	
XOO0450	-	leucine aminopeptidase	1.54	2.09	1.32	1.21	5.67	3.58	8.36	7.04	7.76	6.55	0.00
XOO0451	-	hydrolase	0.59	0.62	0.60	0.57	9.58	8.97	11.16	10.56	10.76	10.19	0.00
XOO0452	<i>yhhT</i>	transporter	0.36	0.50	0.36	0.22	9.50	9.00	9.44	9.07	8.90	8.68	0.00
XOO0453	<i>ubiA</i>	4-hydroxybenzoate octaprenyltransferase	2.04	2.05	1.85	2.22	8.74	6.69	9.98	8.13	9.31	7.10	0.00
XOO0454	<i>comF</i>	competence protein F	0.05	0.14	-0.12	0.12	10.95	10.81	12.09	12.21	11.20	11.08	0.00
XOO0455	<i>bioB</i>	biotin synthase	0.96	0.92	1.01	0.94	11.60	10.68	11.70	10.69	11.58	10.64	0.00
XOO0456	<i>bioF</i>	8-amino-7-oxononanoate synthase	0.93	0.16	1.18	1.46	6.83	6.67	9.16	7.97	8.89	7.42	0.00
XOO0459	<i>fabG</i>	3-ketoacyl-ACP reductase	1.92	2.22	0.80	2.74	8.79	6.57	5.25	4.45	9.23	6.49	0.00
XOO0460	-	halogenase	0.78	0.88	0.50	0.96	8.04	7.16	5.33	4.83	9.70	8.74	0.00
XOO0461	-	dolichyl-phosphate mannose synthase-like protein	0.88	1.15	0.76	0.74	9.81	8.66	11.16	10.40	10.79	10.05	0.00
XOO0462	-	hypothetical protein	0.81	0.80	0.45	1.16	8.16	7.36	8.36	7.90	5.17	4.00	0.00
XOO0463	<i>fabF</i>	3-oxoacyl-ACP synthase	0.21	0.00	0.36	0.27	9.51	9.51	10.27	9.91	9.43	9.16	0.00
XOO0464	-	hypothetical protein	1.58	1.76	1.40	1.56	9.83	8.06	11.37	9.96	10.93	9.37	0.00
XOO0466	-	hypothetical protein	-0.18	0.20	-0.34	-0.39	9.27	9.07	9.39	9.74	8.98	9.37	0.00
XOO0467	<i>zwf</i>	glucose-6-phosphate 1-dehydrogenase	1.25	1.62	0.77	1.35	8.20	6.58	9.23	8.46	9.04	7.68	0.00
XOO0469	<i>kefC</i>	glutathione-regulated potassium-efflux system protein	2.07	1.59	2.25	2.36	7.16	5.58	8.64	6.39	7.70	5.34	0.00
XOO0470	<i>mgtE</i>	Mg <sup>++</sup> transporter	0.68	0.63	0.71	0.71	10.20	9.57	11.17	10.46	10.95	10.24	0.00
XOO0471	-	hypothetical protein	0.88	1.58	1.03	0.04	7.52	5.94	5.14	4.12	7.91	7.88	0.00
XOO0472	-	hypothetical protein	-1.14	0.13	-2.85	-0.69	4.02	3.90	1.73	4.58	7.18	7.87	0.00
XOO0473	-	hypothetical protein	-0.78	-0.47	-0.74	-1.12	7.54	8.00	8.71	9.45	8.24	9.37	0.00
XOO0474	<i>nrdA</i>	ribonucleotide-diphosphate reductase subunit alpha	-1.14	-0.97	-1.16	-1.28	9.12	10.09	9.65	10.80	9.40	10.68	0.00
XOO0475	<i>nrdF</i>	ribonucleotide-diphosphate reductase subunit beta	-0.46	-0.39	-0.49	-0.49	11.80	12.19	12.34	12.84	11.71	12.20	0.00
XOO0476	-	flavodoxin	-0.53	-0.57	-0.66	-0.36	8.47	9.03	9.36	10.02	8.99	9.35	0.00
XOO0477	<i>trxA</i>	thioredoxin	-0.80	-0.82	-0.69	-0.91	7.87	8.69	9.85	10.54	9.28	10.19	0.00
XOO0481	<i>pcaF</i>	beta-ketoacyl CoA thiolase	-0.07	0.05	-0.13	-0.12	10.55	10.50	11.69	11.81	10.63	10.75	0.00
XOO0482	<i>pcaH</i>	protocatechuate 3,4-dioxygenase subunit beta	2.99	2.99			7.52	4.53	1.58	NA	5.85	NA	0.00
XOO0484	<i>pcaB</i>	3-carboxy-cis,cis-muconate cycloisomerase	0.68	0.96	0.47	0.63	3.01	2.05	7.23	6.76	6.74	6.11	0.00
XOO0485	<i>catD</i>	b-ketoacyl enol-lactone hydrolase	-0.24	-0.26	-0.16	-0.29	8.45	8.70	9.72	9.88	8.90	9.19	0.00
XOO0486	<i>pcaC</i>	4-carboxymuconolactone decarboxylase	2.34	4.14	4.21	-1.34	5.89	1.75	7.44	3.23	6.03	7.37	0.00
XOO0487	-	hydrolase	1.81		0.79	2.83	2.54	NA	1.73	0.94	5.42	2.59	0.00
XOO0488	<i>pcaR</i>	transcriptional regulator	-0.23	-0.14	-0.28	-0.26	8.45	8.59	9.15	9.43	8.42	8.68	0.00
XOO0489	-	hypothetical protein	-0.22	-0.24	-0.20	-0.23	9.39	9.63	10.38	10.57	10.02	10.25	0.00
XOO0491	-	oxidoreductase	0.55	0.35	0.30	0.99	9.79	9.44	10.43	10.13	9.32	8.34	0.00
XOO0493	-	hypothetical protein	0.57	0.37	0.37	0.97	9.79	9.42	10.25	9.88	9.57	8.61	

XOO0502	wbnF	nucleotide sugar epimerase	0.19	-0.25	-3.95	4.78	3.25	3.51	4.13	8.08	7.69	2.91	0.00
XOO0503	mcrB	mitomycin resistance protein	0.47	0.14	0.38	0.89	9.20	9.07	10.01	9.63	9.37	8.48	0.00
XOO0504	parB	chromosome partitioning protein	0.69	0.47	0.63	0.96	10.07	9.60	10.55	9.91	10.31	9.36	0.00
XOO0505	parA	chromosome partitioning protein	0.53	0.31	0.37	0.91	9.61	9.30	10.05	9.68	8.89	7.98	0.00
XOO0506	-	hypothetical protein	1.39	1.28	1.20	1.70	10.54	9.26	11.23	10.04	10.55	8.85	0.00
XOO0509	exoA	exodeoxyribonuclease III	1.26	1.41	1.19	1.17	8.60	7.19	10.60	9.40	10.34	9.17	0.00
XOO0510	ampG	signal transducer	0.37	0.28	0.42	0.42	10.69	10.41	11.62	11.20	11.25	10.83	0.00
XOO0512	anmK	anhydro-N-acetyl muramic acid kinase	2.04	-0.69	4.77		7.00	7.69	6.64	1.86	3.48	NA	0.00
XOO0513	-	hypothetical protein	0.91	0.83	0.83	1.08	10.60	9.77	11.89	11.06	11.41	10.33	0.00
XOO0519	-	two-component system sensor protein	0.53	0.63	0.51	0.46	9.79	9.16	11.00	10.48	10.86	10.41	0.00
XOO0521	-	hypothetical protein	0.63	0.41	0.72	0.77	8.24	7.83	10.13	9.40	10.04	9.26	0.00
XOO0522	-	hypothetical protein	1.34	1.36	1.13	1.54	8.77	7.40	9.92	8.80	9.29	7.75	0.00
XOO0523	-	hypothetical protein	0.55	0.30	0.55	0.81	9.89	9.59	10.47	9.92	9.94	9.14	0.00
XOO0525	-	iron-sulfur cluster insertion protein ErpA	0.44	0.42	0.33	0.56	12.34	11.92	13.06	12.74	12.28	11.72	0.00
XOO0526	-	hypothetical protein	0.59	0.50	0.54	0.72	9.74	9.24	9.96	9.42	9.35	8.63	0.00
XOO0527	nudC	NADH pyrophosphatase	1.93	1.85	1.88	2.07	6.39	4.54	9.57	7.69	8.71	6.65	0.00
XOO0528	ampE	hypothetical protein	1.43		1.51	1.34	5.51	NA	8.06	6.54	8.33	6.99	0.00
XOO0529	-	hypothetical protein	0.75	0.30	1.08	0.86	9.26	8.96	9.60	8.52	9.72	8.86	0.00
XOO0530	aas	2-acylglycerophosphoethanolamine acyltransferase	1.47	1.57	1.21	1.62	8.94	7.37	10.08	8.88	9.21	7.59	0.00
XOO0535	-	hypothetical protein	2.48	3.69	1.66	2.08	6.23	2.54	7.37	5.71	7.43	5.36	0.00
XOO0536	-	hypothetical protein	0.25	0.38	0.18	0.18	10.15	9.77	11.94	11.75	11.69	11.51	0.00
XOO0537	purD	phosphoribosylamine--glycine ligase	0.46	0.57	0.47	0.34	7.31	6.74	9.60	9.13	8.75	8.41	0.00
XOO0538	-	ATPase	0.06	0.02	0.11	0.04	12.13	12.11	13.11	13.00	12.65	12.61	0.00
XOO0539	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase	0.88	0.85	0.86	0.92	12.34	11.49	13.01	12.15	12.84	11.92	0.00
XOO0543	-	hypothetical protein	1.79	2.43	1.14		6.68	4.25	7.47	6.33	3.12	NA	0.00
XOO0544	-	hypothetical protein	0.57		0.57		4.84	NA	5.80	5.23	5.96	NA	0.00
XOO0548	fis	Fis family transcriptional regulator	0.10	0.04	0.23	0.01	10.08	10.04	11.78	11.54	11.51	11.50	0.00
XOO0554	-	hypothetical protein	2.02	2.13	2.13	1.80	8.41	6.28	9.12	6.99	8.89	7.09	0.00
XOO0556	accC	acetyl-CoA carboxylase biotin carboxylase subunit	0.53	0.54	0.53	0.53	10.01	9.47	10.88	10.34	10.36	9.83	0.00
XOO0557	-	hypothetical protein	0.04	0.05	0.16	-0.09	11.29	11.24	12.32	12.16	12.29	12.38	0.00
XOO0561	dsbD	C-type cytochrome biogenesis protein (copper tolerance)	1.62	1.88	1.57	1.40	8.70	6.82	9.70	8.14	9.42	8.01	0.00
XOO0562	cutA	divalent cation tolerance protein	1.11	1.21	1.11	0.99	9.38	8.17	10.00	8.89	9.78	8.79	0.00
XOO0567	priA	primosome assembly protein PriA	2.40	2.40			3.62	1.23	4.54	NA	NA	NA	0.01
XOO0568	-	hypothetical protein	1.86	2.26	1.54	1.79	8.50	6.23	10.35	8.82	9.99	8.20	0.00
XOO0569	-	hypothetical protein	0.79	0.26	0.83	1.27	7.38	7.12	9.54	8.71	8.85	7.58	0.00
XOO0572	norM	multidrug efflux protein	0.99	1.17	0.77	1.04	8.77	7.60	10.52	9.74	10.18	9.14	0.00
XOO0573	sppA	endopeptidase IV	1.46	2.13	1.10	1.15	8.66	6.53	9.36	8.26	8.97	7.82	0.00
XOO0575	trn2	tropinone reductase	0.89	1.08	0.77	0.81	10.23	9.15	11.36	10.59	10.79	9.97	0.00
XOO0576	-	hypothetical protein	0.67	0.40	1.01	0.60	8.06	7.66	8.82	7.82	8.59	7.99	0.00
XOO0577	-	hypothetical protein	0.19	-0.20	0.46	0.31	6.91	7.12	8.64	8.18	8.55	8.24	0.00
XOO0579	topA	DNA topoisomerase I	0.91	0.49	0.92	1.32	9.79	9.30	11.74	10.82	10.83	9.51	0.00
XOO0580	-	hypothetical protein	0.24	0.17	0.30	0.24	8.59	8.42	9.88	9.57	9.82	9.58	0.00
XOO0582	smg	hypothetical protein	1.04	1.12	1.02	0.97	11.89	10.77	12.53	11.51	12.32	11.35	0.00
XOO0583	smf	DNA processing protein DprA	1.12	0.15	0.51	2.70	8.17	8.02	8.86	8.35	7.12	4.42	0.00
XOO0584	-	hypothetical protein	0.24	0.68	0.00	0.03	9.46	8.79	11.12	11.12	10.76	10.73	0.00
XOO0585	def	peptide deformylase	0.62	0.73	0.57	0.57	10.70	9.97	12.46	11.89	12.14	11.57	0.00
XOO0586	fmt	methionyl-tRNA formyltransferase	-0.04	0.13	-0.06	-0.20	8.96	8.83	10.39	10.45	10.29	10.50	0.00
XOO0587	sun	hypothetical protein	0.25	0.35	0.23	0.18	8.29	7.93	9.22	9.00	8.89	8.71	0.00
XOO0588	-	hypothetical protein	0.48	0.57	0.49	0.39	9.17	8.60	10.39	9.89	9.52	9.14	0.00
XOO0589	-	hypothetical protein	0.12	0.36	-0.04	0.05	7.56	7.20	8.15	8.20	8.27	8.21	0.00
XOO0590	-	lipopolysaccharide core biosynthesis glycosyl transferase	3.95	5.67	2.79	3.38	7.69	2.02	10.00	7.21	9.84	6.46	0.00
XOO0591	-	hypothetical protein	1.09	0.69	0.51	2.06	2.98	2.28	4.07	3.56	8.30	6.24	0.00
XOO0592	-	hypothetical protein	1.72	0.29	0.69	4.20	3.18	2.89	7.71	7.03	6.82	2.62	0.00
XOO0593	-	hypothetical protein	2.03	3.90	0.80	1.38	7.07	3.17	7.69	6.89	7.75	6.36	0.00
XOO0594	ribA	GTP cyclohydrolase	0.99	0.92	0.97	1.10	9.60	8.68	10.72	9.75	10.05	8.95	0.00
XOO0595	yncA	phosphinothricin acetyltransferase	2.44	2.84	3.05	1.44	8.46	5.61	9.22	6.17	4.67	3.23	0.00
XOO0596	htrB	lipid A biosynthesis lauroyl acyltransferase	3.96			3.96	4.73	NA	6.08	NA	6.22	2.26	0.00
XOO0597	-	D-tyrosyl-tRNA(Tyr) deacylase	1.10	1.11	1.09	1.12	8.10	6.99	10.13	9.04	9.64	8.53	0.00
XOO0598	rpoD	RNA polymerase sigma factor RpoD	0.92	0.91	0.92	0.94	10.58	9.67	12.14	11.22	12.07	11.13	0.00
XOO0599	-	phage integrase family site specific recombinase	1.92			4.94	NA	6.08	4.16	2.08	NA	0.00	
XOO0600	-	hypothetical protein	#DIV/0!				5.58	NA	3.38	NA	2.71	NA	0.00
XOO0601	-	transposase	0.15		0.15		NA	NA	4.81	4.65	2.12	NA	0.00
XOO0603	traF	TraF protein	#DIV/0!				1.90	NA	2.23	NA	2.16	NA	0.00
XOO0604	-	hypothetical protein	1.34	1.78	0.80	1.44	4.68	2.90	6.55	5.75	4.69	3.25	0.00
XOO0605	traH	TraH protein	0.12	-0.06		0.29	3.76	3.82	2.23	NA	7.96	7.67	0.00
XOO0606	-	XorII very-short-patch-repair endonuclease	#DIV/0!				NA	NA	4.67	NA	2.20	NA	0.01
XOO0607	-	modification methylase XorII	#DIV/0!				NA	NA	NA	NA	NA	NA	NA
XOO0608	afa22MI-R	endonuclease	#DIV/0!				0.50	NA	NA	NA	NA	NA	0.63
XOO0609	int	phage-related integrase	2.55	0.47	4.63	3.08	NA	7.90	7.43	8.15	3.52	0.00	
XOO0611	-	hypothetical protein	1.31	2.04	0.59	NA	NA	4.92	2.89	3.56	2.97	0.00	
XOO0624	-	hypothetical protein	3.14	3.33	2.89	3.19	10.28	6.95	11.03	8.14	11.08	7.89	0.00
XOO0625	-	hypothetical protein	3.05	2.97	3.06	3.10	10.16	7.19	10.61	7.54	10.62	7.52	0.00
XOO0626	-	ferrichrome-iron receptor 3	0.13	0.04	0.14	0.20	14.41	14.37	15.08	14.93	14.56	14.35	0.00
XOO0627	-	hypothetical protein	2.41	4.10	1.42	1.72	7.33	3.23	9.47	8.05	9.42	7.70	0.00
XOO0628	-	hypothetical protein	1.30	2.91	0.43	0.56	6.04	3.12	8.48	8.06	8.12	7.55	0.00
XOO0629	-	hypothetical protein	0.68	0.29	0.81	0.94	3.77	3.47	8.66	7.85	8.51	7.58	0.00
XOO0630	-	hypothetical protein	0.23	-0.32	0.96	0.04	7.20	7.52	8.30	7.34	8.05	8.00	0.00
XOO0632	-	hypothetical protein	-0.02	0.14	0.03	-0.23	8.97	8.83	10.40	10.36	10.04	10.27	0.00
XOO0635	ybdR	Zn-dependent alcohol dehydrogenase	1.05	0.36	1.27	1.51	3.93	3.56	7.89	6.63	8.05	6.54	0.00
XOO0638	cioB	cyanide insensitive terminal oxidase	0.61	0.88	0.48	0.48	8.72	7.84	9.29	8.81	8.71	8.23	0.00
XOO0639	cioA	cyanide insensitive terminal oxidase	0.57	0.13	0.59	0.99	2.86	2.74	3.56	2.97	7.65	6.67	0.00
XOO0640	-	hypothetical protein	#DIV/0!				2.54	NA	2.32	NA	NA	NA	0.01
XOO0641	-	NtrC family transcriptional regulator	0.71	0.52	0.89	0.72	7.30	6.79	8.48	7.58	8.56	7.84	0.00
XOO0642	-	hypothetical protein	2.30	3.44	1.51	1.95	6.03	2.59	7.92	6.42	8.13	6.18	0.00
XOO0643	exsF	regulatory protein	2.27	1.88	3.68	1.25	5.08	3.20	7.38	3.70	7.61		

XOO0660	-	hypothetical protein	2.44	2.07	2.45	2.79	10.93	8.87	12.08	9.63	11.50	8.71	0.00
XOO0662	-	metallopeptidase	1.30	1.54	1.35	1.00	8.77	7.24	9.90	8.54	9.51	8.51	0.00
XOO0664	-	oxidoreductase	1.66	2.65	3.87	-1.56	5.79	3.14	6.71	2.83	5.29	6.85	0.00
XOO0666	-	hypothetical protein	1.32	0.98	1.52	1.46	7.91	6.94	8.92	7.40	8.68	7.22	0.00
XOO0669	-	hypothetical protein	0.97	0.66	1.10	1.15	8.27	7.61	9.58	8.48	8.86	7.71	0.00
XOO0670	-	DNA polymerase related protein	0.20	0.05	0.20	0.34	6.25	6.20	4.16	3.97	4.20	3.85	0.00
XOO0671	-	hypothetical protein	1.68	2.04	0.93	2.08	9.21	7.17	5.33	4.41	9.56	7.48	0.00
XOO0675	<i>yjcE</i>	Na <sup>+</sup> :H <sup>+</sup> antiporter	1.41	1.16	0.97	2.09	9.38	8.23	9.94	8.97	8.64	6.55	0.00
XOO0676	<i>yadG</i>	ABC transporter ATP-binding protein	1.28	4.92	-0.22	-0.88	5.90	0.98	7.21	7.42	6.80	7.68	0.00
XOO0677	-	ABC transporter	0.12	-0.20	-0.19	0.74	8.70	8.90	8.42	8.61	8.31	7.57	0.00
XOO0678	-	hypothetical protein	0.22	0.19	0.21	0.28	9.70	9.52	11.28	11.07	10.31	10.03	0.00
XOO0679	-	hypothetical protein	0.94	0.66	1.13	1.02	9.25	8.58	10.03	8.90	9.80	8.79	0.00
XOO0682	<i>cvgSY</i>	histidine kinase/response regulator hybrid protein	2.34	1.98	2.71	3.32	NA	3.53	1.55	5.79	3.09	0.00	
XOO0683	-	two-component response regulator	#DIV/0!				2.90	NA	6.10	NA	2.04	NA	0.01
XOO0688	<i>motA</i>	flagellar motor protein MotA	-0.54	-2.19	-2.81	3.38	0.79	2.98	5.08	7.90	7.60	4.22	0.00
XOO0689	-	hypothetical protein	2.21	3.49	1.26	1.87	5.62	2.13	3.78	2.53	6.00	4.13	0.00
XOO0690	-	methionine sulfoxide reductase B	2.67	1.75	1.54	4.71	8.29	6.53	8.92	7.38	8.00	3.29	0.00
XOO0692	<i>lrp</i>	leucine responsive regulatory protein	2.35	1.63	4.26	1.17	7.72	6.09	7.86	3.60	4.42	3.25	0.00
XOO0693	<i>dadA</i>	D-amino acid dehydrogenase small subunit	1.05	0.93	0.82	1.41	8.33	7.41	9.56	8.74	8.99	7.58	0.00
XOO0694	<i>alr</i>	alanine racemase	3.57	5.24	2.52	2.94	7.84	2.60	10.19	7.67	9.96	7.02	0.00
XOO0695	-	hypothetical protein	1.87	0.96	1.34	3.32	7.78	6.82	9.74	8.40	8.55	5.23	0.00
XOO0696	-	hypothetical protein	-2.95	-3.11	-2.72	-3.03	7.47	10.58	8.42	11.13	7.62	10.65	0.00
XOO0698	-	sensor histidine kinase	-1.08	-1.05	-1.08	-1.13	7.31	8.36	8.82	9.90	8.22	9.35	0.00
XOO0699	-	hypothetical protein	-0.53	-0.63	-0.45	-0.51	8.29	8.91	9.39	9.84	9.39	9.90	0.00
XOO0700	<i>sndH</i>	L-sorbose dehydrogenase	0.77	0.99	0.45	0.86	8.26	7.26	9.29	8.84	8.97	8.12	0.00
XOO0701	-	hypothetical protein	0.06	-0.72	0.59	0.31	6.76	7.47	8.28	7.69	8.03	7.71	0.00
XOO0702	<i>rsmC</i>	ribosomal RNA small subunit methyltransferase C	2.24	1.38	0.74	4.60	7.39	6.01	8.62	7.89	9.11	4.52	0.00
XOO0703	<i>rsuA</i>	ribosomal small subunit pseudouridylate synthase	0.92	0.77	-0.39	2.37	7.96	7.19	7.78	8.17	8.52	6.15	0.00
XOO0704	-	hypothetical protein	2.72	1.77	2.19	4.19	8.55	6.78	8.46	6.27	7.82	3.62	0.00
XOO0706	-	oxidoreductase	-1.09	-2.95	-0.17	-0.16	4.35	7.31	10.18	10.36	9.77	9.93	0.00
XOO0707	-	hypothetical protein	0.86	0.95	0.85	0.79	8.54	7.58	10.37	9.52	9.99	9.20	0.00
XOO0708	-	hypothetical protein	#DIV/0!				2.64	NA	2.82	NA	5.14	NA	0.00
XOO0712	-	hypothetical protein	-0.58	-1.04	-0.43	-0.27	8.62	9.66	9.38	9.80	9.35	9.63	0.00
XOO0713	<i>metN</i>	DL-methionine transporter ATP-binding subunit	0.61	0.45	1.24	0.13	3.46	3.01	8.64	7.40	7.98	7.85	0.00
XOO0714	<i>yaeE</i>	ABC transporter permease	1.53	-0.94	4.12	1.42	3.66	4.60	7.40	3.29	7.94	6.52	0.00
XOO0715	-	hypothetical protein	2.02	2.27	2.32	1.49	9.27	7.00	7.41	5.09	10.42	8.93	0.00
XOO0716	-	hypothetical protein	1.35	2.91	0.62	0.51	6.87	3.96	4.87	4.25	4.78	4.27	0.00
XOO0717	<i>ompW</i>	hypothetical protein	0.99	0.99	1.02	0.96	11.93	10.94	12.17	11.15	11.59	10.63	0.00
XOO0718	-	hypothetical protein	1.40	1.30	1.44	1.46	8.63	7.33	9.65	8.21	8.83	7.37	0.00
XOO0719	-	hypothetical protein	0.85	0.75	0.95	1.90	NA	2.86	2.12	2.56	1.61	0.00	
XOO0720	<i>phdB</i>	dihydroipoamide acetyltransferase	0.89	0.89	0.85	0.92	10.43	9.54	11.95	11.10	11.47	10.55	0.00
XOO0722	<i>lpdA</i>	dihydroipoamide dehydrogenase	0.86	0.90	0.74	0.95	10.98	10.07	12.56	11.82	11.94	10.99	0.00
XOO0724	-	hypothetical protein	-0.31	-0.05	-0.48	-0.39	8.69	8.75	10.21	10.68	9.65	10.04	0.00
XOO0725	-	hypothetical protein	-0.17	-0.08	-0.15	-0.27	13.85	13.92	14.58	14.73	14.22	14.50	0.00
XOO0726	<i>atpB</i>	ATP synthase FOF1 subunit A	0.33	0.39	0.34	0.27	12.70	12.32	13.41	13.07	13.30	13.03	0.00
XOO0727	<i>atpE</i>	ATP synthase FOF1 subunit C	1.04	1.21	0.99	0.93	9.68	8.47	10.25	9.26	10.05	9.13	0.00
XOO0728	<i>atpF</i>	ATP synthase FOF1 subunit B	0.87	1.22	0.45	0.95	11.13	9.91	6.47	6.02	12.03	11.08	0.00
XOO0729	<i>atpH</i>	ATP synthase FOF1 subunit delta	1.07	0.98	1.59	0.63	10.39	9.41	10.93	9.34	11.32	10.69	0.00
XOO0730	<i>atpA</i>	ATP synthase FOF1 subunit alpha	1.53	1.70	1.33	1.57	11.50	9.80	12.21	10.88	11.89	10.31	0.00
XOO0731	<i>atpG</i>	ATP synthase FOF1 subunit gamma	1.34	1.37	1.23	1.43	11.76	10.40	12.37	11.14	11.67	10.24	0.00
XOO0732	<i>atpD</i>	ATP synthase FOF1 subunit beta	1.10	1.16	0.95	1.17	12.86	11.70	13.46	12.51	13.00	11.82	0.00
XOO0733	<i>atpC</i>	ATP synthase FOF1 subunit epsilon	1.07	1.23	1.06	0.92	12.47	11.24	13.86	12.81	13.53	12.61	0.00
XOO0734	<i>pheA</i>	chorismate mutase	0.02	0.28	0.03	-0.26	7.42	7.14	8.77	8.73	8.91	9.17	0.00
XOO0736	<i>glmU</i>	UDP-N-acetylglucosamine pyrophosphorylase	0.95	2.88	0.95	-0.97	6.13	3.25	8.49	7.54	3.36	4.33	0.00
XOO0745	<i>ybjY</i>	ABC transporter permease	3.69	3.86	3.52	3.17	NA	6.92	3.06	6.65	3.13	0.00	
XOO0746	<i>glmS</i>	glucosamine–fructose-6-phosphate aminotransferase	0.80	0.65	0.68	1.07	9.39	8.74	10.50	9.82	9.53	8.46	0.00
XOO0747	-	hypothetical protein	-0.21	-0.13	0.22	-0.72	6.12	6.25	7.46	7.24	6.92	7.64	0.00
XOO0748	-	hypothetical protein	-1.62	-2.42	-0.78	-1.67	5.62	8.04	4.17	4.95	7.54	9.21	0.00
XOO0754	<i>gloA</i>	lactoylglutathione lyase	1.45	3.59	1.87	-1.11	6.62	3.03	6.32	4.45	7.59	8.70	0.00
XOO0755	<i>copB</i>	copper resistance protein B	-0.22	-1.72	0.31	0.76	5.54	7.26	8.32	8.01	7.83	7.06	0.00
XOO0756	<i>copA</i>	copper resistance protein A	1.88	2.38	0.54	2.73	5.10	2.72	5.63	5.09	5.71	2.98	0.00
XOO0757	-	hypothetical protein	1.02	1.14	0.85	1.06	9.92	8.77	10.04	9.19	9.58	8.53	0.00
XOO0758	<i>cysM</i>	cysteine synthase	2.44	3.56	1.86	1.91	6.99	3.43	9.57	7.70	8.61	6.70	0.00
XOO0759	<i>prlC</i>	oligopeptidase A	0.46	-0.08	0.80	0.66	7.10	7.18	9.48	8.68	8.96	8.30	0.00
XOO0761	<i>fabB</i>	beta-ketoacyl- synthase I	2.38	3.32	1.54	2.29	8.02	4.70	9.91	8.37	10.20	7.91	0.00
XOO0762	<i>fabA</i>	3-hydroxydecanoyl-ACP dehydratase	1.42	1.62	1.06	1.59	8.34	6.73	9.69	8.63	9.38	7.79	0.00
XOO0763	<i>dinP</i>	DNA polymerase IV	0.81	0.69	0.74	1.00	10.58	9.89	11.54	10.80	10.96	9.96	0.00
XOO0764	<i>gph</i>	phosphoglycolate phosphatase	0.98	1.03	0.72	1.19	8.20	7.17	8.79	8.07	8.03	6.84	0.00
XOO0767	<i>bioD</i>	dithiobiotin synthetase	1.41	1.58	0.81	1.84	3.72	2.14	6.68	5.87	6.41	4.57	0.00
XOO0768	-	hypothetical protein	0.57	0.37	1.18	0.15	11.16	10.79	10.43	9.25	12.28	12.13	0.00
XOO0769	<i>ptps</i>	6-pyruvoyl tetrahydrobiopterin synthase	-0.20	-0.03	-0.27	-0.30	11.10	11.13	12.62	12.88	12.14	12.44	0.00
XOO0770	<i>rhlE</i>	ATP-dependent RNA helicase	-2.00	-2.14	-1.90	-1.95	8.53	10.67	9.57	11.47	9.29	11.24	0.00
XOO0771	<i>uptA</i>	fumarylacetoacetate hydrolase	0.84	0.81	1.75	-0.03	3.12	2.32	7.52	5.77	3.50	3.53	0.00
XOO0772	<i>uptB</i>	maleylacetoacetate isomerase	1.82	0.82	1.22	3.40	8.14	7.31	8.85	7.62	6.86	3.46	0.00
XOO0773	<i>uptC</i>	type II secretion system protein-like protein	1.11	0.91	1.06	1.35	10.20	9.29	11.34	10.28	11.00	9.64	0.00
XOO0774	<i>uptD</i>	hypothetical protein	0.70	0.91	0.71	0.50	10.11	9.21	11.84	11.13	11.46	10.96	0.00
XOO0775	<i>uptE</i>	hypothetical protein	0.95	0.94	0.99	0.91	9.15	8.22	11.03	10.05	10.69	9.77	0.00
XOO0776	-	hypothetical protein	1.33	1.50	1.22	1.28	13.01	11.52	14.70	13.48	14.38	13.10	0.00
XOO0777	<i>cysB</i>	cystathione beta-synthase	0.75	0.74	0.59	0.90	10.00	9.26	11.48	10.89	11.26	10.36	0.00
XOO0778	<i>metB</i>	cystathione gamma-synthase	0.32	0.38	0.16	0.41	10.74	10.36	12.04	11.87	11.48	11.07	0.00
XOO0779	<i>smtA</i>	hypothetical protein	0.03	0.01	0.00	0.09	13.56	13.55	14.60	14.60	14.37	14.28	0.0

XOO0795	<i>rmlD</i>	dTDP-4-dehydrorhamnose reductase	1.23	1.42	1.01	1.25	8.26	6.83	9.88	8.87	9.31	8.06	0.00	
XOO0796	<i>xanB</i>	phosphomannose isomerase; GDP-mannose pyrophosphorylase	0.18	0.24	0.26	0.03	8.62	8.38	10.26	10.00	9.73	9.70	0.00	
XOO0797	<i>xanA</i>	phosphoglcomutase; phosphomannomutase	-0.13	0.02	-0.22	-0.17	10.77	10.75	12.11	12.34	11.64	11.81	0.00	
XOO0798	<i>ipsI</i>	IpsJ protein	0.73	0.93	0.58	0.68	8.92	7.99	10.20	9.62	10.15	9.48	0.00	
XOO0799	<i>ipsJ</i>	IpsJ protein	-0.16	-0.10	-0.25	-0.12	9.92	10.03	11.71	11.96	11.17	11.29	0.00	
XOO0801	<i>etf-QO</i>	flavoprotein-ubiquinone oxidoreductase	0.41		0.55	0.27	4.31	NA	3.62	3.07	4.80	4.53	0.00	
XOO0802	<i>alkB</i>	DNA repair system specific for alkylated DNA	0.38	0.45	0.03	0.67	8.10	7.65	8.71	8.68	8.00	7.32	0.00	
XOO0803	-	hypothetical protein	0.06	0.03	0.08	0.09	9.61	9.58	9.99	9.90	8.56	8.47	0.00	
XOO0804	-	hypothetical protein	-0.29	-0.37	-0.23	-0.27	8.96	9.33	10.77	11.00	10.42	10.70	0.00	
XOO0805	<i>yrbF</i>	ABC transporter ATP-binding protein	-0.04	-0.06	0.00	-0.05	8.15	8.20	9.81	9.82	9.53	9.58	0.00	
XOO0806	<i>yrbE</i>	ABC transporter permease	-0.32	-0.11	-0.36	-0.49	9.27	9.38	10.92	11.28	10.45	10.95	0.00	
XOO0807	-	hypothetical protein	0.90	1.05	0.68	0.98	9.83	8.78	11.28	10.60	10.03	9.05	0.00	
XOO0808	-	DNA-binding protein	0.84	0.88	0.84	0.81	14.55	13.68	15.58	14.73	14.80	13.99	0.00	
XOO0810	-	hypothetical protein	1.27	1.39	1.22	1.20	11.41	10.01	12.87	11.65	12.76	11.55	0.00	
XOO0811	<i>pssA</i>	phosphatidylserine synthase	0.80	0.74	0.83	0.83	9.44	8.70	10.85	10.02	10.53	9.70	0.00	
XOO0812	<i>rml</i>	ribosomal-protein-alanine acetyltransferase	1.12	1.10	0.56	1.70	8.80	7.70	9.51	8.96	9.71	8.01	0.00	
XOO0820	<i>slt</i>	soluble lytic murein transglycosylase	0.05	0.15	0.10	-0.09	8.30	8.15	8.77	8.67	8.84	8.93	0.00	
XOO0821	<i>pel</i>	pectate lyase	0.91	0.72	0.99	1.03	7.14	6.42	8.20	7.21	7.18	6.15	0.00	
XOO0826	-	SAM-dependent methyltransferase	2.03	0.89	0.92	4.29	10.34	9.44	10.98	10.06	9.65	5.36	0.00	
XOO0831	<i>valS</i>	valyl-tRNA synthetase	2.78		0.82	4.74	6.85	NA	8.92	8.11	8.54	3.80	0.00	
XOO0834	<i>pepA</i>	leucyl aminopeptidase	4.53	5.56	3.06	4.98	6.74	1.17	8.42	5.36	8.17	3.20	0.00	
XOO0836	-	hypothetical protein	0.11	-0.04	0.17	0.20	8.32	8.36	9.81	9.64	9.36	9.16	0.00	
XOO0839	<i>xerD</i>	site-specific tyrosine recombinase XerD	0.59		0.59		1.50	NA	1.79	1.20	3.75	NA	0.01	
XOO0840	<i>dsbC</i>	disulfide isomerase	-0.47	-1.36	-0.25	0.20	5.40	6.76	9.27	9.51	9.27	9.07	0.00	
XOO0841	<i>purL</i>	phosphoribosylformylglycinamide synthase	1.23	0.97	1.26	1.46	8.76	7.79	10.44	9.18	9.70	8.24	0.00	
XOO0842	<i>xadA</i>	hypothetical protein	1.81	1.75	1.77	1.92	10.36	8.62	11.63	9.86	11.33	9.41	0.00	
XOO0847	<i>xpsE</i>	general secretion pathway protein E	2.16	1.16	1.06	4.24	9.56	8.39	10.19	9.13	8.90	4.66	0.00	
XOO0848	<i>xpsF</i>	general secretion pathway protein F	0.90	0.70	0.91	1.09	7.57	6.87	10.27	9.36	9.64	8.55	0.00	
XOO0849	<i>xpsG</i>	general secretion pathway protein G	2.07	2.67	1.70	1.84	8.97	6.30	10.59	8.89	10.32	8.48	0.00	
XOO0850	<i>xpsH</i>	general secretion pathway protein H	0.06	-0.06	-0.11	0.34	7.90	7.95	9.91	10.02	9.63	9.29	0.00	
XOO0851	<i>xpsI</i>	general secretion pathway protein I	2.46		2.00	2.91	6.90	NA	8.23	6.23	7.85	4.94	0.00	
XOO0852	<i>xpsJ</i>	general secretion pathway protein J	1.38	1.63	1.20	1.33	8.25	6.63	9.15	7.95	8.69	7.36	0.00	
XOO0853	<i>xpsK</i>	general secretion pathway protein K	1.09	1.10	1.14	1.05	11.10	10.01	12.42	11.28	12.20	11.14	0.00	
XOO0854	<i>xpsL</i>	general secretion pathway protein L	1.48	1.32	1.22	1.89	6.85	5.53	9.61	8.39	9.42	7.53	0.00	
XOO0855	<i>xpsM</i>	general secretion pathway protein M	2.85	0.62	5.92	2.02	5.03	4.41	9.37	3.46	9.30	7.28	0.00	
XOO0856	<i>xpsN</i>	general secretion pathway protein N	1.11	1.24	0.82	1.27	9.21	7.98	10.42	9.61	9.83	8.56	0.00	
XOO0857	<i>xpsD</i>	general secretion pathway protein D	1.04	1.10	1.06	0.96	10.69	9.59	11.69	10.63	11.41	10.45	0.00	
XOO0859	-	transcriptional regulator	1.47	1.01	1.03	2.36	8.71	7.70	9.78	8.75	8.98	6.62	0.00	
XOO0860	-	transporter	1.34	1.44	1.43	1.17	8.63	7.19	9.02	7.60	8.19	7.02	0.00	
XOO0861	<i>bfrC</i>	iron permease	2.75	2.35	1.87	4.02	6.28	3.93	8.88	7.00	8.30	4.28	0.00	
XOO0862	-	hypothetical protein	#DIV/0!					3.79	NA	6.65	NA	2.26	NA	0.00
XOO0863	-	glycosyl transferase family protein	0.72	1.07	0.63	0.46	7.75	6.68	9.71	9.08	9.67	9.20	0.00	
XOO0866	-	hypothetical protein	1.76	2.49	1.44	1.35	8.52	6.03	9.93	8.48	9.95	8.61	0.00	
XOO0867	-	hypothetical protein	2.93	3.59	2.60	2.61	9.02	5.43	10.28	7.68	9.92	7.31	0.00	
XOO0868	-	endonuclease	2.62	2.23	2.91	2.72	8.58	6.35	9.65	6.73	9.44	6.72	0.00	
XOO0869	-	hypothetical protein	2.32	2.45	2.19	2.32	8.84	6.40	10.27	8.08	10.22	7.90	0.00	
XOO0870	-	hypothetical protein	1.74	1.84	1.58	1.80	11.34	9.49	13.21	11.63	12.49	10.70	0.00	
XOO0871	-	hypothetical protein	1.42	1.22	1.40	1.65	9.06	7.84	10.33	8.93	9.44	7.79	0.00	
XOO0872	-	hypothetical protein	1.67	1.94	1.56	1.52	9.85	7.91	11.18	9.63	10.81	9.29	0.00	
XOO0876	<i>maf</i>	Maf-like protein	2.78		4.67	0.90	4.70	NA	6.59	1.93	3.31	2.41	0.00	
XOO0877	-	hypothetical protein	0.14	0.20	0.09	0.13	13.96	13.76	14.77	14.68	14.68	14.55	0.00	
XOO0878	<i>fabH</i>	3-oxoacyl-ACP synthase	2.41	5.10	0.84	1.29	7.59	2.49	9.04	8.20	8.78	7.48	0.00	
XOO0879	-	hypothetical protein	0.82		0.78	0.87	4.87	NA	8.36	7.58	7.84	6.98	0.00	
XOO0880	<i>fabD</i>	ACP S-malonyltransferase	0.91	0.86	1.04	0.83	11.15	10.29	10.46	9.43	10.17	9.34	0.00	
XOO0881	<i>fabG</i>	3-ketoacyl-ACP reductase	0.99	1.04	1.05	0.87	9.79	8.74	10.80	9.75	10.68	9.81	0.00	
XOO0882	<i>acpP</i>	acyl carrier protein	1.09	1.60	0.67	1.02	15.36	13.77	15.99	15.99	15.99	14.98	0.00	
XOO0883	<i>fabF</i>	3-oxoacyl-ACP synthase	1.49	1.47	1.69	1.30	9.57	8.11	10.54	8.85	10.77	9.46	0.00	
XOO0884	<i>trpE</i>	hypothetical protein	3.53		4.71	2.34	6.34	NA	7.20	2.49	7.12	4.78	0.00	
XOO0885	-	hypothetical protein	1.97	3.45	1.25	1.22	6.53	3.08	8.91	7.66	8.25	7.03	0.00	
XOO0886	<i>holB</i>	DNA polymerase III subunit delta'	1.95	3.32	1.39	1.13	7.73	4.41	11.13	9.74	11.01	9.89	0.00	
XOO0887	<i>pilZ</i>	type IV fimbriae assembly protein	0.45	0.51	0.43	0.39	8.99	8.47	10.01	9.57	9.78	9.38	0.00	
XOO0890	-	hypothetical protein	1.29	1.43	1.05	1.40	9.23	7.81	10.61	9.56	10.14	8.74	0.00	
XOO0891	<i>pprR</i>	propionate catabolism regulatory protein	1.93	2.44	1.38	1.98	6.04	3.61	8.11	6.72	7.96	5.99	0.00	
XOO0892	<i>pprB</i>	2-methylisocitrate lyase	3.22				3.22	1.50	NA	NA	5.72	2.50	0.01	
XOO0893	<i>prpC</i>	methylcitrate synthase	-0.01	0.20	-0.02	-0.20	6.47	6.27	9.17	9.19	8.68	8.88	0.00	
XOO0894	<i>acnA</i>	aconitate hydratase	0.22	-0.45	0.63	0.48	5.90	6.36	8.84	8.21	8.36	7.89	0.00	
XOO0896	-	hypothetical protein	0.25	1.80	-0.13	-0.91	5.89	4.09	8.18	8.31	7.55	8.46	0.00	
XOO0897	<i>fyuA</i>	TonB-dependent receptor	1.14	1.39	0.91	1.13	8.37	6.98	8.89	7.98	9.28	8.15	0.00	
XOO0898	-	inosine-uridine preferring nucleoside hydrolase	2.50	2.02	2.57	2.91	4.22	2.20	6.95	4.38	6.10	3.19	0.00	
XOO0900	-	hypothetical protein	#DIV/0!					5.32	NA	2.99	NA	5.00	NA	0.00
XOO0901	<i>fecA</i>	TonB-dependent receptor	0.07		-0.43	0.57	6.08	NA	7.57	8.00	7.80	7.23	0.00	
XOO0902	<i>glpQ</i>	glycerophosphodiester phosphodiesterase	1.58		1.29	1.86	3.78	NA	9.06	7.77	8.86	7.00	0.00	
XOO0903	-	hypothetical protein	4.17				3.22	5.06	NA	7.29	2.18	6.49	3.27	0.00
XOO0907	-	bacterioferritin	0.09	0.18	-0.06	0.14	9.33	9.15	10.56	10.62	10.03	9.89	0.00	
XOO0908	-	peroxiredoxin	#DIV/0!					5.32	NA	5.02	NA	4.57	NA	0.00
XOO0909	<i>hspA</i>	low molecular weight heat shock protein	2.67	4.01	2.00	1.99	6.01	2.00	10.01	8.01	9.54	7.54	0.00	
XOO0910	<i>cbaP</i>	curved DNA binding protein	1.39	3.72	0.22	0.24	7.26	3.54	9.61	9.40	9.33	9.09	0.00	
XOO0911	<i>pilH</i>	PilH family regulatory protein	1.06	1.58	0.95	0.65	8.89	7.31	11.28	10.33	11.11	10.46	0.00	
XOO0912	<i>hflK</i>	integral membrane protease subunit	0.69	0.79	0.55	0.73	10.83	10.04	12.01	11.46	11.61	10.89	0.00	
XOO0913	<i>hflC</i>	integral membrane proteinase subunit	0.47	0.44	0.49	0.49	9.64	9.21	10.64	10.15	10.69	10.20	0.00	
XOO0915	<i>purA</i>	adenylosuccinate synthetase	1.08	1.21	1.05	0.99	10.37	9.16	11.70	10.66	11.67	10.67	0.00	
XOO0916	<i>pepN</i>	aminopeptidase	1.69	2.21	1.60	1.26	8.06							

XOO0928	<i>pcm</i>	L-isoaspartate protein carboxylmethyltransferase	0.86	0.94	0.78	0.87	10.13	9.19	10.78	10.00	10.63	9.76	0.00	
XOO0929	-	transcriptional regulator	-0.49	-0.47	-0.44	-0.55	9.14	9.61	9.77	10.21	9.72	10.27	0.00	
XOO0930	-	hypothetical protein	0.06	-0.63	0.74	4.67	NA	2.04	2.67	3.64	2.90	0.00		
XOO0935	-	LysR family transcriptional regulator	2.82	2.54	2.27	3.64	7.87	5.32	8.96	6.68	8.64	5.00	0.00	
XOO0936	<i>leuC</i>	isopropylmalate isomerase large subunit	1.80	1.75	1.89	1.77	11.27	9.51	11.49	9.60	11.46	9.69	0.00	
XOO0937	<i>leuD</i>	isopropylmalate isomerase small subunit	2.10	2.12	2.12	2.05	10.52	8.40	11.22	9.10	10.45	8.40	0.00	
XOO0940	<i>leuB</i>	3-isopropylmalate dehydrogenase	1.30	1.22	1.33	1.36	9.33	8.11	10.66	9.33	10.29	8.94	0.00	
XOO0941	<i>leuA</i>	2-isopropylmalate synthase	0.69	0.59	0.62	0.85	9.40	8.81	11.59	10.97	10.94	10.09	0.00	
XOO0945	<i>ilvG</i>	acetolactate synthase 2 catalytic subunit	-0.54	-0.62	-0.38	-0.63	9.49	10.11	10.26	10.63	10.26	10.89	0.00	
XOO0947	<i>thiC</i>	thiamine biosynthesis protein ThiC	1.73	1.71	1.64	1.85	9.68	7.97	10.60	8.95	10.24	8.38	0.00	
XOO0948	-	hypothetical protein	0.00	0.01	0.05	-0.07	9.38	9.37	10.28	10.23	9.23	9.30	0.00	
XOO0949	-	transcriptional regulator	1.69	0.94	2.97	1.15	9.14	8.21	7.27	4.29	9.06	7.91	0.00	
XOO0950	<i>btuB</i>	TonB-dependent receptor	2.46	2.47	2.38	2.52	14.44	11.97	15.19	12.80	14.34	11.82	0.00	
XOO0951	-	response regulator	2.11	1.64	1.52	3.15	9.69	8.04	10.18	8.65	7.06	3.91	0.00	
XOO0952	<i>ppa</i>	inorganic pyrophosphatase	0.40	0.52	0.33	0.34	10.60	10.09	12.25	11.92	11.78	11.44	0.00	
XOO0953	-	hypothetical protein	#DIV/0!				3.13	NA	2.81	NA	2.12	NA	0.00	
XOO0955	-	H <sup>+</sup> translocating pyrophosphate synthase	3.24	3.24	-	-	5.71	2.48	2.88	NA	3.08	NA	0.00	
XOO0957	-	H <sup>+</sup> translocating pyrophosphate synthase	-0.18	-0.09	-0.28	-0.18	12.28	12.37	13.02	13.31	12.56	12.74	0.00	
XOO0958	-	hypothetical protein	-1.21	-1.22	-1.17	-1.24	8.96	10.17	9.99	11.16	9.83	11.07	0.00	
XOO0962	<i>pfkA</i>	6-phosphofructokinase	1.68	2.22	1.78	1.04	7.28	5.06	8.55	6.77	8.32	7.29	0.00	
XOO0963	<i>adk</i>	adenylate kinase	0.75	0.78	0.73	0.73	10.94	10.16	11.90	11.17	11.42	10.69	0.00	
XOO0964	<i>mpl</i>	UDP-N-acetylmuramate-L-alanine ligase	1.11	0.93	0.90	1.51	7.74	6.81	8.91	8.02	8.35	6.84	0.00	
XOO0965	-	hypothetical protein	0.33	0.30	0.19	0.48	9.31	9.00	5.37	5.18	9.59	9.11	0.00	
XOO0966	-	hypothetical protein	0.63	0.84	0.56	0.48	12.61	11.76	13.63	13.07	12.85	12.36	0.00	
XOO0970	<i>gst</i>	glutathione S-transferase	2.66	2.66	-	-	4.87	NA	6.07	3.41	6.34	NA	0.00	
XOO0971	<i>mdh</i>	malate dehydrogenase	0.66	0.89	0.53	0.56	8.90	8.01	11.03	10.50	10.74	10.18	0.00	
XOO0972	<i>ppiB</i>	peptidyl-prolyl cis-trans isomerase	-0.28	-0.11	-0.30	-0.43	10.41	10.52	12.28	12.58	12.00	12.43	0.00	
XOO0973	<i>typA</i>	GTP-binding elongation factor protein	0.21	0.16	0.08	0.38	11.48	11.31	12.97	12.89	12.29	11.91	0.00	
XOO0974	-	hypothetical protein	-0.69	-1.07	-0.33	-0.65	7.30	8.37	8.51	8.84	7.69	8.34	0.00	
XOO0975	<i>getAX</i>	Glu-tRNAGln amidotransferase A subunit	1.39	3.24	0.32	0.62	7.48	4.23	10.23	9.92	10.06	9.44	0.00	
XOO0978	<i>cirA</i>	colicin I receptor	0.39	0.43	0.21	0.54	11.17	10.74	12.57	12.37	11.90	11.36	0.00	
XOO0979	<i>dsbB</i>	disulfide bond formation protein B	1.39	0.92	1.79	1.45	9.63	8.71	7.11	5.31	10.61	9.16	0.00	
XOO0986	-	hypothetical protein	0.19	0.17	0.14	0.24	13.54	13.37	13.66	13.51	13.33	13.09	0.00	
XOO1002	-	pseudouridylate synthase	1.44	1.60	1.62	1.11	8.10	6.51	8.19	6.57	8.52	7.41	0.00	
XOO1004	-	hypothetical protein	1.34	0.19	3.47	0.37	8.54	8.36	7.01	3.54	7.31	6.93	0.00	
XOO1014	-	hypothetical protein	-1.23	-1.48	-1.02	-1.18	8.15	9.62	9.90	10.92	9.65	10.82	0.00	
XOO1018	<i>glpQ</i>	glycerophosphodiester phosphodiesterase	2.91	-	0.96	4.86	4.91	NA	7.43	6.48	7.42	2.56	0.00	
XOO1024	<i>icd</i>	isocitrate dehydrogenase	0.83	1.02	0.78	0.69	11.47	10.45	12.61	11.83	12.76	12.07	0.00	
XOO1025	-	hypothetical protein	-0.29	-0.29	-0.18	-0.39	14.55	14.84	15.29	15.46	14.92	15.32	0.00	
XOO1030	-	DNA replication protein	1.44	2.07	0.97	1.29	7.51	5.44	8.00	7.03	4.22	2.92	0.00	
XOO1032	<i>tig</i>	trigger factor	0.60	0.75	0.34	0.72	11.64	10.88	6.82	6.48	12.53	11.82	0.00	
XOO1033	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit	0.86	0.64	1.11	0.82	12.55	11.91	11.93	10.82	12.79	11.97	0.00	
XOO1034	<i>clpX</i>	ATP-dependent protease ATP-binding subunit ClpX	1.18	1.19	1.02	1.32	12.80	11.61	13.47	12.44	12.85	11.54	0.00	
XOO1035	<i>lon</i>	ATP-dependent serine proteinase La	0.12	0.06	0.09	0.23	11.16	11.10	11.91	11.82	11.21	10.98	0.00	
XOO1036	<i>hupB</i>	histone-like protein	0.94	0.95	0.77	1.10	15.14	14.19	15.60	14.82	15.29	14.19	0.00	
XOO1037	<i>ppiD</i>	peptidyl-prolyl cis-trans isomerase	-1.07	-1.23	-1.04	-0.92	11.66	12.88	12.70	13.74	12.43	13.36	0.00	
XOO1038	<i>dnlR</i>	murein hydrolase D	-0.31	-0.17	-0.38	-0.37	8.03	8.20	9.77	10.15	9.73	10.10	0.00	
XOO1040	-	hypothetical protein	0.49	0.41	0.54	0.53	9.84	9.43	10.58	10.04	10.48	9.95	0.00	
XOO1041	<i>rnhA</i>	ribonuclease H	-0.35	-0.33	-0.22	-0.49	11.13	11.45	11.65	11.87	11.46	11.95	0.00	
XOO1042	<i>dnaQ</i>	DNA polymerase III subunit epsilon	0.71	0.85	0.60	0.69	9.38	8.53	10.67	10.08	10.15	9.46	0.00	
XOO1051	-	hypothetical protein	2.01	2.01	2.01	2.01	7.79	5.78	7.42	5.41	8.74	6.73	0.00	
XOO1054	-	integrase	1.74	-	2.57	0.90	2.40	NA	5.34	2.77	4.39	3.49	0.00	
XOO1055	-	hypothetical protein	2.30	0.71	1.67	4.52	7.48	6.77	8.39	6.72	8.33	3.81	0.00	
XOO1056	<i>opsX</i>	saccharide biosynthesis regulatory protein	2.19	2.30	2.04	2.24	8.91	6.61	9.24	7.21	8.54	6.30	0.00	
XOO1057	-	3-deoxy-D-manno-octulonic-acid kinase	0.27	0.36	0.10	0.34	10.51	10.15	11.23	11.13	10.80	10.46	0.00	
XOO1058	-	hypothetical protein	1.00	2.08	0.42	0.49	7.84	5.76	9.32	8.90	8.66	8.17	0.00	
XOO1059	<i>moaA</i>	mobdenum cofactor biosynthesis protein A	-0.37	-0.94	-0.07	-0.11	8.64	9.58	8.42	8.48	7.26	7.37	0.00	
XOO1060	-	hypothetical protein	-1.95	-	-3.93	0.03	4.29	NA	5.43	9.36	7.01	6.99	0.00	
XOO1061	<i>moaC</i>	mobdenum cofactor biosynthesis protein MoaC	-1.21	-1.16	-1.09	-1.37	8.29	9.45	9.40	10.49	8.56	9.93	0.00	
XOO1063	<i>moaE</i>	mobdopterin-converting factor subunit 2	-0.25	0.51	-0.08	-1.20	7.31	6.80	7.40	7.48	5.94	7.13	0.00	
XOO1064	<i>dnaX</i>	DNA polymerase III subunits gamma and tau	0.46	0.52	0.35	0.52	9.05	8.52	10.29	9.94	10.03	9.52	0.00	
XOO1066	<i>recR</i>	recombination protein RecR	-0.14	0.33	-0.39	-0.37	6.88	6.55	3.83	4.22	6.77	7.14	0.00	
XOO1067	-	histidine triad-like protein	0.24	-0.02	0.27	0.48	6.93	6.96	8.46	8.19	7.77	7.29	0.00	
XOO1068	<i>sip</i>	outer membrane protein Sip	1.03	1.04	1.02	1.05	10.93	9.90	11.73	10.71	11.54	10.49	0.00	
XOO1069	-	hypothetical protein	0.32	0.26	0.11	0.59	6.97	6.71	8.16	8.05	7.93	7.33	0.00	
XOO1070	-	hypothetical protein	2.08	3.84	-0.07	2.46	6.95	3.11	5.31	5.38	5.53	3.07	0.00	
XOO1071	<i>moxR</i>	methanol dehydrogenase regulator	3.37	-	3.46	3.28	6.00	NA	5.57	2.11	5.45	2.17	0.00	
XOO1072	-	hypothetical protein	0.96	0.44	1.28	1.15	9.23	8.79	8.85	7.57	8.27	7.12	0.00	
XOO1075	<i>def</i>	peptide deformylase	0.60	0.68	0.58	0.55	9.73	9.05	11.31	10.74	10.85	10.30	0.00	
XOO1076	<i>celS</i>	cellulase S	0.64	-	0.52	0.76	5.50	NA	7.07	6.55	6.91	6.15	0.00	
XOO1077	-	cellulase S	0.71	0.87	0.56	0.70	12.18	11.32	13.43	12.86	13.36	12.65	0.00	
XOO1078	<i>rhgB</i>	rhamnogalacturonase B	2.07	2.15	1.87	2.19	9.02	6.87	10.38	8.52	10.03	7.84	0.00	
XOO1084	-	hypothetical protein	1.18	-	3.16	0.78	-0.42	5.33	2.17	7.31	6.53	5.62	6.04	0.00
XOO1087	-	hypothetical protein	-0.11	0.27	-0.48	-0.12	4.11	3.84	8.14	8.62	7.58	7.71	0.00	
XOO1090	-	glutaredoxin-like protein	-0.66	-0.76	-0.66	-0.57	10.69	11.45	11.62	12.28	11.12	11.69	0.00	
XOO1091	<i>nodB</i>	acetylxylylan esterase	-0.92	-3.59	-0.77	1.60	4.17	7.76	6.86	7.63	4.55	2.95	0.00	
XOO1092	-	hypothetical protein	-0.29	-0.03	-0.41	-0.44	7.97	8.00	8.30	8.70	8.19	8.62	0.00	
XOO1093	-	hypothetical protein	0.23	0.01	0.22	0.47	9.36	9.35	10.16	9.94	9.16	8.69	0.00	
XOO1096	-	hypothetical protein	1.31	-	-0.44	3.07	1.66	NA	5.00	5.44	6.09	3.02	0.00	
XOO1097	<i>nonF</i>	NonF-like protein	-1.65	-1.98	-0.98	-2.00	5.42	7.40	8.21	9.19	7.22	9.22	0.00	
XOO1098	-	amylosucrase or alpha amylase	-0.10	-0.20	0.00	2.75	NA	7.73	7.93</td					

XOO1111	<i>mocA</i>	rhizopine catabolism protein mocA	2.33	3.34	1.33	2.92	NA	7.02	3.68	5.12	3.79	0.00	
XOO1112	<i>ybhD</i>	transcriptional regulator	-0.42	-0.48	-0.37	6.01	NA	7.05	7.52	6.73	7.10	0.00	
XOO1113	-	hypothetical protein	-0.29	-0.80	0.23	2.40	NA	5.13	5.93	5.54	5.31	0.00	
XOO1114	<i>cit1</i>	citrate carrier protein	0.20	0.32	0.12	0.17	9.36	9.04	10.19	10.08	9.57	9.41	0.00
XOO1115	-	sensor histidine kinase	1.22	2.83	-0.47	1.29	5.72	2.89	7.57	8.03	6.96	5.68	0.00
XOO1116	<i>oprO</i>	polyphosphate-selective porin O	-0.67	-0.40	0.29	-1.92	7.88	8.27	8.53	8.24	6.03	7.95	0.00
XOO1117	<i>dctA</i>	C4-dicarboxylate transporter DctA	-0.48	-0.49	-0.18	-0.75	7.00	7.49	7.82	8.01	7.25	8.01	0.00
XOO1118	<i>maeB</i>	malic enzyme	-0.47	-0.31	-0.38	-0.71	9.31	9.61	9.97	10.35	9.63	10.34	0.00
XOO1123	<i>thiE</i>	thiamine-phosphate pyrophosphorylase	0.18	-0.01	0.15	0.40	10.93	10.94	11.18	11.03	10.50	10.10	0.00
XOO1125	-	hypothetical protein	-0.64	-0.24	-0.66	-1.04	3.36	3.60	8.93	9.59	8.11	9.15	0.00
XOO1126	-	hypothetical protein	0.13	0.22	0.11	0.07	8.12	7.90	9.69	9.58	9.17	9.10	0.00
XOO1128	-	hypothetical protein	-0.85	-0.87	-0.78	-0.89	8.78	9.66	9.94	10.72	9.76	10.65	0.00
XOO1129	-	hypothetical protein	-1.09	-1.37	-0.75	-1.14	7.25	8.62	8.56	9.31	8.17	9.31	0.00
XOO1131	-	hypothetical protein	0.24	0.23	0.24	0.24	10.68	10.45	12.03	11.79	11.68	11.44	0.00
XOO1132	-	hypothetical protein	-1.18	-1.25	-1.05	-1.25	7.16	8.40	8.06	9.11	7.61	8.85	0.00
XOO1133	<i>pepP</i>	aminopeptidase	-0.44	-0.53	-0.26	-0.54	8.56	9.09	10.03	10.30	9.58	10.11	0.00
XOO1138	-	hypothetical protein	1.48	1.30	1.92	1.21	8.57	7.27	9.21	7.29	8.95	7.74	0.00
XOO1139	-	hypothetical protein	1.91	1.31	1.46	2.95	10.20	8.89	10.77	9.31	9.67	6.72	0.00
XOO1140	-	coproporphyrinogen III oxidase	0.15	2.85	-0.98	-1.42	2.20	-0.65	7.96	8.94	7.29	8.71	0.00
XOO1141	-	deoxyribonucleotide triphosphate pyrophosphatase	-0.69	-0.14	-0.86	-1.07	7.55	7.70	8.93	9.79	8.34	9.42	0.00
XOO1142	-	hypothetical protein	-0.89	0.27	-1.24	-1.71	5.80	5.53	8.11	9.35	7.60	9.30	0.00
XOO1144	-	hypothetical protein	0.04	0.02	0.03	0.07	9.88	9.86	10.92	10.90	10.19	10.11	0.00
XOO1145	<i>gmk</i>	guanylate kinase	-0.50	-0.44	-0.52	-0.55	9.71	10.15	10.77	11.29	10.47	11.02	0.00
XOO1149	<i>spot</i>	pentaphosphate guanosine-3'-pyrophosphohydrolase	0.16	0.21	0.04	0.24	8.87	8.66	10.49	10.45	10.32	10.08	0.00
XOO1150	<i>yigF</i>	translation initiation inhibitor	-0.53	-0.84	-0.37	-0.38	8.17	9.01	9.58	9.95	9.31	9.70	0.00
XOO1151	<i>recG</i>	ATP-dependent DNA helicase RecG	1.51	0.81	2.21	2.66	1.85	6.07	3.86	NA	NA	0.00	
XOO1152	-	inosine-uridine preferring nucleoside hydrolase	0.08	-0.16	0.05	0.34	8.21	8.37	9.46	9.41	8.74	8.40	0.00
XOO1153	<i>rpmE2</i>	50S ribosomal protein L31	-0.43	-0.33	-0.42	-0.53	13.33	13.66	14.13	14.55	13.74	14.27	0.00
XOO1154	<i>gltA</i>	type II citrate synthase	0.11	-0.01	0.13	0.20	10.75	10.76	11.22	11.09	10.85	10.65	0.00
XOO1155	-	hypothetical protein	#DIV/0!				2.60	NA	NA	2.73	NA	0.01	
XOO1156	<i>mrcA</i>	penicillin-binding protein 1A	-0.05	0.44	-0.27	-0.31	7.43	6.99	9.30	9.57	8.96	9.28	0.00
XOO1157	<i>pilM</i>	fimbrial assembly membrane protein	0.16	0.16	0.21	0.10	4.02	3.85	10.18	9.98	9.92	9.83	0.00
XOO1158	<i>pilN</i>	fimbrial assembly membrane protein	0.57	0.69	0.51	0.52	9.73	9.04	11.40	10.89	11.07	10.55	0.00
XOO1159	<i>pilO</i>	fimbrial assembly membrane protein	0.31	0.23	0.51	0.19	11.74	11.51	12.65	12.14	12.38	12.19	0.00
XOO1160	<i>pilP</i>	fimbrial assembly protein	0.32	0.32	0.36	0.27	11.48	11.16	12.71	12.35	12.48	12.21	0.00
XOO1161	<i>pilQ</i>	fimbrial assembly protein	0.69	0.75	0.66	0.68	10.39	9.65	11.50	10.84	11.56	10.88	0.00
XOO1167	<i>moxR</i>	methanol dehydrogenase regulatory protein	-0.44	-0.37	-0.49	-0.46	7.22	7.59	9.22	9.70	8.41	8.86	0.00
XOO1168	-	hypothetical protein	-0.33	-0.31	-0.20	-0.48	8.15	8.46	8.69	8.89	8.22	8.70	0.00
XOO1169	-	hypothetical protein	-0.35	-0.11	-0.51	-0.44	7.97	8.08	9.49	9.99	9.20	9.64	0.00
XOO1170	-	hypothetical protein	-0.54	-0.45	-0.54	-0.63	8.56	9.02	9.09	9.64	8.12	8.74	0.00
XOO1171	-	hypothetical protein	-0.34	-0.24	-0.37	-0.39	10.39	10.63	10.72	11.10	10.48	10.87	0.00
XOO1174	-	hypothetical protein	2.60	2.60	2.60	3.58	NA	3.66	NA	5.47	2.88	0.00	
XOO1175	<i>gltP</i>	proton glutamate symport protein	0.01	0.34	-0.11	-0.19	9.26	8.92	11.06	11.17	10.80	10.99	0.00
XOO1176	<i>tktA</i>	transketolase	-0.68	-1.00	-0.32	-0.73	6.03	7.03	4.37	4.69	7.74	8.46	0.00
XOO1177	<i>fhuE</i>	outer membrane receptor for ferric iron uptake	#DIV/0!				1.50	NA	3.02	NA	NA	0.03	
XOO1178	-	hypothetical protein	-0.77	-0.89	-0.60	-0.84	7.52	8.41	8.88	9.48	8.54	9.37	0.00
XOO1182	-	hypothetical protein	0.14	0.14	0.14	2.50	NA	2.78	2.64	2.70	NA	0.00	
XOO1183	-	hypothetical protein	1.30	1.30	1.30	4.77	NA	2.78	1.48	2.54	NA	0.00	
XOO1184	-	long-chain acyl-CoA synthetase	#DIV/0!				1.50	NA	5.05	NA	3.83	NA	0.01
XOO1185	-	hypothetical protein	-0.10	-0.59	-0.61	0.92	7.33	7.93	6.68	7.29	6.34	5.42	0.00
XOO1186	-	short chain dehydrogenase	1.39	-0.05	1.66	2.56	2.32	2.37	8.40	6.74	6.02	3.46	0.00
XOO1187	<i>pflu4968</i>	hypothetical protein	#DIV/0!				5.50	NA	2.79	NA	NA	0.01	
XOO1188	-	response regulator	3.09	3.09	2.32	NA	6.18	3.09	2.26	NA	0.00		
XOO1189	-	Signal transduction histidine kinase	0.31	0.32	0.34	0.27	8.75	8.43	9.39	9.05	9.15	8.88	0.00
XOO1190	<i>blal</i>	Blal family transcriptional regulator	1.76	3.37	-0.26	2.18	6.58	3.21	7.43	7.69	6.31	4.13	0.00
XOO1191	-	TonB-like protein	0.73	-0.05	0.34	1.90	6.82	6.88	7.42	7.08	5.27	3.37	0.00
XOO1192	-	hypothetical protein	-2.20	-3.17	-1.22	2.92	NA	4.35	7.53	1.40	2.63	0.00	
XOO1193	<i>modC</i>	molybdate ABC transporter ATP-binding protein	0.70	2.39	-0.48	0.18	5.65	3.27	3.25	3.72	6.98	6.80	0.00
XOO1194	<i>modB</i>	molybdate ABC transporter permease	-0.52	-0.59	-0.61	-0.36	7.59	8.18	8.62	9.23	7.87	8.23	0.00
XOO1195	<i>modA</i>	molybdate-binding periplasmic protein; permease	-0.42	-0.35	-0.30	-0.61	7.86	8.21	9.09	9.39	8.56	9.17	0.00
XOO1197	-	endonuclease	-0.17	-0.17	-0.07	-0.28	10.58	10.75	11.21	11.28	11.24	11.52	0.00
XOO1201	<i>omp21</i>	hypothetical protein	#DIV/0!				3.99	NA	1.85	NA	3.94	NA	0.00
XOO1202	<i>ompW</i>	outer membrane protein W	-1.13	-0.89	-1.13	-1.38	7.41	8.29	7.86	8.98	7.30	8.68	0.00
XOO1203	<i>gapA</i>	glyceraldehyde-3-phosphate dehydrogenase	0.43	0.60	0.37	0.32	8.44	7.84	10.43	10.06	9.99	9.67	0.00
XOO1207	<i>colS</i>	two-component system sensor protein	-2.23	-3.33	-1.63	-1.71	5.21	8.54	7.43	9.06	7.01	8.72	0.00
XOO1208	<i>colR</i>	two-component system regulatory protein	-1.56	-1.66	-1.41	-1.60	8.59	10.24	10.01	11.43	9.61	11.21	0.00
XOO1209	-	hypothetical protein	-1.81	-2.14	-1.66	-1.64	6.81	8.94	8.20	9.86	7.05	8.69	0.00
XOO1210	<i>rimK</i>	ribosomal protein S6 modification protein	0.87	1.83	0.70	0.09	8.70	6.87	7.70	7.00	6.45	6.36	0.00
XOO1212	-	hypothetical protein	-0.29	-0.52	-0.54	0.18	5.65	6.17	7.52	8.06	7.15	6.97	0.00
XOO1213	-	serine/threonine protein kinase	-1.49	-1.42	-2.95	-0.10	5.71	7.13	3.72	6.67	3.71	3.81	0.00
XOO1216	-	hypothetical protein	-0.79	-0.87	-0.93	-0.58	2.04	2.91	2.68	3.60	3.11	3.70	0.00
XOO1217	-	hypothetical protein	1.08	1.08	NA	NA	NA	NA	NA	4.85	3.77	0.00	
XOO1220	-	hydrolase	0.69	-0.02	2.09	-0.01	6.77	6.79	5.83	3.74	3.40	3.41	0.00
XOO1226	<i>tdcF</i>	hypothetical protein	-0.19	-0.41	-0.31	0.13	8.64	9.05	10.24	10.55	9.02	8.88	0.00
XOO1229	<i>az1</i>	electron transfer protein azurin I	-0.52	-0.15	-0.68	-0.73	7.23	7.38	6.57	7.25	7.26	7.99	0.00
XOO1232	<i>hemL</i>	glutamate-1-semialdehyde aminotransferase	0.62	2.12	-0.76	0.51	5.37	3.25	6.67	7.43	3.71	3.20	0.00
XOO1233	-	Oar protein	-0.59	-0.87	-0.26	-0.65	8.28	9.15	9.67	9.92	8.88	9.53	0.00
XOO1236	-	hypothetical protein	0.14	0.27	0.02	0.15	9.00	8.73	9.99	9.97	9.43	9.28	0.00
XOO1242	<i>hemE</i>	uroporphyrinogen decarboxylase	-0.81	-1.07	-0.66	-0.70	8.75	9.82	9.08	9.74	8.44	9.14	0.00
XOO1243	<i>aroB</i>	3-dehydroquinate synthase	-0.39	-1.02	-1.16	1.01	6.98	8.00	7.21	8.37	5.16	4.15	0.00
XOO1245	<i>pdxH</i>	pyridoxamine 5'-phosphate oxidase	0.16	0.40	0.14	-0.06	9.21	8.81	10.47	10.33	9.98	10.04	0.00
XOO1246	-	hypothetical protein	-0.81	-0.77	-0.88	-0.77	8.06	8.83	9.91	10.78	9.40	10.17	0.00
XOO1247	-	hypothetical protein	0.85	1.86	-0.85	1.55	5.16	3.30	7.04	7.89	7.6		

XOO1260	<i>fecA</i>	TonB-dependent receptor	2.12	3.35	0.78	2.23	6.01	2.66	8.79	8.01	6.61	4.38	0.00
XOO1261	-	hypothetical protein	-1.27		-1.27		5.14	NA	4.36	5.63	NA	NA	0.00
XOO1262	-	hypothetical protein	1.34	1.36	1.71	0.94	7.49	6.13	8.91	7.20	8.84	7.91	0.00
XOO1263	<i>pnaA</i>	tryptophan halogenase	1.89	4.42	0.61	0.63	7.43	3.01	7.69	7.08	7.64	7.00	0.00
XOO1264	-	hydrolase	0.96	0.43	1.26	1.19	7.65	7.23	8.35	4.61	4.30	2.57	4.09
XOO1265	-	hypothetical protein	0.68	-0.77	1.73	1.08	3.85					3.01	0.00
XOO1266	-	endoproteinase ArgC					#DIV/0!		2.35	NA	2.00	NA	4.75
XOO1267	-	amino acid transporter	-0.85	-0.52	-0.40	-1.64	7.97	8.49	8.17	8.58	6.08	7.72	0.00
XOO1268	<i>ahyR</i>	AhyR/AsaR family transcriptional regulator	0.99	-0.64	-0.19	3.79	7.50	8.15	4.55	4.73	8.39	4.60	0.00
XOO1269	-	proline imino-peptidase	1.14	0.84	0.54	2.04	5.74	4.90	6.02	5.48	5.14	3.09	0.00
XOO1270	<i>gabP</i>	amino acid transporter	0.46	0.47	-0.18	1.10	2.84	2.37	3.31	3.49	2.98	1.88	0.00
XOO1273	-	quinol oxidase subunit I	-1.13	0.50	-3.62	-0.27	6.57	6.07	1.40	5.02	4.27	4.54	0.00
XOO1274	<i>qxtB</i>	quinol oxidase subunit II	-0.41	-0.09	0.21	-1.35	9.08	9.18	9.02	8.81	7.27	8.62	0.00
XOO1275	-	hypothetical protein	0.46	1.90	0.04	-0.55	4.73	2.82	7.92	7.88	6.01	6.57	0.00
XOO1276	<i>mgtE</i>	Mg <sup>++</sup> transporter	-0.32	-1.82	-0.22	1.07	5.56	7.38	7.79	8.01	7.98	6.91	0.00
XOO1277	<i>ptsI</i>	phosphotransferase system enzyme I	-0.10	-0.08	-0.15	-0.06	8.67	8.76	9.93	10.08	9.33	9.39	0.00
XOO1278	<i>ptsH</i>	phosphotransferase system HPr enzyme	-0.19	-0.06	-0.35	-0.16	7.87	7.93	8.72	9.07	8.34	8.51	0.00
XOO1279	-	hypothetical protein	-0.04	-0.08	-0.09	0.06	8.04	8.13	9.73	9.82	9.53	9.46	0.00
XOO1280	-	hypothetical protein	1.06	-0.74	0.37	3.55	4.99	5.73	8.44	8.06	7.04	3.49	0.00
XOO1281	<i>ptsK</i>	HPr kinase/phosphorylase	0.24	0.53	0.07	0.13	7.50	6.97	5.44	5.37	9.35	9.21	0.00
XOO1282	<i>ptsN</i>	nitrogen regulatory IIA protein	-0.66	-0.58	-0.75	-0.64	9.78	10.37	9.79	10.55	9.59	10.23	0.00
XOO1284	<i>rpoN</i>	RNA polymerase factor sigma-54	0.14	-0.48	0.88	0.02	7.46	7.94	7.79	6.91	3.47	3.45	0.00
XOO1285	<i>yhbG</i>	ABC transporter ATP-binding protein	0.34	-0.05	-0.68	1.75	8.42	8.47	8.40	9.08	8.75	7.00	0.00
XOO1286	-	hypothetical protein	-0.48	-0.53	-0.45	-0.46	9.40	9.93	11.30	11.75	10.98	11.44	0.00
XOO1287	-	hypothetical protein	-0.57	0.34	-0.80	-1.26	7.39	7.04	8.64	9.44	7.90	9.16	0.00
XOO1290	<i>murA</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	-0.81	-0.58	-0.82	-1.02	8.09	8.67	9.57	10.39	9.11	10.14	0.00
XOO1291	-	hypothetical protein	0.71	0.83	0.61	0.68	14.98	14.15	15.90	15.29	15.21	14.53	0.00
XOO1292	-	hypothetical protein	-0.77	-0.91	-0.70	-0.72	9.46	10.37	11.04	11.74	10.59	11.31	0.00
XOO1294	<i>purN</i>	phosphoribosylglycinamide formyltransferase	0.68	2.49	-0.40	-0.06	5.59	3.10	3.40	3.81	5.24	5.30	0.00
XOO1295	-	hypothetical protein	0.64	-0.09	1.69	0.34	7.80	7.89	6.38	4.70	9.27	8.93	0.00
XOO1296	-	hypothetical protein	0.02	-0.32	-0.89	1.28	7.12	7.45	6.47	7.36	5.04	3.76	0.00
XOO1298	-	hypothetical protein	1.31	0.11	0.33	3.50	8.47	8.36	8.34	8.01	7.79	4.29	0.00
XOO1299	<i>perM</i>	permease	-0.05	-0.27	-0.02	0.12	7.75	8.02	9.63	9.64	9.29	9.17	0.00
XOO1303	-	hypothetical protein	-0.89	-1.88	-0.23	-0.56	6.63	8.51	7.78	8.01	8.22	8.78	0.00
XOO1304	-	hypothetical protein	-0.31	-0.35	-0.17	-0.40	8.50	8.85	10.24	10.40	10.06	10.47	0.00
XOO1308	<i>dapE</i>	succinyl-diaminopimelate desuccinylase	-1.32	-1.12	-2.11	-0.72	5.56	6.68	5.73	7.84	3.23	3.95	0.00
XOO1309	<i>comEA</i>	DNA transport competence protein	0.03	0.23	-0.03	-0.11	15.99	15.76	15.99	16.02	15.99	16.11	0.00
XOO1317	-	alpha-L-arabinofuranosidase	0.23	0.06	0.24	0.39	8.38	8.32	4.95	4.72	8.63	8.23	0.00
XOO1318	<i>galM</i>	aldose 1-epimerase	0.46	1.24	0.26	-0.12	6.90	5.66	4.40	4.14	8.73	8.85	0.00
XOO1319	-	hypothetical protein	0.24	0.13	0.27	0.32	11.34	11.21	11.52	11.25	10.70	10.38	0.00
XOO1321	<i>ffh</i>	signal recognition particle protein	0.17	0.13	0.16	0.22	10.44	10.31	11.05	10.89	10.15	9.93	0.00
XOO1322	-	hypothetical protein	-0.58	-1.43	-0.27	-0.05	6.38	7.81	7.63	7.90	4.07	4.12	0.00
XOO1323	-	2-nitropropane dioxygenase	1.36	0.23	0.57	3.27	6.35	6.13	6.59	6.02	6.96	3.70	0.00
XOO1325	<i>rpsP</i>	30S ribosomal protein S16	-0.22	-0.21	-0.21	-0.24	13.74	13.94	15.12	15.33	14.67	14.91	0.00
XOO1326	<i>rimM</i>	16S rRNA-processing protein RimM	-1.99	-2.02	-2.00	-1.95	10.22	12.24	11.21	13.21	10.95	12.90	0.00
XOO1327	<i>trmD</i>	tRNA (guanine-N(1))-methyltransferase	-0.92	-1.04	-0.91	-0.81	9.76	10.80	11.38	12.29	10.85	11.66	0.00
XOO1328	<i>rplS</i>	50S ribosomal protein L19	0.07	0.08	-0.02	0.15	11.72	11.64	12.83	12.85	12.23	12.08	0.00
XOO1329	-	hypothetical protein	0.11	0.14	-0.01	0.22	7.45	7.31	8.19	8.20	8.19	7.97	0.00
XOO1330	<i>hsfR</i>	heat shock protein 15-like protein	-0.93	-0.47	-0.49	-1.83	7.00	7.46	8.25	8.74	6.73	8.56	0.00
XOO1335	-	glutathione transferase	2.72		1.55	3.88	5.68	NA	4.92	3.37	5.79	1.91	0.00
XOO1337	<i>cipB</i>	ATP-dependent Clp protease subunit	0.18	-0.01	0.25	0.31	8.85	8.85	9.56	9.31	9.32	9.01	0.00
XOO1338	-	hypothetical protein	1.42	1.86	0.99	5.44			7.93	6.94	5.91	NA	0.00
XOO1345	<i>btuB</i>	outer membrane receptor for transport of vitamin B	3.27		3.27		1.95	NA	6.22	2.96	3.82	NA	0.00
XOO1347	-	hypothetical protein	1.93	3.02	0.22	2.56	6.31	3.29	6.98	6.76	5.64	3.08	0.00
XOO1348	-	hypothetical protein	0.95	0.11	1.69	1.05	5.67	5.56	7.77	6.08	8.01	6.96	0.00
XOO1349	<i>btuR</i>	cob(I)alamin adenosyltransferase	0.80	0.93	0.68	4.67	NA		8.69	7.77	7.82	7.14	0.00
XOO1350	<i>cobU</i>	adenosylcobinamide kinase	1.03	2.40	0.62	0.07	6.11	3.71	9.10	8.48	8.30	8.23	0.00
XOO1351	<i>cobT</i>	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltrans-	-1.29	-0.02	-0.84	-3.01	3.27	3.29	6.91	7.75	5.11	8.12	0.00
XOO1353	<i>cobS</i>	cobalamin synthase	0.23		0.23		2.04	NA	2.16	1.93	2.23	NA	0.00
XOO1354	<i>lysA</i>	diaminopimelate decarboxylase	0.29		0.29		2.52	NA	3.13	2.84	2.12	NA	0.00
XOO1355	<i>iucA</i>	iron transporter	1.58	1.28	1.42	2.05	7.69	6.41	9.25	7.83	8.55	6.50	0.00
XOO1356	<i>yceE</i>	transporter	0.15	0.45	-0.24	0.25	7.75	7.30	7.17	7.41	3.61	3.36	0.00
XOO1358	-	hypothetical protein	5.21	5.61	4.81		8.15	2.54	8.51	3.69	7.73	NA	0.00
XOO1359	<i>fecA</i>	citrate-dependent iron transporter	4.36	3.37	3.46	6.24	10.11	6.75	10.61	7.15	9.96	3.72	0.00
XOO1360	<i>mphE</i>	4-hydroxy-2-oxovalerate aldolase	4.22	3.32	3.86	5.47	9.40	6.08	9.90	6.04	9.04	3.57	0.00
XOO1365	-	hypothetical protein	0.19		0.19		2.12	NA	2.75	2.56	2.43	NA	0.00
XOO1367	<i>yheS</i>	ABC transporter ATP-binding protein	-0.67	-0.62	-1.15	-0.23	6.82	7.44	7.42	8.57	7.33	7.56	0.00
XOO1368	-	hypothetical protein	-0.89	-0.13	-1.38	-1.17	2.66	2.79	6.96	8.34	6.54	7.70	0.00
XOO1369	<i>ampR</i>	transcriptional activator ampR family	2.09		2.09		2.82	NA	7.78	5.69	7.02	NA	0.00
XOO1370	<i>bla</i>	beta lactamase	2.75		2.75	2.58	NA	5.15	NA	5.02	2.27	0.00	
XOO1371	<i>xynB</i>	xylanase	2.07	0.12	3.41	2.68	5.90	5.78	6.56	3.15	5.48	2.79	0.00
XOO1376	-	hypothetical protein	-0.74	0.22	-0.94	-1.51	7.68	7.46	6.98	7.92	7.50	9.01	0.00
XOO1379	<i>hrgG</i>	HrpG protein	0.82	0.25	1.13	1.09	7.60	7.35	8.62	7.49	7.34	6.25	0.00
XOO1380	<i>hpxXct</i>	HrpX protein	2.20		2.38	2.02	NA		5.55	3.17	5.11	3.09	0.00
XOO1381	<i>hsp90xc</i>	heat shock protein 90	-0.56	1.64	-1.48	-1.82	5.81	4.17	6.55	8.03	6.69	8.51	0.00
XOO1382	-	hypothetical protein	-0.09	-0.02	-0.27	0.03	8.87	8.89	10.23	10.50	9.48	9.45	0.00
XOO1387	-	glutamine synthetase	-1.33	-1.64	-1.47	-0.88	6.33	7.98	7.45	8.92	7.48	8.36	0.00
XOO1388	-	homoserine O-succinyltransferase	-1.11	-1.17	-0.99	-1.17	9.90	11.07	10.35	11.33	10.35	11.52	0.00
XOO1389	<i>rtxC</i>	protein RtxC	-0.68	-0.91	-0.56	-0.57	8.04	8.95	9.12	9.68	8.19	8.76	0.00
XOO1390	<i>rtxA</i>	protein RtxA	-0.26	-0.32	-0.33	-0.13	7.01	7.33	9.28	9.61	8.34	8.47	0.00
XOO1391	-	hypothetical protein	-0.74	-0.26	-1.13	-0.83	3.52	3.78	7.77	8.90	6.87	7.70	0.00
XOO1402	<i>nifS</i>	cysteine desulfurase	0.22	0.24	0.25	0.15	11.83	11.58	12.31	12.05	11.19	11.03	0.00
XOO1403	<i>ynhC</i>	ABC transporter permease	1.04	-0.42	0.33	3.23	7.32	7.74					

XOO1416	<i>proC</i>	pyrroline-5-carboxylate reductase	0.29	0.94	0.29	-0.35	7.66	6.72	7.87	7.58	6.26	6.62	0.00
XOO1417	-	hypothetical protein	1.89	2.23	1.61	1.83	5.60	3.37	6.92	5.31	5.09	3.26	0.00
XOO1418	<i>pilT</i>	twitching motility protein	-0.10	-0.33	0.01	0.00	9.70	10.03	10.33	10.32	10.31	10.31	0.00
XOO1419	<i>pilU</i>	twitching motility protein	2.15		1.19	3.10	5.07	NA	6.98	5.78	6.69	3.59	0.00
XOO1423	<i>tag</i>	DNA-3-methyladenine glycosylase I	0.85	2.85	0.24	-0.54	7.10	4.25	6.15	5.91	2.12	2.66	0.00
XOO1424	-	hypothetical protein	1.57		1.57		1.85	NA	5.78	4.21	NA	NA	0.00
XOO1425	<i>algH</i>	hypothetical protein	-0.32	-0.18	-0.29	-0.48	8.86	9.04	10.06	10.35	9.48	9.95	0.00
XOO1427	<i>pyrB</i>	aspartate carbamoyltransferase	-0.94	-1.06	-0.84	-0.93	8.86	9.92	9.87	10.71	9.70	10.63	0.00
XOO1428	<i>osmC</i>	osmotically inducible protein	-0.60	-0.54	-0.72	-0.53	8.54	9.07	9.47	10.19	9.01	9.55	0.00
XOO1429	-	hypothetical protein	-0.26	-0.39	-0.16	-0.25	7.30	7.68	8.94	9.10	8.49	8.74	0.00
XOO1430	-	hypothetical protein	1.82	2.86	0.82	1.79	7.76	4.90	8.42	7.60	7.49	5.70	0.00
XOO1432	-	hypothetical protein	3.08		3.08		2.76	NA	5.29	2.21	5.13	NA	0.00
XOO1433	<i>lysA</i>	bifunctional aspartate kinase/diaminopimelate decarboxylase	-0.45	-0.35	-0.59	-0.40	8.86	9.20	9.80	10.39	9.53	9.93	0.00
XOO1434	-	hypothetical protein	-0.14	-0.04	-0.26	-0.12	10.63	10.67	11.51	11.77	10.57	10.69	0.00
XOO1435	-	hypothetical protein	-0.35	-0.46	-0.25	-0.34	9.98	10.45	10.38	10.63	10.27	10.61	0.00
XOO1436	<i>murD</i>	UDP-N-acetylMuramoyl-L-alanyl-D-glutamate synthetase	-1.09		-1.00	-1.18	1.95	NA	7.49	8.49	6.89	8.06	0.00
XOO1437	-	hypothetical protein	0.64		-1.27	2.56	2.04	NA	6.31	7.57	6.28	3.72	0.00
XOO1439	<i>ssb</i>	single-stranded DNA-binding protein	-0.06	0.01	-0.06	-0.13	11.17	11.16	12.58	12.64	12.23	12.37	0.00
XOO1445	-	hydrolase	-1.12	-1.63	-0.82	-0.90	6.81	8.44	9.18	10.00	8.55	9.45	0.00
XOO1446	-	hypothetical protein	-0.29	-0.28	-0.25	-0.36	8.86	9.14	9.78	10.03	9.20	9.56	0.00
XOO1447	<i>cstA</i>	carbon starvation protein A	0.53	-0.40	2.32	-0.31	6.63	7.03	6.20	3.89	6.30	6.61	0.00
XOO1448	-	pirin	-0.91	0.16	-0.85	-2.04	5.66	5.49	7.22	8.08	6.14	8.17	0.00
XOO1450	-	hypothetical protein	-0.77	-0.78	-0.66	-0.87	12.80	13.58	13.31	13.97	13.31	14.18	0.00
XOO1451	-	hypothetical protein	-0.87	-0.60	-0.88	-1.12	7.40	8.00	8.68	9.56	8.10	9.22	0.00
XOO1452	-	hypothetical protein	0.02	0.22	0.00	-0.16	7.58	7.37	9.27	9.27	8.28	8.45	0.00
XOO1456	-	hypothetical protein	1.90	4.24	-0.04	1.50	5.41	1.16	2.64	2.68	4.47	2.98	0.00
XOO1458	-	pirin	0.58		0.58		2.84	NA	3.45	2.87	NA	NA	0.00
XOO1460	<i>gpmA</i>	phosphoglyceromutase	-0.36	-0.17	-0.50	-0.42	7.23	7.40	8.63	9.14	8.48	8.90	0.00
XOO1462	-	metallopeptidase	-0.31	-1.38	0.75		1.29	2.67	4.31	3.56	4.65	NA	0.00
XOO1466	<i>cheR</i>	response regulator for chemotaxis	0.49	0.28	0.34	0.86	7.45	7.16	7.93	7.60	8.11	7.25	0.00
XOO1467	<i>vieA</i>	response regulator	1.31	0.08		2.54	5.31	5.22	4.23	NA	5.70	3.16	0.00
XOO1468	<i>cheW</i>	chemotaxis protein	-0.14	0.12	-0.04	-0.50	6.14	6.02	4.08	4.12	7.49	7.99	0.00
XOO1469	<i>mcp</i>	chemotaxis protein	#DIV/0!				NA	NA	4.81	NA	2.45	NA	0.01
XOO1470	<i>cheA</i>	chemotaxis histidine protein kinase	-0.13	0.14	-0.16	-0.36	7.86	7.72	8.78	8.94	8.03	8.39	0.00
XOO1471	-	hypothetical protein	0.26			0.26	3.04	NA	5.24	NA	2.79	2.53	0.00
XOO1472	<i>mfd</i>	transcription-repair coupling factor	-0.57	-0.67	-0.46	-0.57	7.46	8.13	8.88	9.33	8.15	8.72	0.00
XOO1473	-	hypothetical protein	-2.09	-2.25	-2.06	-1.96	8.21	10.46	9.77	11.83	9.56	11.52	0.00
XOO1474	-	hypothetical protein	0.01	0.39	-0.37	0.00	6.21	5.83	8.27	8.64	7.97	7.97	0.00
XOO1477	<i>creC</i>	two-component system sensor protein	1.35	3.95	-0.80	0.90	4.87	0.92	5.45	6.25	2.99	2.09	0.00
XOO1498	-	hypothetical protein	1.89		2.35	1.43	NA	NA	5.39	3.03	4.67	3.24	0.00
XOO1502	<i>nthA</i>	nitrilase	0.99	1.29	0.02	1.68	5.25	3.97	6.77	6.75	5.56	3.89	0.00
XOO1503	-	hypothetical protein	1.24	0.95	-0.19	2.98	5.04	4.09	2.54	2.74	5.57	2.60	0.00
XOO1504	<i>gltX</i>	glutamyl-tRNA synthetase	0.35	0.52	0.21	0.33	2.92	2.39	7.79	7.59	7.69	7.36	0.00
XOO1505	-	FUR family transcriptional regulator	0.47		1.91	-0.98	4.42	NA	7.22	5.31	5.17	6.15	0.00
XOO1509	-	hypothetical protein	1.95		1.95		4.65	NA	5.41	3.45	1.29	NA	0.00
XOO1510	<i>cspA</i>	cold-shock protein	2.20	2.33	2.09	2.20	13.65	11.33	14.77	12.68	14.38	12.18	0.00
XOO1511	<i>pcp</i>	peptidoglycan-associated outer membrane lipoprotein	-1.06	-0.92	-1.12	-1.13	6.60	7.53	7.73	8.85	6.48	7.61	0.00
XOO1512	-	hypothetical protein	-0.57	0.19	-0.86	-1.05	6.10	5.91	6.39	7.25	2.68	3.73	0.00
XOO1513	<i>moeB</i>	molybdopterin biosynthesis protein	0.02	1.00	-0.75	-0.19	4.15	3.15	7.24	7.99	7.01	7.20	0.00
XOO1514	-	hypothetical protein	0.38	-2.62	1.50	2.26	3.48	6.11	5.26	3.75	5.75	3.50	0.00
XOO1516	-	hypothetical protein	-0.27	-0.18	-0.35	-0.28	8.86	9.04	9.92	10.27	9.33	9.61	0.00
XOO1517	<i>gcdH</i>	glutaryl-CoA dehydrogenase	1.06	0.99	2.75	-0.58	7.26	6.26	6.63	3.88	7.89	8.47	0.00
XOO1523	-	asparagine synthetase	1.15	0.69	0.35	2.42	6.00	5.31	7.31	6.96	7.60	5.19	0.00
XOO1524	-	hypothetical protein	-1.71	-1.08	-3.14	-0.92	4.66	5.73	5.45	8.59	3.15	4.08	0.00
XOO1525	<i>dnaB</i>	replicative DNA helicase	0.03	0.06	-0.08	0.11	7.96	7.90	9.31	9.39	8.49	8.38	0.00
XOO1526	<i>phr</i>	photolyase	-0.70	-0.26	-0.73	-1.09	8.36	8.62	7.37	8.11	7.02	8.11	0.00
XOO1527	-	OmpA family protein	-0.80	-0.73	-0.84	-0.83	8.90	9.63	9.88	10.72	8.75	9.57	0.00
XOO1528	-	short chain dehydrogenase	-1.13	-0.96	-1.07	-1.37	9.07	10.02	9.35	10.43	9.31	10.68	0.00
XOO1530	<i>fhuA</i>	TonB-dependent receptor	#DIV/0!				2.56	NA	4.03	NA	1.58	NA	0.01
XOO1533	-	hypothetical protein	1.37	0.16	0.11	3.84	8.87	8.71	7.93	7.82	8.51	4.67	0.00
XOO1534	-	hypothetical protein	0.18	0.18	0.09	0.27	9.02	8.84	9.56	9.47	9.00	8.73	0.00
XOO1535	-	alcohol dehydrogenase	0.23	0.35	0.14	0.19	9.04	8.70	9.82	9.68	8.88	8.69	0.00
XOO1536	<i>yadQ</i>	chloride channel	-0.44	-0.54	-0.55	-0.22	9.86	10.40	10.47	11.02	9.41	9.63	0.00
XOO1539	<i>ada</i>	DNA methylation and regulatory protein	0.16		-0.53	0.85	1.29	NA	6.91	7.45	5.83	4.98	0.00
XOO1540	-	hypothetical protein	0.79		0.79		2.16	NA	4.38	3.59	3.97	NA	0.00
XOO1542	-	hypothetical protein	-3.15	-3.43	-3.17	-2.84	7.69	11.12	8.76	11.93	8.13	10.97	0.00
XOO1543	-	hypothetical protein	-1.23	-1.92	-1.12	-0.65	6.17	8.09	7.86	8.98	7.69	8.35	0.00
XOO1544	-	hypothetical protein	-0.73	-0.71	-0.60	-0.88	8.21	8.92	8.67	9.26	8.57	9.44	0.00
XOO1550	<i>deaD</i>	ATP-dependent RNA helicase	-0.04	0.01	-0.12	-0.01	8.67	8.65	9.93	10.05	9.40	9.40	0.00
XOO1551	-	hypothetical protein	1.03	2.27	0.34	0.47	6.87	4.60	6.88	6.54	5.50	5.03	0.00
XOO1552	-	pseudouridylate synthase	0.87	-0.46	2.73	0.35	8.29	8.75	7.15	4.43	8.06	7.71	0.00
XOO1554	-	hypothetical protein	-0.01	0.06	0.25	-0.34	7.80	7.73	4.66	4.41	7.07	7.41	0.00
XOO1555	<i>menG</i>	ribonuclease activity regulator protein RraA	-0.22	0.18	-0.20	-0.65	8.20	8.02	8.85	9.05	8.02	8.67	0.00
XOO1556	-	beta-lactamase	-0.65	-0.62	-0.72	-0.62	7.70	8.33	8.79	9.51	7.43	8.05	0.00
XOO1557	<i>yj094C</i>	cation:proton antiporter	0.55	0.09	0.75	0.82	4.00	3.91	8.74	7.99	8.95	8.13	0.00
XOO1558	<i>baeS</i>	two-component system sensor protein	0.73	0.28	1.54	0.38	4.33	4.05	8.22	6.68	3.56	3.18	0.00
XOO1559	<i>baeR</i>	two-component system regulatory protein	5.24	5.20	3.15	7.37	9.94	4.74	10.65	7.49	10.12	2.74	0.00
XOO1561	-	hypothetical protein	#DIV/0!				2.95	NA	2.79	NA	3.14	NA	0.00
XOO1562	<i>mexC</i>	RND efflux membrane fusion protein	1.61			1.61	3.36	NA	4.59	NA	2.95	1.35	0.00
XOO1563	<i>acr</i>	acriflavin resistance protein	1.50		0.45	2.55	NA	NA	4.20	3.74	4.88	2.33	0.00
XOO1564	-	hypothetical protein	-0.17	0.00	-0.30	-0.23	8.13	8.13	9.25	9.54	8.13	8.36	0.00
XOO1565	<i>bapA</i>	ABC transporter ATP-binding protein	0.28	-0.67	2.43	-0.92	7.76	8.44	7.20	4.77	7.78	8.70	0.00
XOO1577	-	RhsD protein	-0.49	-0.43	-0.60	-0.46	10.54	10.97	11.78	12.37	11.11	11.57	0.00
XOO1580	<i>rhsD</i>	RhsD protein	-0.43	-0.78	-0.17	-0.34	7.01	7.80	9.01	9.18	8.52	8.86	0.00
XOO1													

XOO1590	<i>fic</i>	cell filamentation protein Fic	2.11	2.69	1.53	NA	NA	5.66	2.97	7.16	5.64	0.00	
XOO1591	<i>pilR</i>	two-component system regulatory protein	0.07	-0.19	0.22	0.19	8.10	8.29	8.42	8.20	8.47	8.28	0.00
XOO1593	<i>sucC</i>	succinyl-CoA synthetase subunit beta	0.28	0.44	0.14	0.26	11.05	10.61	11.75	11.61	11.35	11.09	0.00
XOO1594	<i>sucD</i>	succinyl-CoA synthetase subunit alpha	0.31	0.46	0.29	0.18	10.49	10.03	12.16	11.87	11.73	11.55	0.00
XOO1595	<i>nadE</i>	NAD synthetase	1.34	1.58	1.11	4.28	2.70	5.96	4.85	2.12	NA	0.00	
XOO1596	<i>comL</i>	competence lipoprotein	-0.91	-1.01	-0.73	-1.00	8.73	9.74	10.36	11.09	10.21	11.21	0.00
XOO1597	<i>rluD</i>	ribosomal large subunit pseudouridine synthase D	-0.06	0.91	-0.42	-0.66	8.23	7.32	8.80	9.22	8.78	9.44	0.00
XOO1598	-	hypothetical protein	-0.89	-0.64	-0.98	-1.05	5.41	6.04	7.54	8.52	6.76	7.80	0.00
XOO1599	-	hypothetical protein	-0.40	-1.36	-0.79	0.94	5.65	7.01	6.93	7.71	6.81	5.87	0.00
XOO1600	-	hypothetical protein	1.07	0.02	2.12	3.02	3.01	5.67	3.55	2.48	NA	0.00	
XOO1601	<i>ostA</i>	trehalose-6-phosphate synthase	-0.77	-1.34	-0.71	-0.26	7.06	8.39	6.39	7.10	8.13	8.39	0.00
XOO1602	-	hypothetical protein	-1.02	-1.51	-0.09	-1.46	8.07	9.58	8.50	8.59	8.75	10.20	0.00
XOO1603	<i>ostB</i>	trehalose-6-phosphate phosphatase	-2.61	-2.63	-2.92	-2.27	6.17	8.80	6.08	9.00	6.49	8.76	0.00
XOO1604	<i>bfeA</i>	ferric enterobactin receptor	0.24	0.24	0.22	0.28	12.17	11.94	12.96	12.74	12.19	11.91	0.00
XOO1605	-	hypothetical protein	0.84	0.65	0.68	1.18	10.38	9.73	11.03	10.34	10.45	9.27	0.00
XOO1606	-	hypothetical protein	0.85	-0.91	1.71	1.75	6.84	7.75	7.10	5.39	5.35	3.60	0.00
XOO1607	-	hypothetical protein	-0.20	-0.54	-0.09	0.04	9.43	9.97	10.40	10.49	9.67	9.63	0.00
XOO1609	-	hypothetical protein	0.89	2.17	0.49	0.01	5.78	3.61	8.26	7.77	6.91	6.91	0.00
XOO1612	-	hypothetical protein	0.48	0.54	0.41	0.49	11.30	10.77	12.49	12.08	12.01	11.52	0.00
XOO1613	<i>rfaY</i>	RNA polymerase sigma factor	1.32	0.27	-0.40	4.09	3.58	3.31	6.43	6.83	7.23	3.14	0.00
XOO1614	<i>pthX</i>	pathogenicity-like protein	-1.45	-1.41	-1.45	-1.48	1.79	3.20	6.19	7.64	4.64	6.12	0.00
XOO1615	<i>tesB</i>	acyl-CoA thioesterase	0.32	-0.24	1.41	-0.21	7.66	7.90	6.24	4.82	8.22	8.43	0.00
XOO1616	-	hypothetical protein	0.20	-0.17	0.23	0.55	8.39	8.56	4.29	4.06	7.82	7.27	0.00
XOO1617	-	hypothetical protein	1.09	1.32	-0.19	2.15	7.43	6.10	8.05	8.25	9.19	7.04	0.00
XOO1618	-	hypothetical protein	-0.36	-0.29	-0.48	-0.31	10.24	10.53	10.62	11.10	9.57	9.87	0.00
XOO1620	<i>rplU</i>	50S ribosomal protein L21	-0.37	-0.51	-0.25	-0.34	14.75	15.26	15.77	16.02	15.35	15.69	0.00
XOO1622	<i>obgE</i>	GTPase ObgE	-0.35	-0.29	-0.29	-0.46	8.25	8.54	9.96	10.25	9.39	9.86	0.00
XOO1623	<i>rpsT</i>	30S ribosomal protein S20	1.35	2.92	0.60	0.52	8.00	5.08	11.74	11.13	11.67	11.15	0.00
XOO1624	<i>mviN</i>	virulence factor	-0.70	-0.70	-0.58	-0.83	8.04	8.73	9.73	10.31	9.76	10.60	0.00
XOO1625	<i>ribF</i>	bifunctional riboflavin kinase/FMN adenyllytransferase	-0.62	-0.78	-0.54	-0.54	9.26	10.04	10.06	10.59	9.62	10.16	0.00
XOO1626	<i>ileS</i>	isoleucyl-tRNA synthetase	0.25	0.38	0.22	0.16	9.70	9.33	10.67	10.45	9.87	9.71	0.00
XOO1627	<i>lspA</i>	lipoprotein signal peptidase	-0.58	-0.56	-0.61	-0.58	9.29	9.85	10.22	10.83	9.93	10.51	0.00
XOO1628	<i>ispH</i>	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	-0.58	-0.55	-0.27	-0.92	7.30	7.86	7.31	7.58	8.17	9.09	0.00
XOO1629	<i>cyaA</i>	cytochrome O ubiquinol oxidase subunit II	-0.94	-1.02	-0.87	-0.93	7.50	8.52	9.20	10.08	8.70	9.64	0.00
XOO1630	<i>cyoB</i>	cytochrome O ubiquinol oxidase subunit I	-0.57	-0.60	-0.54	-0.59	9.91	10.51	10.83	11.37	10.20	10.78	0.00
XOO1631	<i>cyoC</i>	cytochrome O ubiquinol oxidase subunit III	-0.94	-0.88	-0.92	-1.02	8.74	9.62	9.35	10.27	9.07	10.09	0.00
XOO1632	<i>cyoD</i>	cytochrome O ubiquinol oxidase subunit IV	-0.57	-0.59	-0.54	-0.58	10.50	11.09	10.94	11.48	10.16	10.74	0.00
XOO1633	-	hypothetical protein	0.93	1.08	0.67	1.04	8.88	7.80	9.97	9.30	9.04	8.00	0.00
XOO1634	<i>vrgS</i>	hypothetical protein	1.80	3.33	0.98	1.09	6.41	3.09	9.34	8.37	8.85	7.76	0.00
XOO1635	-	hypothetical protein	0.17	0.49	-0.08	0.10	8.43	7.94	10.59	10.67	10.22	10.12	0.00
XOO1638	-	hypothetical protein	#DIV/0!				2.45	NA	NA	NA	5.10	NA	0.01
XOO1642	<i>mutS</i>	DNA mismatch repair protein MutS	0.28	1.41	-0.38	-0.20	3.87	2.46	7.26	7.64	4.86	5.06	0.00
XOO1651	<i>plcN</i>	phospholipase C	1.77	1.28	2.26	3.89	2.61	0.79	NA	4.96	2.70	0.00	
XOO1654	-	hypothetical protein	-0.33	-0.43	-0.28	-0.29	7.09	7.52	9.02	9.30	8.08	8.37	0.00
XOO1655	-	hypothetical protein	-1.96	-2.96	-1.00	-1.90	6.07	9.03	7.74	8.74	6.87	8.77	0.00
XOO1656	<i>aspS</i>	aspartyl-tRNA synthetase	-0.20	-0.35	-0.16	-0.08	9.74	10.09	10.16	10.32	9.35	9.44	0.00
XOO1657	-	acetyltransferase	-0.31	0.08	0.07	-1.09	8.65	8.57	8.67	8.60	7.80	8.89	0.00
XOO1658	-	hypothetical protein	3.08	3.01	3.15	5.99	2.99	6.72	3.57	2.56	NA	0.00	
XOO1659	-	hypothetical protein	-1.04	-1.25	-0.93	-0.95	7.86	9.10	10.14	11.07	9.57	10.52	0.00
XOO1660	<i>rvuC</i>	Holliday junction resolvase	-1.35	-1.41	-1.34	-1.29	2.43	3.84	7.48	8.81	7.63	8.92	0.00
XOO1661	<i>rvuA</i>	Holliday junction DNA helicase RvuA	-1.26	-1.07	-1.20	-1.50	6.95	8.02	7.91	9.12	7.70	9.20	0.00
XOO1662	<i>kup</i>	potassium uptake protein	-1.17	-1.30	-1.10	-1.11	6.82	8.12	8.69	9.79	8.06	9.17	0.00
XOO1663	<i>rvuB</i>	Holliday junction DNA helicase RvuB	-0.13	-0.21	-0.18	0.01	7.95	8.16	9.59	9.77	9.24	9.23	0.00
XOO1665	<i>tolQ</i>	hypothetical protein	-1.17	-0.94	-1.26	-1.31	7.76	8.70	9.09	10.35	8.73	10.04	0.00
XOO1666	<i>tolR</i>	hypothetical protein	-0.58	-0.55	-0.58	-0.60	8.12	8.67	9.40	9.98	8.93	9.53	0.00
XOO1667	<i>tolA</i>	hypothetical protein	-0.93	-1.02	-0.84	-0.95	8.46	9.47	9.70	10.54	8.75	9.69	0.00
XOO1668	<i>tolB</i>	translocation protein TolB	-1.46	-1.38	-1.56	-1.45	10.56	11.94	10.73	12.29	10.58	12.02	0.00
XOO1669	<i>ompP6</i>	outer membrane protein P6	-0.27	-0.32	-0.27	-0.21	12.99	13.31	13.25	13.52	12.87	13.08	0.00
XOO1670	-	hypothetical protein	-0.60	-0.55	-0.74	-0.49	9.24	9.79	10.13	10.88	9.65	10.15	0.00
XOO1671	-	radical activating enzyme	-1.39	-1.37	-1.31	-1.51	7.37	8.74	9.38	10.68	8.73	10.23	0.00
XOO1679	<i>exsB</i>	transcriptional regulator	0.84	0.97	1.87	-0.32	4.17	3.20	6.63	4.77	3.47	3.79	0.00
XOO1680	<i>int</i>	phage-related integrase	-0.37	-0.31	-0.99	0.17	1.29	1.60	5.76	6.75	6.35	6.18	0.00
XOO1681	-	hypothetical protein	2.90		2.90	5.35	NA	2.84	NA	6.33	3.43	0.00	
XOO1682	-	hypothetical protein	#DIV/0!				3.51	NA	3.84	NA	2.45	NA	0.00
XOO1683	-	hypothetical protein	-0.35		-0.35	4.35	NA	6.38	6.73	3.67	NA	0.00	
XOO1684	-	hypothetical protein	#DIV/0!				0.79	NA	4.21	NA	4.51	NA	0.01
XOO1685	-	hypothetical protein	2.03		4.18	-0.12	3.48	NA	5.21	1.03	1.58	1.70	0.00
XOO1687	-	hypothetical protein	-0.64	-0.52	-0.94	-0.47	7.14	7.66	8.31	9.25	7.15	7.62	0.00
XOO1688	-	hypothetical protein	-1.03	-1.13	-0.91	-1.04	9.53	10.66	9.95	10.86	9.80	10.84	0.00
XOO1689	-	phage-related tail protein	-0.18	-1.26	0.90	6.22	7.48	6.64	5.73	2.85	NA	0.00	
XOO1690	-	phage-related tail protein	0.97	-1.29	1.71	2.50	8.31	9.59	7.09	5.39	5.74	3.24	0.00
XOO1691	-	phage-related tail protein	#DIV/0!				2.00	NA	NA	NA	NA	NA	0.12
XOO1693	-	phage-related tail protein	4.08		4.08	3.22	NA	5.84	1.76	3.70	NA	0.00	
XOO1694	-	phage-related tail protein	0.40		-2.00	2.81	4.28	NA	5.30	7.30	6.04	3.24	0.00
XOO1695	-	phage-related tail protein	-0.22	-0.13	-0.15	-0.38	6.71	6.84	8.10	8.25	7.12	7.49	0.00
XOO1697	-	phage-related baseplate protein	-0.14	-0.98	0.38	0.18	7.34	8.32	8.13	7.74	8.22	8.04	0.00
XOO1698	-	hypothetical protein	1.06	3.61	-0.04	-0.39	5.92	2.30	7.64	7.68	3.64	4.03	0.00
XOO1699	-	phage-related tail protein	0.79	1.13	1.37	-0.12	3.66	2.53	6.35	4.98	2.94	3.06	0.00
XOO1700	-	phage-related baseplate assembly protein	2.18		2.18	2.66	NA	6.47	4.29	NA	NA	0.00	
XOO1701	-	hypothetical protein	-0.36	-0.95	-0.04	-0.11	6.75	7.70	8.56	8.60	9.44	9.55	0.00
XOO1702	-	phage-related tail protein	-1.27	-1.17	-1.38	2.66	3.83	8.07	9.45	3.22	NA	0.00	
XOO1703	-	phage-related tail protein	-0.61	-0.70	-0.45	-0.68	8.28	8.97	8.88	9.33	7.97	8.65	0.00
XOO1704	-	hypothetical protein	0.01	-0.83	-1.08	1.93	4.06	4.90	3.85	4.92	3.09	1.16	0

XOO1720	-	hypothetical protein	0.43	0.47	0.29	0.54	7.69	7.23	8.91	8.62	8.59	8.06	0.00
XOO1721	-	response regulator	-2.18	-2.01	-2.23	-2.31	9.94	11.95	10.92	13.15	10.82	13.13	0.00
XOO1722	-	hypothetical protein	-0.59	-0.53	-0.55	-0.68	9.32	9.85	10.01	10.56	9.19	9.86	0.00
XOO1723	recQ	DNA helicase	-0.37	-0.23	-0.40	-0.48	8.20	8.42	8.27	8.68	8.24	8.72	0.00
XOO1724	-	DNA-binding related protein	-0.71	-0.63	-0.65	-0.84	8.39	9.02	10.72	11.36	10.47	11.31	0.00
XOO1725	hrpA	ATP-dependent RNA helicase	1.19	4.45	-0.85	-0.04	7.18	2.73	7.91	8.76	7.73	7.77	0.00
XOO1727	fepA	TonB-dependent receptor	-0.23		0.41	-0.86	NA	NA	3.99	3.58	2.66	3.52	0.00
XOO1730	glk	glucose kinase	0.88	2.47	0.36	-0.20	5.63	3.16	7.36	7.00	5.69	5.89	0.00
XOO1731	-	hypothetical protein	0.47	-1.60	2.75	0.28	6.51	8.11	5.39	2.65	3.00	2.72	0.00
XOO1732	-	hypothetical protein	1.81	1.84	2.93	0.67	5.95	4.11	6.60	3.67	7.38	6.71	0.00
XOO1733	pqqE	pyrroloquinoline quinone biosynthesis protein PqqE	2.72	3.95	0.77	3.46	6.97	3.03	8.34	7.57	6.82	3.37	0.00
XOO1734	pqqC	pyrroloquinoline quinone biosynthesis protein PqqC	4.12		4.12		4.76	NA	5.43	1.30	3.71	NA	0.00
XOO1735	pqqG	pyrroloquinoline quinone biosynthesis protein PqqB	-0.22	-0.24	-0.16	-0.26	8.38	8.62	9.47	9.62	9.13	9.40	0.00
XOO1736	relA	ATP:GTP 3'-pyrophosphotransferase	0.11	0.26	-0.14	0.21	8.33	8.07	8.80	8.94	8.50	8.28	0.00
XOO1739	ponB	penicillin-binding protein 1B	-0.08	0.12	-0.40	0.06	5.01	4.89	8.04	8.44	7.46	7.40	0.00
XOO1740	-	hypothetical protein	-0.19	-0.17	-0.09	-0.32	3.69	3.86	8.29	8.37	7.76	8.08	0.00
XOO1741	yoaA	ATP-dependent helicase	0.49	-0.93	2.02	0.40	2.43	3.36	7.04	5.02	6.41	6.01	0.00
XOO1743	draG	dinitrogenase reductase activationg glycohydrolase	0.69	2.53	0.33	-0.79	6.07	3.54	7.32	6.99	6.05	6.84	0.00
XOO1744	tonB	TonB protein	1.51		0.86	2.16	4.92	NA	7.11	6.25	3.92	1.75	0.00
XOO1745	gshB	glutathione synthetase	0.03	0.13	-0.14	0.11	8.12	8.00	8.91	9.05	8.76	8.65	0.00
XOO1746	pilG	pilus protein	-0.26	-0.12	-0.28	-0.37	13.19	13.31	14.89	15.18	14.71	15.08	0.00
XOO1747	pilH	PilH protein	-0.72	-0.79	-0.71	-0.67	9.35	10.14	11.07	11.78	10.48	11.15	0.00
XOO1748	pill	pilus biogenesis protein	-0.28	-0.21	-0.30	-0.33	9.39	9.60	10.76	11.06	10.68	11.00	0.00
XOO1749	pilJ	pilus biogenesis protein	0.28	0.46	0.14	0.25	11.00	10.54	12.10	11.96	11.40	11.15	0.00
XOO1752	-	hypothetical protein	0.07	0.36	0.00	-0.16	9.81	9.45	11.50	11.50	11.19	11.35	0.00
XOO1753	-	hypothetical protein	0.28	0.23	0.28	0.35	9.94	9.71	11.16	10.88	11.01	10.67	0.00
XOO1754	rimJ	ribosomal protein alanine acetyltransferase	1.82		2.46	1.18	3.85	NA	6.47	4.01	4.40	3.22	0.00
XOO1760	aspG	asparaginase	-0.03	-0.03	-0.02	-0.03	10.15	10.18	11.20	11.22	10.75	10.77	0.00
XOO1761	cutC	copper homeostasis protein	-0.33	-0.24	-0.29	-0.45	8.07	8.31	9.54	9.83	8.77	9.23	0.00
XOO1763	-	hypothetical protein	3.18	1.80	4.56		4.11	2.32	7.62	3.06	2.75	NA	0.00
XOO1768	-	hypothetical protein	#DIV/0!				5.03	NA	1.95	NA	2.32	NA	0.01
XOO1769	bga	beta-galactosidase	-0.99	-1.08	-0.64	-1.25	6.27	7.35	6.45	7.09	6.59	7.84	0.00
XOO1770	-	hypothetical protein	-0.36		-0.02	-0.70	6.16	NA	8.20	8.22	7.36	8.06	0.00
XOO1771	-	hypothetical protein	-0.35	-0.25	-0.28	-0.51	7.73	7.98	9.49	9.77	9.05	9.56	0.00
XOO1772	-	membrane-fusion protein	-0.11	0.85	-0.42	-0.76	4.34	3.48	8.21	8.63	6.74	7.51	0.00
XOO1774	-	hypothetical protein	0.06		0.24	-0.12	NA	NA	3.45	3.21	3.10	3.22	0.00
XOO1778	-	colicin V secretion ABC transporter ATP-binding protein	-1.01		-1.81	-0.21	NA	NA	5.83	7.65	3.60	3.82	0.00
XOO1779	-	glucan 1,4-beta-glucosidase	-1.95	-0.89	-0.73	-4.22	7.06	7.95	7.48	8.20	3.33	7.55	0.00
XOO1780	-	beta-mannosidase	1.60		1.60		2.79	NA	4.05	2.45	1.58	NA	0.00
XOO1781	nahA	beta-hexosaminidase	-4.12	-2.64	-6.00	-3.72	6.65	9.29	5.00	10.99	6.17	9.89	0.00
XOO1782	-	hypothetical protein	-0.67	-0.81	0.43	-1.61	6.63	7.44	5.01	4.58	5.25	6.86	0.00
XOO1783	fucA1	alpha-L-fucosidase	0.52	-1.02	-0.40	2.96	7.33	8.34	7.17	7.57	7.33	4.36	0.00
XOO1784	iroN	TonB-dependent receptor	-0.12	-0.02	-0.29	-0.05	10.50	10.52	11.60	11.89	10.90	10.95	0.00
XOO1785	glk	glucokinase	-1.12	-1.21	-1.05	-1.09	7.39	8.60	9.06	10.10	8.68	9.77	0.00
XOO1787	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	-0.57	-0.45	-0.46	-0.80	7.00	7.44	8.80	9.26	7.96	8.76	0.00
XOO1790	mazG	nucleoside triphosphate pyrophosphohydrolase	-0.47	-0.87	-0.10	-0.43	7.40	8.26	9.33	9.43	8.59	9.02	0.00
XOO1792	-	hypothetical protein	-0.57	-0.70	-0.12	-0.88	4.63	5.33	7.18	7.29	2.92	3.80	0.00
XOO1793	-	hypothetical protein	-0.34	-0.26	-0.38	-0.37	7.45	7.72	7.91	8.29	8.33	8.69	0.00
XOO1794	gcvT	glycine cleavage system aminomethyltransferase T	0.19	0.45	0.03	0.09	8.55	8.09	10.00	9.97	9.54	9.45	0.00
XOO1795	gcvH	glycine cleavage system protein H	0.41	0.52	0.36	0.35	10.71	10.18	11.64	11.29	11.28	10.93	0.00
XOO1796	-	hypothetical protein	-0.32	-0.22	-0.36	-0.38	9.81	10.02	9.70	10.06	8.94	9.32	0.00
XOO1797	bla	beta-lactamase	0.99	1.35	0.67	0.95	9.67	8.33	10.97	10.30	9.83	8.87	0.00
XOO1798	-	hypothetical protein	0.10		0.10		NA	NA	2.85	2.75	2.23	NA	0.00
XOO1800	-	hypothetical protein	0.05	0.15	0.02	-0.01	7.45	7.30	9.02	9.00	8.56	8.58	0.00
XOO1803	-	hypothetical protein	-0.37	-1.01	-0.56	0.46	4.27	5.28	6.43	7.00	3.07	2.61	0.00
XOO1804	-	transcriptional regulator	1.16	0.95	0.81	1.70	9.18	8.23	9.61	8.79	8.77	7.07	0.00
XOO1805	-	hypothetical protein	0.31	0.36	0.36	0.22	11.94	11.58	12.89	12.54	12.87	12.66	0.00
XOO1806	-	hypothetical protein	0.63	0.70	0.58	0.62	8.81	8.10	10.12	9.54	9.53	8.92	0.00
XOO1807	-	heat shock protein	-1.11	-2.18	-0.51	-0.66	5.87	8.05	7.69	8.20	7.15	7.81	0.00
XOO1809	gtrB	glucosyl transferase	-0.10	-0.07	-0.39	0.18	7.96	8.03	6.58	6.98	8.16	7.99	0.00
XOO1810	-	hypothetical protein	4.72	4.00	5.50	4.68	11.85	7.85	13.01	7.51	12.07	7.39	0.00
XOO1814	hly3	hemolysin III	1.31	1.94	0.93	1.07	5.55	3.61	8.43	7.50	8.28	7.21	0.00
XOO1815	prfC	peptide chain release factor 3	-0.73	-0.49	-0.69	-0.99	7.43	7.92	9.09	9.78	3.64	4.63	0.00
XOO1818	metB	cystathione gamma-synthase	1.16	0.06	0.21	3.22	9.03	8.97	8.92	8.72	7.28	4.06	0.00
XOO1823	-	cold shock domain-containing protein	1.45		1.45		2.70	NA	3.63	2.18	NA	NA	0.00
XOO1824	-	hypothetical protein	-0.05	0.00	0.00	-0.13	10.43	10.43	11.13	11.13	11.07	11.20	0.00
XOO1825	yodB	cytochrome B561	0.57	0.83	0.29	0.57	7.85	7.01	9.43	9.14	9.02	8.45	0.00
XOO1826	-	hypothetical protein	0.26	0.42	0.18	0.20	8.59	8.17	10.28	10.10	9.87	9.67	0.00
XOO1827	-	histidine kinase-response regulator hybrid protein	0.52	-0.13	-0.55	2.25	3.40	3.53	3.19	3.73	6.05	3.81	0.00
XOO1828	-	histidine kinase/response regulator hybrid protein	2.52	1.98	2.29	3.28	8.20	6.22	6.63	4.34	6.96	3.69	0.00
XOO1829	-	histidine kinase-response regulator hybrid protein	0.36	0.47	0.35	0.26	7.08	6.61	7.85	7.50	4.47	4.21	0.00
XOO1831	-	histidine kinase-response regulator hybrid protein	0.97	-0.02	-0.64	3.57	7.02	7.04	7.84	8.47	7.13	3.56	0.00
XOO1833	-	hypothetical protein	0.52	-0.06	0.78	0.85	6.61	6.67	9.56	8.78	8.72	7.87	0.00
XOO1835	-	hypothetical protein	1.47	3.35	0.09	0.98	7.08	3.73	8.28	8.20	8.22	7.24	0.00
XOO1836	-	hypothetical protein	-2.01	-2.22	-1.93	-1.87	5.63	7.85	8.01	9.94	7.65	9.52	0.00
XOO1838	bga	beta-galactosidase	-0.17	-0.44	0.10		6.33	6.76	7.68	7.58	2.38	NA	0.00
XOO1842	mmsA	methylmalonate-semialdehyde dehydrogenase	0.45	0.34	0.28	0.72	9.04	8.69	5.15	4.87	9.00	8.28	0.00
XOO1843	fadE9	acyl-CoA dehydrogenase	0.19	1.17	-0.18	-0.41	6.30	5.13	3.75	3.92	6.62	7.03	0.00
XOO1844	paaF	enoyl-CoA hydratase	-0.14	-0.79	-0.34	0.70	6.93	7.72	7.63	7.97	6.59	5.89	0.00
XOO1845	-	enoyl-CoA hydratase	-1.26	-2.05	-2.35	0.63	1.29	3.35	4.56	6.91	4.25	3.62	0.00
XOO1846	mmsB	3-hydroxyisobutyrate dehydrogenase	0.35		-0.58	1.28	3.99	NA	2.45	3.03	4.55	3.27	0.00
XOO1847	czcD	cobalt-zinc-cadmium resistance protein	-6.74	-6.62	-6.87	NA	NA	4.52	11.14	2.66	9.53	0.00	
XOO1848	fadB	3-hydroxyacyl-CoA dehydrogenase	2.24		0.40	4.08	2.86	NA	6.61	6.21	7.15	3.07	0.00
XOO1849	algU	RNA polymerase sigma factor RpoE	0.90	0.88	0.74	1.07	9.25	8.37	10.78	10.03	9		

XOO1856	<i>era</i>	GTP-binding protein Era	-0.23	-0.37	-0.38	0.06	9.26	9.63	9.84	10.22	5.06	5.00	0.00
XOO1857	<i>recO</i>	DNA repair protein RecO	-0.43	-0.29	-0.43	-0.59	8.65	8.94	8.85	9.28	8.30	8.89	0.00
XOO1858	-	hypothetical protein	0.84		1.12	0.55	2.86	NA	4.74	3.61	4.45	3.90	0.00
XOO1859	<i>rumA</i>	23S rRNA 5-methyluridine methyltransferase	-1.12	-1.05	-1.71	-0.61	8.24	9.29	7.59	9.30	7.68	8.29	0.00
XOO1860	-	hypothetical protein	0.78	0.78	0.84	0.72	8.14	7.35	9.47	8.63	9.12	8.40	0.00
XOO1864	<i>frnE</i>	polyketide synthase	#DIV/0!				2.62	NA	2.58	NA	5.21	NA	0.00
XOO1865	-	hypothetical protein	#DIV/0!				1.16	NA	5.70	NA	2.26	NA	0.02
XOO1866	-	hypothetical protein	#DIV/0!				1.40	NA	NA	NA	NA	NA	0.22
XOO1867	<i>nagZ</i>	beta-hexosaminidase	-0.43		-0.26	-0.61	2.71	NA	3.85	4.11	7.04	7.64	0.00
XOO1869	<i>deoD</i>	5'-methylthioadenosine phosphorylase	-0.11	-0.03	-0.05	-0.25	8.88	8.91	5.07	5.12	9.35	9.60	0.00
XOO1870	<i>scoF</i>	cold shock protein	2.56	2.70	2.32	2.65	10.93	8.23	12.29	9.97	11.92	9.27	0.00
XOO1873	-	hypothetical protein	1.87	0.56	3.19		2.43	1.87	5.02	1.83	3.88	NA	0.00
XOO1874	<i>lhr2</i>	helicase-like protein	1.76	2.45		1.07	3.99	1.54	5.17	NA	2.60	1.54	0.00
XOO1876	-	mRNA 3'-end processing factor	-0.70	-1.08	-2.65	1.63	4.39	5.47	4.37	7.02	6.96	5.33	0.00
XOO1877	-	hypothetical protein	-0.13	-0.18	-0.18	-0.04	11.91	12.09	12.91	13.09	12.39	12.43	0.00
XOO1878	-	hypothetical protein	-0.09	1.48	-1.86	0.11	2.52	1.04	4.44	6.29	2.82	2.71	0.00
XOO1879	-	sensor histidine kinase	-0.70	-0.85	-0.81	-0.43	5.67	6.52	7.42	8.23	6.94	7.37	0.00
XOO1881	<i>atoB</i>	acetoacetyl-CoA thiolase	2.07	1.08	4.23	0.91	9.42	8.33	9.52	5.29	10.64	9.73	0.00
XOO1882	-	serine protease	-0.56	-0.68	-1.11	0.12	2.62	3.31	5.69	6.80	3.55	3.43	0.00
XOO1883	<i>leu</i>	leucine dehydrogenase	1.30		-0.51	3.10	2.78	NA	6.40	6.90	5.88	2.78	0.00
XOO1884	-	hypothetical protein	-0.72	-0.47	-0.78	-0.90	8.09	8.56	8.82	9.60	8.47	9.37	0.00
XOO1888	-	hypothetical protein	-0.57	-0.34	-0.73	-0.64	8.78	9.12	9.01	9.74	8.60	9.24	0.00
XOO1892	<i>yegD</i>	heat shock protein	-0.44	-0.48	-0.29	-0.55	8.33	8.81	8.57	8.86	8.32	8.87	0.00
XOO1897	<i>catA</i>	cation transport protein	-1.97	-1.05	-2.04	-2.83	6.04	7.10	7.61	9.66	6.55	9.37	0.00
XOO1898	-	hypothetical protein	-0.33	-0.27	-0.65	-0.06	3.08	3.35	7.87	8.53	9.44	9.50	0.00
XOO1899	-	hypothetical protein	0.16	0.10	-0.03	0.41	8.47	8.38	9.43	9.46	8.81	8.40	0.00
XOO1900	<i>nerA</i>	GTN reductase	-0.32	-0.33	-0.05	-0.57	6.98	7.30	8.32	8.37	7.67	8.24	0.00
XOO1901	<i>araJ</i>	MFS transporter	-0.53	-0.28	-0.48	-0.83	3.28	3.57	3.45	3.93	6.73	7.56	0.00
XOO1902	-	hypothetical protein	-2.69	-3.16	-2.46	-2.47	5.50	8.66	7.08	9.54	6.88	9.35	0.00
XOO1903	-	hypothetical protein	-0.47	-0.38	-0.62	-0.41	10.20	10.58	10.77	11.38	10.06	10.47	0.00
XOO1904	-	hypothetical protein	0.27	1.87	-0.68	-0.38	4.34	2.47	3.25	3.93	6.63	7.00	0.00
XOO1906	<i>acvB</i>	virulence protein	0.85	-0.76	-0.04	3.34	5.15	5.91	4.13	4.17	6.97	3.63	0.00
XOO1910	-	hypothetical protein	0.95	0.89	0.95	1.02	10.12	9.23	10.82	9.87	10.14	9.12	0.00
XOO1911	-	hypothetical protein	0.08		-0.05	0.21	2.90	NA	7.41	7.46	4.00	3.79	0.00
XOO1912	-	hypothetical protein	0.30	0.49	-0.03	0.43	7.56	7.07	9.25	9.27	8.93	8.50	0.00
XOO1913	-	hypothetical protein	-0.25	3.35	-3.36	-0.76	5.66	2.30	4.81	8.17	6.39	7.14	0.00
XOO1916	-	dehydrogenase	-0.71	-1.52	-0.56	-0.05	5.28	6.80	7.67	8.24	7.61	7.66	0.00
XOO1917	<i>desC</i>	delta 9 acyl-lipid fatty acid desaturase	-0.12	-0.13	-0.19	-0.03	9.62	9.75	10.94	11.13	10.30	10.33	0.00
XOO1918	-	hypothetical protein	0.56	0.66	0.75	0.27	7.83	7.17	7.87	7.12	8.36	8.09	0.00
XOO1921	-	hypothetical protein	-0.23	-3.13	-0.72	3.16	0.79	3.92	2.89	3.61	6.02	2.86	0.00
XOO1923	-	hypothetical protein	-0.12		1.27	-1.52	1.50	NA	5.71	4.44	2.12	3.64	0.00
XOO1924	<i>metG</i>	methionyl-tRNA synthetase	-0.05	0.10	0.02	-0.28	7.23	7.13	8.33	8.31	4.13	4.41	0.00
XOO1925	-	hypothetical protein	0.53	0.99	0.24	0.36	8.96	7.97	11.17	10.93	10.69	10.33	0.00
XOO1929	<i>ykfD</i>	S-methylmethionine transporter	0.75	-0.72	-0.76	3.73	9.15	9.88	5.71	6.47	6.74	3.01	0.00
XOO1930	<i>mmuM</i>	homocysteine methyltransferase	0.22	0.03	0.63	-0.01	7.97	7.94	8.44	7.81	7.74	7.76	0.00
XOO1932	-	hypothetical protein	0.32	-0.24	0.53	0.68	5.00	5.24	7.99	7.46	7.56	6.87	0.00
XOO1934	-	hypothetical protein	#DIV/0!				0.79	NA	NA	NA	1.50	NA	0.13
XOO1951	-	hypothetical protein	-0.98	-1.50	-0.52	-0.94	6.75	8.25	7.90	8.42	7.86	8.80	0.00
XOO1953	-	hypothetical protein	0.76	0.64	0.66	0.96	6.29	5.65	5.97	5.30	6.75	5.79	0.00
XOO1954	-	hypothetical protein	0.13	0.40	-0.62	0.62	4.28	3.88	7.28	7.90	4.49	3.87	0.00
XOO1956	-	hypothetical protein	-0.86	-0.96	-0.80	-0.83	9.77	10.73	10.55	11.35	10.00	10.83	0.00
XOO1957	-	hypothetical protein	-1.19	-1.30	-1.27	-1.02	7.29	8.58	7.62	8.88	8.76	9.78	0.00
XOO1958	-	ABC transporter ATP-binding protein	-0.54	-0.53	-0.73	-0.35	7.98	8.51	9.40	10.13	9.00	9.35	0.00
XOO1959	-	outer membrane receptor proteins, mostly Fe transport	-0.62	-0.66	-0.66	-0.55	7.92	8.58	10.13	10.79	9.77	10.31	0.00
XOO1961	<i>accA</i>	acetyl-CoA carboxylase carboxyltransferase subunit alpha	-0.71	-0.67	-0.73	-0.73	8.96	9.63	10.58	11.31	9.96	10.69	0.00
XOO1963	<i>rmbB</i>	ribonuclease III	1.45	3.26	0.34	0.76	6.04	2.78	7.87	7.53	7.90	7.15	0.00
XOO1964	<i>lpdB</i>	lipid A-disaccharide synthase	0.15	0.02	0.29	0.15	8.32	8.30	9.13	8.84	8.92	8.78	0.00
XOO1965	<i>lpdA</i>	UDP-N-acetylglucosamine acyltransferase	0.22	-0.14	0.26	0.54	5.70	5.83	7.33	7.06	3.95	3.41	0.00
XOO1966	<i>fabZ</i>	(3R)-hydroxymyristoyl-ACP dehydratase	-0.39	-0.36	-0.47	-0.34	7.69	8.05	9.49	9.96	9.52	9.86	0.00
XOO1967	<i>lpdD</i>	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	-0.39	-0.12	-0.67	-0.39	9.08	9.19	10.95	11.62	10.46	10.85	0.00
XOO1968	<i>oma</i>	outer membrane antigen	-0.16	-0.11	-0.18	-0.18	9.42	9.53	11.03	11.21	10.95	11.14	0.00
XOO1969	-	hypothetical protein	-0.57	-0.57	-0.49	-0.65	10.75	11.32	11.44	11.93	11.18	11.82	0.00
XOO1970	<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	-0.76	-0.73	-0.85	-0.70	10.32	11.05	11.02	11.87	10.76	11.46	0.00
XOO1971	<i>cdsA</i>	phosphatidate cytidylyltransferase	-0.64	-0.73	-0.42	-0.78	7.32	8.06	8.41	8.83	8.53	9.30	0.00
XOO1972	<i>uppS</i>	undecaprenyl pyrophosphate synthase	0.70	2.37	-0.24	-0.04	5.66	3.29	7.93	8.17	7.47	7.51	0.00
XOO1973	<i>frr</i>	ribosome recycling factor	-0.40	-0.34	-0.44	-0.43	10.55	10.89	12.10	12.54	11.65	12.07	0.00
XOO1975	-	hypothetical protein	0.12	0.17	-0.01	0.19	10.27	10.10	11.53	11.54	11.30	11.12	0.00
XOO1976	<i>tsf</i>	elongation factor Ts	1.14	1.38	1.03	1.00	9.51	8.14	10.70	9.67	10.42	9.41	0.00
XOO1978	-	pili assembly chaperone	-1.22	-1.60	-1.14	-0.91	6.24	7.84	8.11	9.26	7.63	8.54	0.00
XOO1979	-	hypothetical protein	0.32		0.13	0.51	5.82	NA	3.24	3.10	7.20	6.69	0.00
XOO1980	<i>fasD</i>	outer membrane usher protein FasD	#DIV/0!				2.54	NA	1.90	NA	2.26	NA	0.00
XOO1981	<i>ecpD</i>	pili assembly chaperone	-0.69		-0.69		2.26	NA	4.99	5.68	5.01	NA	0.00
XOO1982	<i>pru</i>	protein U	0.21	0.26	0.15	0.21	8.03	7.77	7.68	7.53	7.28	7.07	0.00
XOO1983	<i>map</i>	methionine aminopeptidase	-0.54	-0.78	-0.43	-0.41	7.67	8.45	9.76	10.19	9.67	10.07	0.00
XOO1984	<i>glnD</i>	PII uridyl-transferase	0.63	-0.04	1.61	0.33	4.78	4.82	6.73	5.12	5.15	4.82	0.00
XOO1985	<i>dapD</i>	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase	-1.26	-1.64	-1.05	-1.08	7.18	8.82	8.91	9.96	8.46	9.54	0.00
XOO1989	<i>dapE</i>	succinyl-diaminopimelate desuccinylase	-0.37	-2.20	-1.09	2.19	4.36	6.57	6.89	7.98	6.14	3.96	0.00
XOO1990	<i>asnB</i>	asparagine synthetase B	1.79	0.75	1.61	3.03	8.61	7.86	7.39	5.78	7.12	4.10	0.00
XOO1991	-	hypothetical protein	-0.40	-0.36	-0.40	-0.43	9.61	9.96	10.90	11.29	10.53	10.96	0.00
XOO1992	<i>fhuA</i>	iron permease	4.01	4.46	4.01	3.58	9.16	4.70	10.05	6.04	10.21	6.64	0.00
XOO1993	<i>acylI</i>	penicillin acylase II	2.52	3.56	1.70	2.31	6.22	2.67	8.80	7.10	8.07	5.76	0.00
XOO1996	<i>parC</i>	DNA topoisomerase IV subunit A	0.95	1.02	0.85	0.99	8.32	7.30	9.94	9.09	9.53	8.54	0.00
XOO1997	-	transcriptional regulator	0.07	0.66	-0.24	-0.21	4.32	3.66	7.20	7			

XOO2020	-	hypothetical protein	-0.51	-0.34	-0.67	-0.51	7.48	7.82	8.54	9.21	8.30	8.81	0.00
XOO2023	<i>smpB</i>	SsrA-binding protein	-0.78	-0.69	-0.83	-0.82	9.02	9.72	10.67	11.50	10.32	11.14	0.00
XOO2024	-	hypothetical protein	-1.04	-0.72	-1.17	-1.23	7.06	7.78	7.95	9.13	7.73	8.96	0.00
XOO2026	<i>smpA</i>	hypothetical protein	-0.35	-0.16	-0.41	-0.49	11.41	11.57	12.21	12.63	11.95	12.44	0.00
XOO2027	<i>fur</i>	ferric uptake regulator Fur	-0.29	-0.29	-0.13	-0.44	10.98	11.27	11.55	11.68	11.64	12.08	0.00
XOO2028	<i>recN</i>	recombination protein N	-0.62	-0.27	-0.23	-1.35	3.19	3.46	8.15	8.38	6.94	8.29	0.00
XOO2029	<i>hrcA</i>	heat-inducible transcription repressor	2.55	4.99	-0.08	2.73	6.31	1.32	5.72	5.80	5.51	2.78	0.00
XOO2030	<i>grpE</i>	heat shock protein GrpE	-0.50	-0.16	-0.61	-0.72	9.07	9.23	10.62	11.22	10.63	11.35	0.00
XOO2031	<i>dnaK</i>	molecular chaperone DnaK	0.37	0.51	0.35	0.26	12.72	12.21	14.03	13.68	13.17	12.91	0.00
XOO2032	<i>dnaJ</i>	molecular chaperone DnaJ	-0.22	-0.27	-0.16	-0.24	10.21	10.48	11.34	11.50	11.03	11.27	0.00
XOO2033	<i>pdxY</i>	pyridoxine kinase	0.16	-	-0.05	0.36	2.89	NA	2.99	3.04	3.04	2.68	0.00
XOO2034	<i>tyrA</i>	prephenate dehydrogenase	0.66	3.26	-0.65	-0.63	6.54	3.28	7.86	8.50	7.44	8.07	0.00
XOO2038	<i>oxyR</i>	hydrogen peroxide-inducible genes activator	#DIV/0!				2.04	NA	2.35	NA	NA	NA	0.02
XOO2039	<i>draA</i>	ABC transporter ATP-binding protein	1.01	0.17	-0.23	3.09	7.25	7.08	8.03	8.26	7.18	4.09	0.00
XOO2041	-	hypothetical protein	-1.38	-1.38	-1.61	-1.15	6.83	8.22	7.08	8.69	7.83	8.98	0.00
XOO2043	<i>sucB</i>	dihydrolipoamide succinyltransferase	-0.10	0.10	-0.22	-0.19	10.06	9.96	11.44	11.67	11.28	11.47	0.00
XOO2045	-	hypothetical protein	-0.25	-0.03	-0.44	-0.27	7.87	7.90	8.86	9.30	8.80	9.06	0.00
XOO2046	-	hypothetical protein	0.09	0.23	0.06	-0.02	8.73	8.50	9.78	9.72	9.38	9.40	0.00
XOO2049	-	hypothetical protein	1.03	1.08	1.04	0.96	7.21	6.13	8.52	7.48	8.31	7.35	0.00
XOO2050	-	hypothetical protein	0.03	-0.08	0.99	-0.82	2.79	2.87	3.20	2.21	3.33	4.15	0.00
XOO2057	<i>fumC</i>	fumarate hydratase	0.05	0.10	-0.28	0.35	7.02	6.93	8.15	8.43	4.25	3.90	0.00
XOO2058	-	hypothetical protein	0.35	0.49	-0.22	0.80	7.98	7.50	9.28	9.51	8.27	7.47	0.00
XOO2059	-	hypothetical protein	1.76	1.15	0.96	3.17	7.88	6.73	7.42	6.46	6.61	3.44	0.00
XOO2060	-	hypothetical protein	0.55	0.26	0.66	0.74	7.53	7.27	9.10	8.44	8.42	7.67	0.00
XOO2061	-	hypothetical protein	2.08	3.44	3.25	-0.44	5.86	2.42	8.01	4.76	4.98	5.42	0.00
XOO2062	<i>nodI</i>	ABC transporter ATP-binding protein	2.07	4.34	1.29	0.59	7.06	2.72	7.95	6.66	4.13	3.54	0.00
XOO2063	-	GntR family transcriptional regulator	0.33	0.59	0.18	0.22	8.20	7.61	9.96	9.78	9.51	9.29	0.00
XOO2064	<i>btuE</i>	vitamin B12 uptake ABC transporter permease	-0.12	-0.04	-0.16	-0.17	10.15	10.19	11.05	11.21	10.37	10.53	0.00
XOO2065	<i>fkpA</i>	FKBP-type peptidylprolyl isomerase	-0.02	0.02	0.01	-0.10	12.31	12.30	13.04	13.02	13.15	13.24	0.00
XOO2066	<i>ugd</i>	UDP-glucose dehydrogenase	-0.35	-0.38	-0.29	-0.39	8.49	8.86	10.13	10.42	9.73	10.12	0.00
XOO2067	-	hypothetical protein	-0.09	0.11	-0.14	-0.25	9.98	9.87	11.18	11.32	10.82	11.07	0.00
XOO2068	-	hypothetical protein	-0.20	-0.24	-0.23	-0.13	3.84	4.08	8.92	9.15	8.44	8.58	0.00
XOO2069	-	transcriptional regulator	0.41	0.05	-0.26	1.44	7.62	7.57	7.94	8.21	5.71	4.27	0.00
XOO2070	<i>fucP</i>	glucose-galactose transporter	-0.80	-0.88	-0.71	-0.81	8.04	8.91	9.58	10.29	9.22	10.04	0.00
XOO2071	<i>scrK</i>	fructokinase	-0.69	-0.77	-0.57	-0.72	7.95	8.72	8.55	9.12	8.01	8.73	0.00
XOO2072	-	hypothetical protein	0.12	0.25	0.05	0.05	10.04	9.78	11.67	11.62	11.16	11.11	0.00
XOO2073	<i>metH2</i>	5-methyltetrahydrofolate--homocysteine methyltransferase	-1.16	-0.70	-1.43	-1.36	6.81	7.51	7.66	9.09	7.25	8.62	0.00
XOO2074	<i>metH</i>	5-methyltetrahydrofolate--homocysteine methyltransferase	-0.98	-0.94	-0.86	-1.13	9.70	10.63	10.56	11.42	9.26	10.39	0.00
XOO2075	-	transcriptional regulator	0.27	0.29	0.28	0.25	9.67	9.38	11.50	11.22	11.07	10.82	0.00
XOO2076	<i>acdA</i>	acyl-CoA dehydrogenase	-0.76	-0.63	-0.70	-0.95	8.52	9.15	9.42	10.12	8.39	9.34	0.00
XOO2079	-	acetylhydrolase	0.45	1.20	0.50	-0.36	6.37	5.18	7.69	7.19	6.45	6.81	0.00
XOO2080	<i>vacB</i>	RNase R	-1.25	-1.52	-0.85	-1.37	7.49	9.01	9.64	10.49	8.96	10.33	0.00
XOO2083	-	hypothetical protein	-0.40	-0.21	-0.58	-	3.73	3.95	3.81	4.39	2.12	NA	0.00
XOO2084	-	tRNA/rRNA methyltransferase	-0.35	-0.62	-0.27	-0.16	9.89	10.51	10.16	10.43	9.70	9.86	0.00
XOO2093	<i>metX</i>	homoserine O-acetyltransferase	2.23	3.38	-0.07	3.38	6.39	3.02	8.47	8.54	7.11	3.73	0.00
XOO2114	-	TonB-like protein	-2.15	2.28	-4.55	-4.18	5.99	3.71	3.67	8.22	3.67	7.84	0.00
XOO2115	-	hypothetical protein	-0.35	-0.19	-0.56	-0.29	8.08	8.27	8.79	9.35	7.66	7.95	0.00
XOO2116	<i>serS</i>	seryl-tRNA synthetase	-0.17	-0.75	-0.34	0.58	6.57	7.31	8.85	9.20	8.77	8.19	0.00
XOO2123	<i>acpD</i>	ACP phosphodiesterase	-0.44	-0.60	-0.38	-0.32	8.73	9.34	10.03	10.41	9.55	9.87	0.00
XOO2124	-	transcriptional regulator	0.59	0.49	0.63	0.65	9.71	9.23	11.31	10.68	10.79	10.14	0.00
XOO2133	-	hypothetical protein	1.81	3.13	0.78	1.51	6.47	3.34	8.29	7.51	7.83	6.32	0.00
XOO2136	-	hypothetical protein	-0.47	-0.33	-0.30	-0.78	7.21	7.54	8.41	8.71	8.03	8.80	0.00
XOO2137	-	enolase	0.16	0.01	0.22	0.26	9.57	9.56	10.17	9.95	9.73	9.47	0.00
XOO2138	-	dioxygenase	0.04	0.06	0.04	0.01	11.66	11.60	12.83	12.79	12.39	12.38	0.00
XOO2139	-	methylthioribulose-1-phosphate dehydratase	-0.14	-0.13	-0.05	-0.25	8.98	9.11	11.06	11.12	11.16	11.41	0.00
XOO2140	<i>yhdG</i>	cationic amino acid transporter	1.06	0.70	1.65	0.82	9.14	8.44	6.84	5.19	9.54	8.72	0.00
XOO2141	<i>yhdG</i>	cationic amino acid transporter	0.46	0.41	0.71	0.26	8.87	8.46	9.37	8.65	8.29	8.04	0.00
XOO2142	-	hypothetical protein	-0.09	0.09	-0.24	-0.11	7.79	7.70	8.46	8.70	4.04	4.15	0.00
XOO2144	-	oxidoreductase	1.65	3.46	0.97	0.53	6.10	2.64	8.64	7.66	8.78	8.26	0.00
XOO2145	-	hypothetical protein	0.01	-0.37	0.71	-0.31	5.20	5.57	8.57	7.86	7.24	7.56	0.00
XOO2148	<i>cycL</i>	C-type cytochrome biogenesis protein	-0.56	-0.45	-0.56	-0.66	9.78	10.24	10.27	10.83	9.20	9.86	0.00
XOO2149	<i>dsbE</i>	C-type cytochrome biogenesis protein/thioredoxin	-0.76	-0.77	-0.66	-0.84	7.79	8.56	8.70	9.36	7.79	8.64	0.00
XOO2150	<i>cycK</i>	C-type cytochrome biogenesis membrane protein	-0.64	-0.34	-0.57	-1.00	6.86	7.20	7.69	8.25	7.45	8.45	0.00
XOO2151	<i>cycJ</i>	cytochrome c-type biogenesis protein CcmE	-0.06	0.27	-0.43	-0.03	7.60	7.33	8.79	9.22	8.68	8.71	0.00
XOO2157	-	hydrolase	0.42	0.20	0.96	0.10	8.77	8.57	9.61	8.65	8.81	8.71	0.00
XOO2159	-	glutamine cyclotransferase	0.96	2.16	0.93	-0.20	6.58	4.42	4.18	3.25	6.47	6.67	0.00
XOO2160	-	hypothetical protein	-1.30	-1.30	-1.35	-1.24	9.32	10.62	9.82	11.17	9.04	10.28	0.00
XOO2161	-	pseudouridylate synthase	-1.72	-1.54	-1.68	-1.95	7.81	9.35	8.54	10.22	6.10	8.05	0.00
XOO2162	-	hypothetical protein	-1.53	-1.55	-1.65	-1.40	10.23	11.78	11.62	13.27	10.49	11.89	0.00
XOO2164	-	hypothetical protein	0.09	-1.30	-1.08	2.65	7.74	9.04	8.31	9.39	7.45	4.79	0.00
XOO2166	-	hypothetical protein	0.01	0.05	0.07	-0.07	15.33	15.28	15.64	15.57	14.58	14.65	0.00
XOO2168	-	hypothetical protein	0.22	0.20	0.22	0.25	9.86	9.66	10.92	10.70	10.53	10.28	0.00
XOO2169	-	hypothetical protein	0.55	0.34	0.51	0.81	9.18	8.84	9.07	8.56	8.81	8.00	0.00
XOO2170	<i>malE</i>	sugar ABC transporter substrate-binding protein	-0.57	-1.38	0.18	-0.51	5.84	7.22	8.83	8.65	7.86	8.37	0.00
XOO2171	<i>lacF</i>	sugar ABC transporter permease	-0.04	-0.81	0.29	0.40	6.12	6.93	4.65	4.36	7.87	7.47	0.00
XOO2172	<i>lacG</i>	sugar ABC transporter permease	0.36	0.29	0.43	0.36	9.38	9.09	9.55	9.12	10.12	9.76	0.00
XOO2173	-	hypothetical protein	0.14	0.33	-0.04	0.14	6.56	6.23	4.03	4.07	7.14	7.00	0.00
XOO2174	<i>traB</i>	pheromone shutdown protein	0.00	-0.14	-0.68	0.83	7.92	8.06	8.20	8.88	5.09	4.26	0.00
XOO2175	<i>pat</i>	phosphinothricin N-acetyltransferase	0.84	1.13	0.51	0.87	9.46	8.33	10.54	10.03	10.02	9.15	0.00
XOO2176	-	beta-alanine synthetase	-0.24	-0.06	-0.38	-0.27	8.16	8.22	9.68	10.07	9.15	9.42	0.00
XOO2177	-	hypothetical protein	0.09	-0.67	0.27	0.66	7.44	8.11	9.81	9.54	9.07	8.41	0.00
XOO2178	-	hypothetical protein	0.76	0.69	0.77	0.83	10.40	9.71	11				

XOO2192	-	hypothetical protein	0.12	0.13	0.10	0.13	8.67	8.55	11.07	10.97	10.70	10.57	0.00
XOO2193	<i>folD</i>	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10	-0.64	0.02	-0.57	-1.37	6.46	6.44	7.96	8.52	6.79	8.17	0.00
XOO2194	<i>guaB</i>	inosine 5'-monophosphate dehydrogenase	-0.56	-0.42	-0.59	-0.68	8.53	8.94	10.06	10.65	9.62	10.30	0.00
XOO2195	<i>guaA</i>	GMP synthase	-0.23	-0.52	-0.04	-0.13	7.35	7.87	8.62	8.66	8.31	8.44	0.00
XOO2197	-	NADH dehydrogenase	1.33				2.04	NA	2.43	NA	3.29	1.96	0.00
XOO2198	-	LysR family transcriptional regulator	-1.92	-2.66	-1.03	-2.07	5.35	8.01	2.29	3.32	2.73	4.80	0.00
XOO2199	-	hypothetical protein	0.33	0.35	0.45	0.18	6.76	6.41	8.23	7.78	7.51	7.33	0.00
XOO2200	-	hypothetical protein	1.52	1.00	2.30	1.25	6.76	5.76	6.21	3.90	7.35	6.10	0.00
XOO2202	-	hypothetical protein	1.93	1.26	2.61		4.05	2.80	5.39	2.78	4.31	NA	0.00
XOO2203	-	hypothetical protein	-1.74	-1.01	-2.13	-2.07	3.25	4.26	6.37	8.50	6.20	8.27	0.00
XOO2204	<i>tipC</i>	methyl-accepting chemotaxis protein	-1.24	-0.76	-1.42	-1.54	3.68	4.44	8.46	9.87	7.78	9.32	0.00
XOO2205	<i>smf2</i>	manganese transport protein MntH	1.84	2.75	1.52	1.25	9.12	6.37	11.27	9.75	10.63	9.38	0.00
XOO2206	-	manganese transport regulator MntR	0.13	0.09	0.17	0.15	9.34	9.25	10.73	10.56	10.48	10.33	0.00
XOO2210	<i>yggB</i>	small conductance mechanosensitive ion channel	0.24	0.37	0.29	0.07	8.86	8.48	10.06	9.77	9.58	9.51	0.00
XOO2212	-	hypothetical protein	0.13	-0.07	0.18	0.28	7.86	7.94	8.92	8.74	8.83	8.55	0.00
XOO2213	-	hypothetical protein	0.74	0.67	0.79	0.76	15.27	14.60	15.77	14.98	14.70	13.94	0.00
XOO2214	<i>mutT</i>	7,8-dihydro-8-oxoguanine-triphosphatase	-1.43	-1.00	-1.63	-1.66	7.15	8.15	7.72	9.34	7.48	9.14	0.00
XOO2218	<i>hbdH1</i>	D-beta-hydroxybutyrate dehydrogenase	2.97	2.72	2.74	3.45	3.97	1.25	6.17	3.43	6.82	3.37	0.00
XOO2219	<i>pssA</i>	CDP-diacylglycerol-serine o-phosphatidyltransferase	0.03	-0.16	-0.26	0.53	7.94	8.10	7.91	8.17	7.85	7.33	0.00
XOO2220	<i>phaE</i>	PHA synthase subunit	0.71	1.23	0.61	0.30	8.11	6.88	8.96	8.34	7.89	7.60	0.00
XOO2221	<i>phbC</i>	poly (3-hydroxybutyric acid) synthase	0.52	0.57	0.29	0.71	8.30	7.74	8.93	8.65	9.07	8.37	0.00
XOO2224	-	hypothetical protein	-2.44	-2.93	-1.99	-2.40	6.02	8.94	8.95	10.94	8.20	10.60	0.00
XOO2225	<i>tex</i>	transcription-like protein	0.03	0.21	-0.01	-0.12	8.68	8.48	9.90	9.90	9.75	9.87	0.00
XOO2227	<i>regR</i>	two-component system regulatory protein	-1.49	-1.67	-1.37	-1.43	8.31	9.98	9.66	11.03	9.02	10.45	0.00
XOO2228	<i>regS</i>	two-component system sensor protein	-2.31	-3.26	-1.77	-1.90	4.77	8.03	5.95	7.71	6.28	8.18	0.00
XOO2229	<i>ispG</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	-0.07	-0.11	-0.08	-0.03	8.70	8.81	10.13	10.21	9.86	9.89	0.00
XOO2230	-	phosphatidylglycerophosphatase B	-2.73	-5.12	-1.50	-1.57	3.98	9.10	7.50	9.00	7.46	9.03	0.00
XOO2231	<i>proP</i>	Prop transport protein	-0.82		-0.82		2.64	NA	3.59	4.41	1.00	NA	0.00
XOO2235	-	hypothetical protein	-1.12		-1.20	-1.04	NA	NA	5.97	7.17	5.49	6.53	0.00
XOO2236	<i>murB</i>	UDP-N-acetylglucosamine reductase	-0.46	-0.80	-0.25	-0.32	7.55	8.36	8.21	8.47	4.23	4.55	0.00
XOO2237	<i>pyrD</i>	dihydroorotate dehydrogenase 2	-0.55	-0.44	-0.27	-0.94	6.38	6.82	8.31	8.58	5.95	6.89	0.00
XOO2238	-	hypothetical protein	0.24	0.41	0.18	0.13	9.38	8.97	10.48	10.30	10.49	10.36	0.00
XOO2241	<i>tspO</i>	tryptophan-rich sensory protein	-0.65	-0.55	-0.72	-0.69	9.24	9.79	11.10	11.82	10.56	11.24	0.00
XOO2242	<i>thrA</i>	bifunctional aspartokinase I/homoserine dehydrogenase I	-0.20	-1.66	-0.71	1.77	6.06	7.72	7.80	8.51	7.42	5.65	0.00
XOO2243	<i>thrB</i>	homoserine kinase	-0.87	-1.01	-0.93	-0.66	7.58	8.59	8.79	9.71	8.51	9.17	0.00
XOO2246	-	hypothetical protein	2.14	-0.37	4.00	2.80	2.70	3.06	5.76	1.77	6.03	3.22	0.00
XOO2247	<i>thrC</i>	threonine synthase	0.10		-0.80	1.01	NA	NA	2.97	3.77	6.65	5.65	0.00
XOO2248	-	hypothetical protein	-0.30	-0.58	-0.02		1.90	2.49	3.35	3.37	2.89	NA	0.00
XOO2251	<i>hisS</i>	histidyl-tRNA synthetase	-0.02	-0.12	0.01	0.05	8.96	9.08	9.68	9.67	9.17	9.12	0.00
XOO2254	-	hypothetical protein	0.12	-0.14	0.03	0.48	7.75	7.88	9.92	9.89	8.92	8.45	0.00
XOO2255	<i>hisG</i>	ATP phosphoribosyltransferase	0.88	1.56	1.21	-0.14	4.40	2.84	7.28	6.06	6.32	6.46	0.00
XOO2256	<i>hisD</i>	histidinol dehydrogenase	1.54	0.77	0.20	3.63	4.05	3.27	8.32	8.12	7.43	3.80	0.00
XOO2257	<i>hisC</i>	histidinol-phosphate aminotransferase	1.23	2.42	0.85	0.41	4.80	2.38	8.78	7.93	7.79	7.38	0.00
XOO2258	<i>hisB</i>	imidazole glycerol-phosphate dehydratase/histidinol phosphatase	0.84	1.50	0.18		3.43	1.93	7.43	7.24	NA	NA	0.00
XOO2259	<i>hisH</i>	imidazole glycerol phosphate synthase subunit HisH	0.42	1.37	-0.45	0.35	4.37	3.00	6.27	6.72	6.88	6.53	0.00
XOO2260	<i>hisA</i>	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylidene]amin	-0.19	0.08	-0.13	-0.51	6.92	6.84	3.56	3.69	3.55	4.07	0.00
XOO2261	<i>hisF</i>	imidazole glycerol phosphate synthase subunit HisF	-0.51	-0.65	-0.48	-0.39	9.23	9.88	10.58	11.05	9.80	10.19	0.00
XOO2262	<i>hisI</i>	bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-A	-1.02		-0.72	-1.33	6.41	NA	7.06	7.78	6.66	7.98	0.00
XOO2263	-	hypothetical protein	1.65		-0.15	3.45	3.10	NA	8.12	8.27	7.54	4.09	0.00
XOO2265	-	pectate lyase L	-0.12	0.48	-0.32	-0.54	3.03	2.55	6.57	6.89	6.01	6.54	0.00
XOO2266	-	phage replication protein RstA	-0.34	-0.37	0.13	-0.80	7.25	7.62	6.73	6.59	6.42	7.22	0.00
XOO2267	-	hypothetical protein	2.12	1.21	2.01	3.13	8.78	7.57	6.49	4.47	6.61	3.48	0.00
XOO2268	-	hypothetical protein	#DIV/0!				NA	NA	3.23	NA	2.12	NA	0.01
XOO2273	-	transposase	2.10		2.10		1.66	NA	6.46	4.36	2.60	NA	0.00
XOO2279	-	avirulence protein	-0.73	-0.78	-0.61	-0.79	8.02	8.80	9.91	10.53	9.49	10.27	0.00
XOO2286	-	RhsD protein	-0.02	-0.14	-0.09	0.17	5.26	5.39	8.41	8.50	8.04	7.86	0.00
XOO2290	-	hypothetical protein	2.73		2.73		4.08	NA	5.97	3.24	4.41	NA	0.00
XOO2291	<i>pgsA</i>	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	0.12	0.16	0.15	0.04	10.05	9.89	11.35	11.19	10.77	10.73	0.00
XOO2292	<i>uvrC</i>	excinuclease ABC subunit C	-1.96	-2.33	-1.83	-1.72	8.11	10.44	9.40	11.23	9.16	10.88	0.00
XOO2293	-	hypothetical protein	-0.07	0.00	-0.05	-0.17	8.05	8.05	9.64	9.69	9.42	9.59	0.00
XOO2294	-	low molecular weight phosphotyrosine protein phosphatase	-0.30	0.42	-0.37	-0.96	7.35	6.93	7.90	8.27	7.32	8.28	0.00
XOO2295	<i>kdsB</i>	3-deoxy-manno-octulose cytidyltransferase	0.11	0.66	-0.28	-0.06	6.58	5.93	6.53	6.81	3.98	4.04	0.00
XOO2296	<i>lpkX</i>	tetraacyldisaccharide 4'-kinase	-0.30	-0.55	-0.33	-0.01	6.16	6.71	8.09	8.42	7.62	7.62	0.00
XOO2297	<i>msbA</i>	ABC transporter ATP-binding protein	1.20	2.41	-0.16	1.36	6.16	3.75	8.18	8.34	5.14	3.78	0.00
XOO2298	<i>exbD</i>	biopolymer transport protein	0.02	-0.02	-0.07	0.15	8.78	8.80	10.25	10.32	9.86	9.70	0.00
XOO2299	<i>exbB</i>	biopolymer transport protein	-0.22	-0.40	-0.09	-0.17	3.64	4.04	9.43	9.53	9.13	9.31	0.00
XOO2300	<i>comA</i>	competence protein	#DIV/0!				1.95	NA	5.07	NA	2.16	NA	0.01
XOO2302	-	hypothetical protein	-2.49	-2.33	-2.56	-2.58	7.52	9.85	8.32	10.88	8.36	10.94	0.00
XOO2303	-	hypothetical protein	0.77		0.26	1.28	2.71	NA	3.95	3.69	6.87	5.59	0.00
XOO2304	<i>ycfV</i>	ABC transporter ATP-binding protein	0.49	0.54	0.42	0.53	8.22	7.68	9.31	8.90	8.36	7.83	0.00
XOO2305	<i>lolC</i>	lipoprotein releasing system transmembrane protein	-0.12	-0.07	-0.09	-0.21	9.05	9.12	10.57	10.66	10.25	10.46	0.00
XOO2306	-	hypothetical protein	0.84	2.88	0.04	-0.40	7.18	4.30	9.70	9.65	8.99	9.39	0.00
XOO2307	<i>sdhB</i>	succinate dehydrogenase iron-sulfur subunit	0.27	0.30	0.37	0.14	10.69	10.39	11.77	11.39	11.43	11.29	0.00
XOO2308	<i>sdhA</i>	succinate dehydrogenase flavoprotein subunit	-0.05	0.01	0.01	-0.17	9.95	9.94	11.07	11.06	10.95	11.12	0.00
XOO2309	<i>sdhD</i>	succinate dehydrogenase membrane anchor subunit	-0.46	-0.37	-0.51	-0.50	7.79	8.16	8.83	9.34	8.52	9.03	0.00
XOO2310	<i>sdhC</i>	succinate dehydrogenase membrane anchor subunit	-0.38	-0.38	-0.36	-0.40	10.50	10.88	10.93	11.29	10.60	11.00	0.00
XOO2313	<i>ugpC</i>	sugar ABC transporter ATP-binding protein	-0.59	-0.37	-0.41	-0.99	6.17	6.55	8.24	8.65	7.27	8.26	0.00
XOO2314	<i>wzf</i>	glucose-6-phosphate 1-dehydrogenase	-0.31	-0.33	-0.37	-0.22	8.86	9.19	10.02	10.40	9.55	9.76	0.00
XOO2315	<i>gik</i>	glucokinase	-0.67	-0.72	-0.66	-0.62	8.45	9.17	9.19	9.85	9.10	9.72	0.00
XOO2316	<i>pgl</i>	6-phosphogluconolactonase	-0.69	-0.76	-0.83	-0.49	8.07	8.84	9.03	9.86	8.54	9.02	0.00
XOO2317	<i>edd</i>	phosphogluconate dehydratase	-0.64	-0.09	-0.94	-0.89	6.73	6.82	7.08	8.02	7.06	7.95	0.00

XOO2338	<i>fpr</i>	ferredoxin-NADP reductase		2.13	4.67	1.15	0.58	6.58	1.91	7.83	6.68	7.21	6.63	0.00
XOO2339	<i>gpo</i>	glutathione peroxidase		2.84		2.84	2.79	NA	6.60	NA	4.29	1.46	0.00	
XOO2341	<i>dcp</i>	peptidyl-dipeptidase	-0.02		-0.02		2.56	NA	5.33	5.36	1.95	NA	0.00	
XOO2342	<i>aprE</i>	extracellular protease		#DIV/0!				NA	NA	3.92	NA	NA	NA	0.02
XOO2343	-	DNA-directed RNA polymerase specialized sigma subunit, sigma2	0.54	0.40	0.63	0.59	9.95	9.55	10.87	10.24	10.41	9.82	0.00	
XOO2344	-	hypothetical protein	1.40	1.38	1.71	1.10	10.97	9.59	11.19	9.48	11.61	10.50	0.00	
XOO2345	-	MarR family transcriptional regulator	0.41	-0.27	0.86	0.65	6.40	6.68	9.22	8.35	8.60	7.95	0.00	
XOO2346	-	hypothetical protein	-0.49	-1.22	-0.17	-0.07	6.41	7.63	9.43	9.60	9.37	9.44	0.00	
XOO2349	-	hypothetical protein	-0.18	-0.39	-0.23	0.07	9.86	10.25	10.61	10.84	10.05	9.98	0.00	
XOO2351	-	hypothetical protein	1.90	2.69	1.11		5.35	2.66	3.59	2.48	NA	NA	0.00	
XOO2352	<i>bgfS</i>	beta-glucosidase	1.96		0.95	2.97	3.94	NA	6.92	5.98	6.68	3.70	0.00	
XOO2354	-	hypothetical protein	-1.79	-0.89	-2.37	-2.12	3.79	4.68	7.31	9.68	6.87	9.00	0.00	
XOO2355	<i>sgT</i>	sodium/glucose cotransport protein		#DIV/0!				2.78	NA	2.40	NA	0.50	NA	0.02
XOO2357	<i>phoX</i>	alkaline phosphatase	0.09	0.35	-0.25	0.16	7.30	6.95	8.34	8.59	7.88	7.72	0.00	
XOO2360	<i>pgi</i>	glucose-6-phosphate isomerase	-0.28	-0.18	-0.38	-0.29	8.61	8.79	9.80	10.17	9.41	9.70	0.00	
XOO2364	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	-0.04	0.21	-0.28	-0.04	9.22	9.00	11.20	11.48	10.85	10.88	0.00	
XOO2366	<i>pcnB</i>	polynucleotide adenylyltransferase	0.82	1.28	0.77	0.40	8.65	7.37	9.38	8.61	8.86	8.46	0.00	
XOO2367	-	GTP cyclohydrolase	3.38	2.80	4.36	2.99	8.58	5.78	9.15	4.79	9.45	6.46	0.00	
XOO2368	<i>amiC</i>	N-acetylmuramoy-L-alanine amidase	4.35	5.32	3.66	4.07	7.46	2.15	9.54	5.88	9.16	5.09	0.00	
XOO2375	-	serine protease	0.54	0.76	0.35	0.52	9.58	8.83	10.40	10.04	9.12	8.61	0.00	
XOO2376	<i>czcB</i>	cation efflux system protein		#DIV/0!				2.54	NA	0.50	NA	2.26	NA	0.03
XOO2377	<i>czcA</i>	cation efflux system protein	3.15		3.15		6.18	NA	5.88	2.73	1.95	NA	0.00	
XOO2378	<i>nodV</i>	nodulation protein	0.46	0.90	0.24	0.23	8.12	7.22	8.48	8.24	4.47	4.24	0.00	
XOO2379	<i>nodW</i>	nodulation protein	0.77	1.17	0.37		2.26	1.09	3.70	3.33	6.18	NA	0.00	
XOO2380	<i>yapH</i>	YapH protein	2.62		2.62		3.00	NA	4.73	2.10	5.37	NA	0.00	
XOO2383	-	hypothetical protein	0.16	0.57	-0.96	0.87	1.40	0.84	6.72	7.68	8.68	7.81	0.00	
XOO2386	<i>aroA</i>	3-phosphoshikimate 1-carboxyvinyltransferase	1.14	2.13	0.39	0.91	7.15	5.02	9.95	9.56	9.30	8.40	0.00	
XOO2387	<i>pheA</i>	P-protein	0.42	0.40	0.44	0.41	10.12	9.72	11.42	10.98	11.12	10.71	0.00	
XOO2388	<i>serC</i>	phosphoserine aminotransferase	0.11	0.07	0.11	0.16	9.82	9.75	10.72	10.61	10.44	10.27	0.00	
XOO2389	-	sulfite oxidase subunit YedY	1.12	1.73	1.45	0.17	7.18	5.44	7.09	5.64	7.07	6.89	0.00	
XOO2393	<i>phaF</i>	poly(hydroxyalcanoate) granule associated protein	-0.52	-1.27	-1.49	1.20	7.20	8.47	9.16	10.65	5.96	4.76	0.00	
XOO2394	-	hypothetical protein	1.10	3.19	-0.10	0.21	5.57	2.38	8.28	8.37	7.02	6.81	0.00	
XOO2398	<i>hutH</i>	histidine ammonia-lyase	-1.02	-1.00	-0.40	-1.67	7.44	8.44	4.41	4.80	6.42	8.09	0.00	
XOO2399	<i>hutG</i>	formylglutamate amidohydrolase	-1.13	0.43	-2.10	-1.72	2.20	1.76	5.89	7.99	6.21	7.93	0.00	
XOO2400	<i>hutU</i>	urocanate hydratase	-1.23		-0.84	-1.61	1.95	NA	5.27	6.11	3.11	4.73	0.00	
XOO2401	-	acyltransferase		#DIV/0!				3.18	NA	2.68	NA	NA	NA	0.01
XOO2402	-	hypothetical protein	0.21		-1.16	1.58	2.89	NA	7.35	8.51	5.21	3.64	0.00	
XOO2406	<i>gyrA</i>	DNA gyrase subunit A	0.17	0.14	0.12	0.24	10.80	10.66	12.03	11.91	11.26	11.02	0.00	
XOO2408	-	hypothetical protein	-2.42	-2.38	-2.27	-2.61	6.09	8.47	8.23	10.50	7.55	10.16	0.00	
XOO2409	<i>lysS</i>	lysyl-tRNA synthetase	-1.57	-1.75	-0.90	-2.07	2.56	4.31	5.62	6.52	4.05	6.12	0.00	
XOO2412	<i>zipA</i>	cell division protein ZipA	0.86	0.76	1.05	0.78	9.97	9.21	10.18	9.13	9.65	8.87	0.00	
XOO2413	<i>smc</i>	chromosome segregation protein	0.38	0.23	-0.14	1.04	6.98	6.75	8.29	8.42	7.69	6.65	0.00	
XOO2414	<i>rplL</i>	50S ribosomal protein L9	-0.03	0.23	-0.34	0.01	10.04	9.81	11.31	11.65	10.48	10.47	0.00	
XOO2415	<i>rpsR</i>	30S ribosomal protein S18	0.05	0.17	-0.11	0.07	11.15	10.98	12.10	12.20	11.47	11.40	0.00	
XOO2416	<i>rpsF</i>	30S ribosomal protein S6	0.11	0.27	-0.02	0.09	11.87	11.60	13.71	13.74	13.03	12.94	0.00	
XOO2417	-	hypothetical protein	-0.40	-0.53	-0.32	-0.34	9.27	9.80	11.08	11.40	10.73	11.07	0.00	
XOO2418	<i>asnC</i>	asparaginyl-tRNA synthetase	0.34	0.36	0.26	0.39	9.73	9.37	10.17	9.91	9.92	9.53	0.00	
XOO2420	-	hypothetical protein	0.78	-0.79	0.80	2.34	3.68	4.48	7.98	7.18	6.23	3.89	0.00	
XOO2422	<i>paiB</i>	transcriptional regulator protein Pai2	-0.91	-1.98	-0.13	-0.64	6.16	8.14	7.61	7.73	7.27	7.91	0.00	
XOO2423	<i>yadF</i>	carbonic anhydrase	-0.03	0.55	-0.25	-0.40	7.45	6.90	8.60	8.85	7.85	8.25	0.00	
XOO2424	<i>haaO</i>	3-hydroxyanthranilate 3,4-dioxygenase	2.20	2.76	0.06	3.77	3.17	0.41	4.48	4.42	7.14	3.37	0.00	
XOO2428	-	kynureninase	0.60	1.54	0.15	0.10	5.25	3.70	4.66	4.51	7.83	7.73	0.00	
XOO2429	-	kynurenine 3-monooxygenase	-0.45	-0.70	0.57	-1.22	4.86	5.56	5.76	5.19	1.73	2.95	0.00	
XOO2430	<i>sbcB</i>	exonuclease I	0.43	0.87	0.13	0.29	6.78	5.91	9.05	8.92	7.53	7.24	0.00	
XOO2431	-	hypothetical protein	1.07	0.11	-0.09	3.17	8.37	8.26	9.04	9.13	7.87	4.70	0.00	
XOO2432	-	oxidoreductase	0.68	-1.01	-0.12	3.18	5.54	6.56	8.98	9.10	7.63	4.45	0.00	
XOO2433	-	hypothetical protein	0.20	0.22	0.16	0.22	15.80	15.57	15.99	15.83	15.58	15.37	0.00	
XOO2434	-	5'-nucleotidase	2.25	1.12	2.97	2.67	4.37	3.25	5.86	2.89	5.80	3.13	0.00	
XOO2438	<i>rmlL</i>	23S rRNA m(2)G2445 methyltransferase	0.13	-0.01	0.23	0.16	8.29	8.30	9.78	9.55	9.16	9.00	0.00	
XOO2440	-	ABC transporter ATP-binding protein	0.41	0.23	0.58	0.42	8.68	8.45	8.98	8.39	8.85	8.43	0.00	
XOO2445	-	hypothetical protein	0.08	0.00	0.58	-0.33	5.21	5.22	3.82	3.24	6.66	6.99	0.00	
XOO2446	-	hypothetical protein	0.61	0.34	0.41	1.07	8.73	8.39	9.50	9.10	8.71	7.64	0.00	
XOO2447	<i>sseA</i>	thiosulfate sulfurtransferase	-0.43	-1.43	0.12	0.03	4.72	6.15	3.94	3.82	3.63	3.60	0.00	
XOO2448	-	MutT/nudix family protein	0.29	-0.04	0.82	0.07	7.58	7.62	9.08	8.26	8.03	7.96	0.00	
XOO2451	-	peptidyl-prolyl cis-trans isomerase	1.38	1.33	1.26	1.56	11.70	10.36	12.19	10.93	11.57	10.01	0.00	
XOO2452	<i>crt</i>	3-hydroxybutyryl-CoA dehydratase	2.02	1.90	1.14	3.01	8.49	6.59	9.13	7.99	6.88	3.87	0.00	
XOO2454	<i>nth</i>	endonuclease III	0.73	-0.37	0.77	1.78	6.25	6.62	9.24	8.46	8.35	6.57	0.00	
XOO2457	<i>cynT</i>	carbonic anhydrase	1.32		1.32		2.70	NA	2.97	1.65	4.01	NA	0.00	
XOO2460	<i>oprO</i>	polyphosphate-selective porin O	-0.33	0.56	-0.69	-0.86	6.98	6.42	7.96	8.65	7.56	8.42	0.00	
XOO2461	<i>phoX</i>	phosphate binding protein	-0.72	-0.79	-0.73	-0.65	9.10	9.88	9.71	10.44	9.98	10.63	0.00	
XOO2462	<i>pstS</i>	phosphate ABC transporter substrate-binding protein	-1.13	-1.30	-0.96	-1.14	6.89	8.18	7.93	8.89	8.36	9.50	0.00	
XOO2463	<i>pstC</i>	phosphate ABC transporter permease	-2.05	-2.85	-1.86	-1.45	5.54	8.39	7.20	9.06	3.72	5.17	0.00	
XOO2464	<i>pstA</i>	phosphate ABC transporter permease	0.12	-0.72	-1.46	2.54	3.76	4.48	8.47	9.94	7.23	4.69	0.00	
XOO2465	<i>pstB</i>	phosphate transporter ATP-binding protein	-0.62	-0.48	-0.66	-0.71	9.85	10.33	9.98	10.65	9.41	10.11	0.00	
XOO2466	<i>phoU</i>	phosphate regulon transcriptional regulator	0.45	1.17	-1.88	2.06	5.38	4.21	5.75	7.62	5.89	3.83	0.00	
XOO2468	<i>rnt</i>	ribonuclease T	-0.63	-0.71	-0.63	-0.56	8.94	9.65	10.05	10.68	9.63	10.18	0.00	
XOO2479	-	site-specific recombinase	1.23		1.23		2.64	NA	5.90	4.67	2.68	NA	0.00	
XOO2482	<i>secD</i>	preprotein translocase subunit SecD	-0.06	-0.49	-0.03	0.35	7.36	7.85	9.63	9.66	9.63	9.28	0.00	
XOO2483	<i>yajC</i>	preprotein translocase subunit YajC	0.11	0.24	0.06	0.04	9.42	9.17	11.28	11.22	10.84	10.81	0.00	
XOO2484	<i>tgt</i>	queueine tRNA-ribosyltransferase	-0.31	-1.07	-0.09	0.23	7.33	8.40	9.31	9.40</				

XOO2508	<i>coaD</i>	phosphopantetheine adenyllyltransferase	-0.03	-0.08	0.09	-0.09	10.55	10.63	11.33	11.25	11.46	11.55	0.00
XOO2510	<i>htpG</i>	heat shock protein 90	0.93	0.83	0.89	1.08	9.88	9.05	11.06	10.16	11.02	9.94	0.00
XOO2514	<i>moeB</i>	molybdopterin biosynthesis protein MoeB	0.18	2.46	-0.63	-1.30	5.94	3.48	8.22	8.85	6.83	8.13	0.00
XOO2528	<i>moeA</i>	molybdopterin biosynthesis	1.40	0.72	0.44	3.05	6.58	5.86	7.89	7.45	6.72	3.67	0.00
XOO2530	-	hypothetical protein	-0.21	0.01	-0.26	-0.37	8.98	8.97	10.36	10.62	10.34	10.71	0.00
XOO2531	-	hypothetical protein	-0.65	-0.66	-0.57	-0.72	9.41	10.07	11.76	12.33	11.20	11.92	0.00
XOO2532	-	hypothetical protein	0.07	0.15	-0.13	0.19	9.55	9.40	11.73	11.86	11.17	10.98	0.00
XOO2533	<i>pilF</i>	fimbrial biogenesis protein	0.40	0.42	0.36	0.44	11.52	11.10	12.87	12.51	12.57	12.13	0.00
XOO2534	-	hypothetical protein	-0.10	-0.10	-0.19	-0.02	10.08	10.18	11.72	11.91	11.19	11.22	0.00
XOO2536	-	TetR family transcriptional regulator	-0.01	-0.27	0.20	0.04	7.64	7.91	8.32	8.12	7.79	7.75	0.00
XOO2537	<i>fadB</i>	3-hydroxyacyl-CoA dehydrogenase	-0.46	-0.55	-0.36	-0.49	8.80	9.35	9.79	10.15	9.93	10.41	0.00
XOO2538	<i>fadA</i>	acetyl-CoA acetyltransferase	-1.39	-2.00	-1.29	-0.89	3.55	5.55	7.62	8.92	8.12	9.01	0.00
XOO2539	-	hypothetical protein	-0.79	-1.02	-0.56	-0.78	5.87	6.89	7.64	8.21	7.62	8.40	0.00
XOO2540	<i>crcB</i>	camphor resistance protein CrcB	1.25	2.40	0.66	0.68	5.59	3.19	9.02	8.36	8.53	7.85	0.00
XOO2541	-	hypothetical protein	2.83	1.45	3.47	3.56	9.20	7.75	6.70	3.23	7.12	3.56	0.00
XOO2543	-	hypothetical protein	-0.35	-0.62	-0.20	-0.23	3.49	4.11	3.73	3.93	4.78	5.01	0.00
XOO2545	-	hypothetical protein	1.78	1.51	2.06	2.48	NA	4.64	3.13	4.53	2.47	0.00	
XOO2546	<i>ftsK</i>	cell division protein	0.65	3.95	-2.27	0.27	5.61	1.65	4.54	6.81	3.40	3.13	0.00
XOO2547	<i>trxB</i>	thioredoxin reductase	0.56	0.43	0.38	0.88	7.58	7.15	8.94	8.56	8.71	7.83	0.00
XOO2548	-	hypothetical protein	1.31	1.45	1.30	1.16	9.40	7.95	10.17	8.87	10.13	8.96	0.00
XOO2549	-	hypothetical protein	1.38	1.44	1.33	NA	NA	5.51	4.08	4.19	2.86	0.00	
XOO2550	-	hypothetical protein	0.86	2.13	-0.39	0.85	4.77	2.64	3.25	3.65	4.36	3.51	0.00
XOO2551	<i>aat</i>	leucyl/phenylalanyl-tRNA--protein transferase	0.00	-0.51	0.52	0.79	NA	7.30	7.82	6.85	6.33	0.00	
XOO2552	<i>infA</i>	translation initiation factor IF-1	-0.25	-0.11	-0.35	-0.28	12.25	12.37	13.43	13.78	13.00	13.28	0.00
XOO2553	<i>cipA</i>	ATP-dependent Clp protease subunit	0.12	0.04	0.21	0.10	10.28	10.24	11.08	10.87	10.89	10.79	0.00
XOO2554	<i>cipS</i>	ATP-dependent Clp protease adaptor protein CipS	-0.22	-0.21	-0.29	-0.16	10.93	11.14	11.80	12.09	11.09	11.25	0.00
XOO2555	<i>mutT</i>	7,8-dihydro-8-oxoguanine-triphosphatase	0.23	0.12	0.39	0.19	9.58	9.45	10.40	10.01	10.37	10.18	0.00
XOO2556	<i>mnmA</i>	tRNA-specific 2-thiouridylase MnmA	-1.72	-2.93	0.37	-2.59	4.72	7.65	7.85	7.48	5.32	7.91	0.00
XOO2557	-	hypothetical protein	1.86	1.86	3.95	NA	4.56	2.70	2.43	NA	NA	0.00	
XOO2558	<i>mcp</i>	chemotaxis protein	-2.90	-3.45	-2.34	NA	NA	5.65	9.11	2.60	4.95	0.00	
XOO2559	-	hypothetical protein	#DIV/0!				1.66	NA	2.00	NA	3.02	NA	0.01
XOO2560	-	hypothetical protein	0.77	0.89	0.85	0.58	7.50	6.61	7.96	7.12	7.84	7.26	0.00
XOO2562	-	HrpX related protein	0.78	0.78	0.79	0.77	8.06	7.28	9.57	8.78	9.41	8.63	0.00
XOO2563	<i>pdeA</i>	c-di-GMP phosphodiesterase A	-0.04	-0.33	0.19	0.01	3.09	3.42	7.96	7.77	6.25	6.25	0.00
XOO2564	-	histidine kinase	0.55	0.64	0.40	0.63	8.40	7.76	9.78	9.38	8.92	8.30	0.00
XOO2566	<i>flgM</i>	flagellar protein	-3.26	-2.95	-3.25	-3.59	8.91	11.85	9.28	12.54	8.12	11.71	0.00
XOO2567	<i>flgA</i>	flagellar basal body P-ring biosynthesis protein FlgA	-2.56	-1.20	-4.59	-1.88	3.12	4.33	4.75	9.34	2.60	4.48	0.00
XOO2568	<i>cheV</i>	chemotaxis protein	-2.50	-1.90	-3.10	NA	3.70	6.02	7.92	4.49	7.58	0.00	
XOO2569	<i>flgB</i>	flagellar basal-body rod protein FlgB	-0.20	2.31	-2.71	7.96	5.66	6.24	8.96	NA	NA	0.00	
XOO2570	<i>flgC</i>	flagellar basal body rod protein FlgC	-1.16	0.66	-1.85	-2.28	4.52	3.87	7.57	9.42	6.86	9.14	0.00
XOO2571	<i>flgD</i>	flagellar basal body rod modification protein	-2.89	-3.40	-2.49	-2.78	5.31	8.71	7.30	9.79	6.90	9.68	0.00
XOO2572	<i>flgE</i>	flagellar hook protein FlgE	-3.82	-4.02	-3.97	-3.47	10.14	14.15	10.38	14.34	9.94	13.41	0.00
XOO2575	<i>flgG</i>	flagellar basal body rod protein FlgG	0.27	2.23	-1.69	1.79	NA	6.22	3.99	6.60	8.30	0.00	
XOO2576	<i>flgH</i>	flagellar basal body L-ring protein	-0.65	-0.91	-0.39	1.85	NA	2.12	3.03	2.16	2.55	0.00	
XOO2577	<i>flgI</i>	flagellar basal body P-ring biosynthesis protein FlgA	-0.81	0.20	0.40	-3.03	3.69	3.49	7.27	6.88	4.46	7.49	0.00
XOO2578	<i>flgJ</i>	flagellar rod assembly protein/muramidase FlgJ	1.24	1.24	2.12	NA	3.06	1.82	3.10	NA	NA	0.00	
XOO2579	<i>flgK</i>	flagellar hook-associated protein FlgK	2.47	2.47	5.22	2.75	1.90	NA	2.58	NA	NA	0.00	
XOO2580	<i>flgL</i>	flagellar hook-associated protein FlgL	-1.14	-0.62	-1.66	2.89	NA	6.88	7.49	6.20	7.86	0.00	
XOO2581	<i>fliC</i>	flagellin	-1.21	-1.64	-2.62	0.62	2.71	4.35	6.64	9.25	5.42	4.80	0.00
XOO2582	<i>fliD</i>	flagellar protein	-1.50	-1.74	-1.34	-1.43	6.19	7.93	8.64	9.98	8.07	9.50	0.00
XOO2583	<i>fliS</i>	flagellar protein	-3.26	-3.17	-3.43	-3.19	5.17	8.35	6.74	10.16	6.81	10.00	0.00
XOO2585	-	hypothetical protein	-1.32	-0.76	-1.22	-1.98	7.28	8.03	6.64	7.86	5.62	7.60	0.00
XOO2586	-	response regulator	-0.02	0.09	-0.14	4.55	4.46	2.64	2.78	NA	NA	0.00	
XOO2587	<i>rpoN</i>	RNA polymerase sigma-54 factor	0.26	-0.16	-0.92	1.85	3.62	3.78	2.89	3.82	5.83	3.98	0.00
XOO2588	-	response regulator	-0.98	-0.84	-0.95	-1.15	8.43	9.27	9.66	10.60	9.29	10.44	0.00
XOO2589	<i>flqQ</i>	transcriptional regulator	-1.33	-1.00	-1.81	-1.20	3.15	4.15	7.81	9.62	7.82	9.02	0.00
XOO2590	<i>vioA</i>	nucleotide sugar transaminase	-0.74	-0.45	-0.65	-1.12	7.26	7.71	8.86	9.50	8.45	9.57	0.00
XOO2591	<i>acp</i>	acyl carrier protein	-1.29	-1.44	-1.01	-1.43	8.41	9.85	9.82	10.83	9.16	10.60	0.00
XOO2592	<i>fabH</i>	3-oxoacyl-ACP synthase	-1.97	-1.63	-1.52	-2.77	6.41	8.04	7.48	9.00	6.51	9.28	0.00
XOO2593	<i>fabG</i>	3-oxoacyl-ACP reductase	-3.12	-3.66	-2.80	-2.91	0.50	4.16	5.78	8.59	5.50	8.41	0.00
XOO2594	-	dehydrogenase	-1.89	-2.65	0.38	-3.38	5.28	7.93	4.76	4.39	5.27	8.65	0.00
XOO2596	-	ring hydroxylating dioxygenase subunit alpha	-1.96	-0.15	-3.30	-2.44	2.66	2.81	5.49	8.79	6.94	9.38	0.00
XOO2597	-	hypothetical protein	-2.41	-3.59	-1.12	-2.51	4.72	8.31	7.39	8.51	7.02	9.53	0.00
XOO2598	-	hypothetical protein	-0.97	-1.14	-0.83	-0.95	8.47	9.61	9.56	10.39	9.44	10.39	0.00
XOO2599	<i>rbfC</i>	O-antigen biosynthesis protein	-2.62	-1.81	-3.44	NA	NA	6.19	8.00	4.33	7.77	0.00	
XOO2600	<i>fliE</i>	flagellar protein	-1.55	-1.49	-1.32	-1.85	1.73	3.22	3.13	4.45	2.54	4.40	0.00
XOO2601	<i>fliF</i>	flagellar MS-ring protein	-1.26	-0.77	-1.08	-1.93	7.18	7.95	7.94	9.02	7.12	9.04	0.00
XOO2602	<i>fliG</i>	flagellar protein	-0.90	-0.38	-1.43	2.20	NA	3.13	3.51	2.35	3.78	0.00	
XOO2604	<i>fliI</i>	flagellar protein	0.17	0.17	1.58	NA	6.02	5.85	NA	1.74	0.01	0.00	
XOO2605	<i>fliJ</i>	flagellar FliJ protein	2.30	2.30	1.29	NA	5.93	3.64	2.94	NA	NA	0.00	
XOO2606	<i>fliK</i>	flagellar protein	0.62	3.00	-0.03	-1.12	6.74	3.74	7.38	7.41	5.33	6.45	0.00
XOO2607	<i>fliL</i>	flagellar protein	-2.37	-2.60	-2.67	-1.84	6.60	9.20	7.58	10.25	6.15	8.00	0.00
XOO2608	<i>fliM</i>	flagellar motor switch protein FliM	-0.93	-0.81	-0.98	-1.00	9.44	10.25	9.06	10.04	9.17	10.17	0.00
XOO2610	<i>fliO</i>	flagellar protein	-0.41	-0.03	-0.44	-0.78	7.96	7.99	9.06	9.50	8.72	9.50	0.00
XOO2611	<i>fliP</i>	flagellar biosynthesis protein FliP	-0.33	-0.19	-0.19	-0.61	7.34	7.53	9.13	9.31	9.09	9.70	0.00
XOO2612	<i>fliQ</i>	flagellar biosynthesis	2.36	2.36	2.26	NA	7.98	5.62	3.27	NA	NA	0.00	
XOO2613	<i>fliR</i>	flagellar biosynthetic protein	-0.59	-0.88	-0.43	-0.47	7.18	8.06	7.61	8.05	8.33	8.80	0.00
XOO2614	-	diguanylate cyclase	0.11	1.50	-0.77	-0.40	3.46	1.96	6.11	6.87	6.61	7.02	0.00
XOO2615	-	diguanylate cyclase	#DIV/0!				2.50	NA	4.94	NA	2.32	NA	0.00
XOO2616	-	diguanylate cyclase	0.52	-	-1.61	2.65	2.38	NA	6.79	8.40	6.24	3.59	0.00
XOO2617	<i>fliB</i>	flagellar biosynthesis protein FliB	-0.57	-0.10	-0.60	-1.02	4.36	4.45	7.54	8.14	6.39	7.40	0.00
XOO2618	<i>fliA</i>	flagellar biosynthesis protein FliA	0.48	-0.77	1.73	1.40	2.17	NA	NA	5.06	3.33	0.00	
XOO2619	<i>fliF</i>	flagellar biosynthesis regulator FliF	-2.42	-0.62	-2.83	-3.81	2.89	3.51	5.98	8.81	4.82	8.63	

XOO2647	-	hypothetical protein	0.48	1.93	-1.56	1.06	2.71	0.78	5.22	6.78	5.61	4.55	0.00
XOO2653	<i>cydC</i>	ABC transporter ATP-binding protein	-0.04	-0.16	0.08		2.58	2.75	3.52	3.44	2.76	NA	0.00
XOO2654	<i>strW</i>	transporter	1.68	1.34	1.39	2.29	8.03	6.69	8.56	7.16	7.07	4.78	0.00
XOO2660	<i>cydA</i>	cytochrome D ubiquinol oxidase subunit I	-0.09	-1.16	0.30	0.59	6.01	7.16	6.88	6.58	7.38	6.79	0.00
XOO2663	<i>cynX</i>	MFS transporter	0.73	4.00	-2.55		7.09	3.09	5.92	8.47	NA	NA	0.00
XOO2664	<i>gaa</i>	glutaryl-7-ACA acylase	0.19	-0.57	0.55	0.60	8.50	9.07	10.90	10.34	8.30	7.70	0.00
XOO2665	<i>proA</i>	gamma-glutamyl phosphate reductase	1.89		3.05	0.74	5.56	NA	6.75	3.70	6.52	5.78	0.00
XOO2668	-	hypothetical protein	0.83	0.65	0.73	1.10	8.66	8.00	9.36	8.64	8.97	7.87	0.00
XOO2669	<i>argH</i>	arginosuccinate lyase	0.21	0.25	0.16	0.22	8.78	8.53	9.46	9.31	9.52	9.30	0.00
XOO2672	<i>argB</i>	acetylglutamate kinase	0.80	0.85	0.63	0.93	8.39	7.55	10.02	9.39	9.46	8.53	0.00
XOO2673	<i>argE</i>	acetylornithine deacetylase	0.27	0.03	0.59	0.21	3.28	3.26	4.24	3.65	3.68	3.48	0.00
XOO2675	<i>argG</i>	argininosuccinate synthase	1.67	0.32	4.38	0.30	8.53	8.20	9.36	4.98	8.83	8.53	0.00
XOO2676	<i>argF</i>	N-acetylornithine carbamoyltransferase	0.57	1.31	0.28	0.13	7.29	5.98	9.80	9.52	9.63	9.50	0.00
XOO2677	-	hypothetical protein	-0.14	-0.34	0.06	-0.14	8.25	8.59	10.73	10.67	9.73	9.88	0.00
XOO2678	<i>cysS</i>	cysteinyl-tRNA synthetase	0.20	0.59	0.12	-0.13	3.27	2.68	7.09	6.97	6.82	6.95	0.00
XOO2679	-	hypothetical protein	1.57	3.69	0.63	0.39	7.74	4.06	8.33	7.70	8.00	7.61	0.00
XOO2680	<i>tetV</i>	drug:proton antiporter	0.32	0.41	0.24		4.16	3.75	7.05	6.81	5.97	NA	0.00
XOO2681	-	interphotoreceptor retinoid-binding protein	#DIV/0!				3.86	NA	3.50	NA	2.58	NA	0.00
XOO2682	<i>dksA</i>	DnaK supressor	0.65	0.88	0.48	0.59	10.34	9.46	11.64	11.16	11.46	10.87	0.00
XOO2683	<i>pyrC</i>	dihydroorotate	-0.06	0.33	-0.23	-0.29	8.34	8.01	9.00	9.22	8.68	8.97	0.00
XOO2684	-	peptidase	-0.66	-0.17	-0.96	-0.87	7.54	7.71	8.57	9.52	3.14	4.01	0.00
XOO2685	<i>eutC</i>	ethanolamine ammonia-lyase light subunit	-2.63		-2.63		NA	NA	1.50	4.13	3.93	NA	0.00
XOO2688	-	hypothetical protein	-2.06	-1.89	-3.51	-0.79	1.50	3.39	1.29	4.80	3.00	3.79	0.00
XOO2689	-	general stress protein	-1.20	-0.75	-1.32	-1.54	8.43	9.18	9.53	10.85	8.20	9.75	0.00
XOO2696	-	pectinesterase	-0.05		-0.10	0.00	1.29	NA	8.08	8.19	7.56	7.56	0.00
XOO2699	<i>pglA</i>	polygalacturonase	0.34	0.23	0.55	0.24	10.16	9.93	11.53	10.97	11.14	10.90	0.00
XOO2700	-	hypothetical protein	0.72	2.14	-0.05	0.06	5.38	3.23	8.04	8.09	7.87	7.81	0.00
XOO2701	<i>cbbZ</i>	phosphoglycolate phosphatase	0.03	1.40	-0.81	-0.51	5.82	4.42	8.47	9.28	4.18	4.68	0.00
XOO2702	<i>ubiG</i>	3-demethylubiquinone-9 3-methyltransferase	0.29	2.21	-0.82	-0.53	5.28	3.07	7.58	8.40	3.49	4.02	0.00
XOO2703	-	N-ethylammonium chlorohydrolase	0.00	0.03	0.00	-0.03	8.69	8.66	9.51	9.51	9.48	9.51	0.00
XOO2704	-	hypothetical protein	2.02	2.04	0.28	3.76	5.26	3.23	8.34	8.06	7.80	4.04	0.00
XOO2705	<i>efP</i>	elongation factor P	0.28	0.38	0.25	0.22	11.07	10.70	12.10	11.85	11.82	11.60	0.00
XOO2708	-	diguanylate cyclase	1.86	3.45	3.06	-0.94	7.75	4.30	8.02	4.96	6.44	7.38	0.00
XOO2709	-	phosphate-binding protein	1.21	1.23	1.29	1.12	9.05	7.82	9.71	8.43	9.10	7.98	0.00
XOO2710	-	tRNA/tRNA methyltransferase	2.69	2.39	3.77	1.92	6.14	3.75	7.88	4.11	7.62	5.70	0.00
XOO2711	<i>suhB</i>	extragenic suppressor protein SuhB	-0.18	0.21	-0.69	-0.04	2.70	2.49	7.84	8.53	8.12	8.16	0.00
XOO2712	<i>sodM</i>	superoxidase dismutase	0.23	0.26	0.23	0.21	10.63	10.37	11.93	11.70	11.42	11.21	0.00
XOO2713	-	ribonuclease	1.41	1.05	3.38	-0.19	5.60	4.56	6.47	3.10	2.56	2.75	0.00
XOO2714	-	hypothetical protein	0.63	-0.13	0.61	1.42	6.90	7.03	9.12	8.52	7.46	6.04	0.00
XOO2715	<i>uup</i>	ABC transporter ATP-binding protein	-0.11	-0.06	-0.16	-0.12	9.20	9.26	10.30	10.46	9.72	9.84	0.00
XOO2716	<i>dbpA</i>	ATP-dependent RNA helicase DbpA	0.37	0.32	0.41	0.37	9.35	9.03	10.37	9.96	10.26	9.89	0.00
XOO2717	<i>apt</i>	adenine phosphoribosyltransferase	-0.91	-1.21	-0.88	-0.65	6.45	7.67	8.09	8.97	8.11	8.76	0.00
XOO2718	-	hypothetical protein	0.60	0.17	0.53	1.10	3.85	3.68	4.92	4.40	5.59	4.50	0.00
XOO2719	-	carboxylesterase	-0.34	0.40		-1.08	3.25	2.85	1.79	NA	5.44	6.52	0.00
XOO2720	<i>gstA</i>	glutathione S-transferase	0.08	-1.79	-0.28	2.29	4.82	6.61	3.63	3.91	4.98	2.69	0.00
XOO2721	<i>cspA</i>	cold-shock protein	-0.17	-0.11	-0.20	-0.20	14.21	14.33	14.90	15.10	14.29	14.48	0.00
XOO2722	-	hypothetical protein	-1.44		-0.63	-2.25	2.86	NA	3.38	4.02	1.58	3.84	0.00
XOO2723	-	hypothetical protein	-1.12	-1.15	-1.03	-1.18	7.22	8.37	8.91	9.94	8.21	9.39	0.00
XOO2724	-	hypothetical protein	-2.17	-1.21	-2.14	-3.15	6.14	7.35	6.64	8.78	5.14	8.28	0.00
XOO2725	-	hypothetical protein	0.86	0.33	1.18	1.06	7.56	7.23	9.01	7.83	8.44	7.37	0.00
XOO2726	<i>htpX</i>	heat shock protein HtpX	1.15	2.49	0.43	0.53	6.31	3.82	8.69	8.26	8.23	7.70	0.00
XOO2728	<i>phbB</i>	acetoacetyl-CoA reductase	0.49	0.64	0.74	0.10	7.49	6.85	8.62	7.87	4.14	4.04	0.00
XOO2729	-	hypothetical protein	0.75	0.66	0.80	0.80	8.84	8.18	10.05	9.25	9.86	9.06	0.00
XOO2730	-	hypothetical protein	0.54	-0.26	1.28	0.61	4.87	5.13	4.96	3.68	3.29	2.68	0.00
XOO2731	-	hypothetical protein	0.28	0.23	0.40	0.21	11.52	11.29	11.04	10.63	12.05	11.85	0.00
XOO2732	<i>mutL</i>	DNA mismatch repair protein	0.65	1.07	0.42	0.47	7.10	6.03	8.78	8.36	8.78	8.31	0.00
XOO2733	<i>amiC</i>	N-acetylmuramoyl-L-alanine amidase	2.02	1.22	1.48	3.37	8.02	6.80	8.37	6.90	7.13	3.77	0.00
XOO2734	-	hypothetical protein	0.52	0.75	0.39	0.42	7.44	6.68	9.04	8.65	8.25	7.83	0.00
XOO2736	<i>yjeS</i>	(Fe-S)-binding protein	-0.20		-0.46	0.07	NA	NA	7.77	8.23	7.64	7.57	0.00
XOO2737	<i>xseA</i>	exodeoxyribonuclease VII large subunit	2.26		0.57	3.95	2.29	NA	4.04	3.46	7.41	3.46	0.00
XOO2738	<i>acvB</i>	virulence protein	1.07	1.22	1.06	0.94	9.81	8.59	10.97	9.91	10.95	10.00	0.00
XOO2742	<i>rnD</i>	ribonuclease D	1.07	0.56	1.29	1.37	2.64	2.08	8.03	6.74	6.96	5.59	0.00
XOO2744	<i>xrvA</i>	virulence regulator	0.58	0.51	0.69	0.52	10.21	9.70	11.24	10.55	11.20	10.67	0.00
XOO2746	-	hypothetical protein	0.05	-0.01	0.21	-0.05	9.36	9.37	9.95	9.74	10.48	10.53	0.00
XOO2750	-	3-methyadenine DNA glycosylase	1.81	1.03		2.59	4.79	3.77	3.02	NA	5.89	3.30	0.00
XOO2756	-	hypothetical protein	0.97	0.92	0.90	1.10	10.26	9.34	10.71	9.82	9.84	8.74	0.00
XOO2757	-	hypothetical protein	-0.76	-0.75	-0.67	-0.86	8.20	8.95	9.45	10.12	9.12	9.98	0.00
XOO2758	<i>sspB</i>	ClpXP protease specificity-enhancing factor	-0.46	-0.43	-0.52	-0.43	9.36	9.80	10.12	10.64	9.84	10.27	0.00
XOO2759	<i>sspA</i>	stringent starvation protein A	0.60	0.75	0.51	0.56	8.79	8.04	10.97	10.46	10.57	10.01	0.00
XOO2760	<i>petC</i>	ubiquinol cytochrome C oxidoreductase, cytochrome C1 subunit	1.67	1.56	1.45	2.01	8.66	7.10	10.15	8.69	9.21	7.20	0.00
XOO2761	<i>petB</i>	ubiquinol cytochrome C oxidoreductase, cytochrome B subunit	1.76	1.80	1.77	1.72	9.50	7.70	10.47	8.70	10.25	8.52	0.00
XOO2762	<i>petA</i>	ubiquinol cytochrome C oxidoreductase, iron-sulfur subunit	3.15	5.15	2.27	2.03	8.66	3.50	10.22	7.95	9.98	7.94	0.00
XOO2765	<i>gstA</i>	glutathione S-transferase	3.13			3.13	5.03	NA	6.25	NA	5.57	2.44	0.00
XOO2766	-	(dimethylallyl)adenosine tRNA methylthiotransferase	0.82	0.75	0.95	0.75	7.98	7.23	9.40	8.45	9.27	8.52	0.00
XOO2767	-	ATP-binding protein	0.22	0.08	0.71	-0.12	1.58	1.51	6.79	6.08	3.49	3.61	0.00
XOO2768	-	hypothetical protein	1.85	1.62	0.49	3.44	6.78	5.16	7.65	7.16	7.07	3.62	0.00
XOO2769	-	metalloprotease	0.48	0.43	0.30	0.70	9.51	9.08	10.39	10.09	9.42	8.72	0.00
XOO2770	-	hypothetical protein	0.93	0.85	0.79	1.15	9.86	9.01	10.39	9.60	9.97	8.82	0.00
XOO2771	<i>ybeX</i>	polar amino acid transporter	-0.44	-0.29	-0.43	-0.61	8.25	8.54	9.42	9.85	9.46	10.07	0.00
XOO2772	-	hypothetical protein	-1.00	-1.04	-0.91	-1.03	7.68	8.73	10.24	11.15	9.86	10.89	0.00
XOO2773	<i>corA</i>	magnesium and cobalt transport protein	-1.37	-1.70	-1.20	-1.20	7.25	8.94	9.03	10.23	7.59	8.79	0.00
XOO2774	<i>gabD</i>	succinate-semialdehyde dehydrogenase	0.16	0.19	0.66	-0.37	3.68	3.49	6.32	5.65	7.03	7.41	0.00
XOO2													

XOO2787	<i>rrpX</i>	transcriptional regulator	-2.03	-5.62	1.57	NA	NA	3.20	8.82	8.01	6.44	0.00		
XOO2788	<i>yhjE</i>	metabolite transport protein	2.06	2.58	0.43	3.17	5.55	2.98	7.18	6.75	6.09	2.93	0.00	
XOO2790	<i>fdsC</i>	formate dehydrogenase accessory protein	-1.92	-3.20	-1.98	-0.58	4.89	8.10	6.71	8.69	7.03	7.61	0.00	
XOO2791	<i>yhjX</i>	integral membrane transporter	-0.20	-0.81	0.41	NA	NA	5.75	6.55	3.22	2.81	0.00		
XOO2793	-	beta alanine-pyruvate transaminase	0.73	0.73		2.66	1.93	5.39	NA	4.80	NA	0.00		
XOO2795	-	hypothetical protein	-0.39		-0.39		NA	NA	4.86	5.24	2.64	NA	0.00	
XOO2796	-	hypothetical protein	-0.09	-0.20	-0.08	0.00	9.45	9.65	10.39	10.47	9.94	9.93	0.00	
XOO2797	-	two-component system sensor protein	0.16	-0.34	-1.27	2.11	3.33	3.67	6.80	8.07	6.39	4.28	0.00	
XOO2798	-	two-component system regulatory protein	1.71	1.55	3.19	0.38	4.78	3.23	7.00	3.80	7.75	7.38	0.00	
XOO2799	<i>yieO</i>	drug resistance translocase	0.65	0.65		5.05	4.40	1.66	NA	NA	NA	NA	0.00	
XOO2803	-	TetR/AcrR family transcriptional regulator	-1.21	-1.09	-1.17	-1.35	8.59	9.68	9.48	10.65	9.05	10.40	0.00	
XOO2804	<i>acrA</i>	multidrug resistance protein	-1.39	-1.29	-1.33	-1.55	8.19	9.49	8.88	10.21	8.53	10.08	0.00	
XOO2805	<i>acrB</i>	multidrug efflux transporter	-0.52	-0.38	-0.45	-0.73	10.55	10.93	11.15	11.60	10.89	11.62	0.00	
XOO2806	-	transposase and inactivated derivative	0.77	0.66	0.72	0.94	8.40	7.74	9.08	8.36	8.82	7.88	0.00	
XOO2808	-	transposase	1.82	3.60	0.56	1.29	6.23	2.63	8.64	8.08	7.74	6.44	0.00	
XOO2809	-	LacI family transcriptional regulator	-0.72	-0.78	-0.54	-0.82	7.47	8.25	9.01	9.55	7.96	8.79	0.00	
XOO2810	<i>fruB</i>	multiphosphoryl transfer protein	1.17	1.80	0.69	1.01	6.98	5.18	8.62	7.92	8.74	7.74	0.00	
XOO2811	<i>fruK</i>	1-phosphofructokinase	0.30		-0.32	0.91	2.56	NA	6.70	7.02	7.01	6.10	0.00	
XOO2812	<i>fruA</i>	PTS system fructose-specific transporter subunit IIBC	0.82	0.58	0.80	1.09	9.51	8.93	10.15	9.35	9.64	8.55	0.00	
XOO2813	<i>rpfN</i>	regulator of pathogenicity factors	0.81	1.06	0.59	0.77	8.59	7.53	10.15	9.56	9.93	9.16	0.00	
XOO2818	-	hypothetical protein	0.62	0.63	0.70	0.51	8.96	8.33	8.67	7.96	7.85	7.33	0.00	
XOO2822	-	hypothetical protein	1.16	2.82	-0.32	0.97	6.88	4.06	8.16	8.48	6.82	5.86	0.00	
XOO2824	-	hypothetical protein	0.40	0.45	0.35	0.38	8.48	8.04	9.64	9.29	9.31	8.93	0.00	
XOO2826	<i>cirA</i>	TonB-dependent receptor	0.90	1.70	0.43	0.58	7.88	6.19	4.12	3.70	3.98	3.39	0.00	
XOO2827	-	outer membrane receptor proteins, mostly Fe transport	1.09	0.03	-0.29	3.53	7.34	7.31	6.76	7.05	7.28	3.74	0.00	
XOO2828	<i>sodM</i>	superoxidase dismutase	0.71	0.40	0.43	1.29	7.45	7.05	8.97	8.54	8.67	7.38	0.00	
XOO2829	-	TonB-dependent siderophore receptor	0.68	0.32	1.05		2.08	1.76	6.47	5.42	2.60	NA	0.00	
XOO2830	<i>motC</i>	flagellar motor protein	-2.33	-1.06	-2.98	-2.95	6.20	7.26	6.60	9.58	6.12	9.07	0.00	
XOO2831	<i>motB</i>	flagellar motor protein MotD	-4.21	-4.31	-4.22	-4.10	6.20	10.51	7.06	11.28	6.85	10.94	0.00	
XOO2832	<i>parA</i>	chromosome partitioning protein	-3.26	-3.85	-2.66	-3.26	5.44	9.30	6.73	9.39	5.94	9.21	0.00	
XOO2833	<i>cheW</i>	chemotaxis protein	-2.44	-2.47	-2.24	-2.61	6.60	9.07	7.89	10.13	7.66	10.27	0.00	
XOO2834	-	hypothetical protein	-3.10	-3.34	-2.84	-3.13	6.77	10.11	8.87	11.71	8.30	11.43	0.00	
XOO2835	<i>cheY</i>	chemotaxis response regulator	-1.06	1.32	-1.90	-2.60	5.49	4.17	7.47	9.36	6.79	9.40	0.00	
XOO2836	<i>cheA</i>	chemotaxis protein	-2.13	-1.98	-2.25	-2.15	7.37	9.35	7.94	10.19	7.67	9.82	0.00	
XOO2838	<i>tsr</i>	chemotaxis protein	2.94	2.85	2.01	3.95	5.71	2.87	5.19	3.18	6.06	2.11	0.00	
XOO2840	<i>tsr</i>	chemotaxis protein	-0.15	-0.72	0.12	0.16	4.51	5.22	8.20	8.07	7.79	7.63	0.00	
XOO2842	<i>tsr</i>	chemotaxis protein	3.29				3.29	1.58	NA	1.73	NA	4.86	1.57	0.01
XOO2844	<i>tsr</i>	chemotaxis protein	-0.17	-0.28	-0.25	0.02	7.72	8.00	8.53	8.78	7.87	7.84	0.00	
XOO2845	<i>tsr</i>	chemotaxis protein	1.54		2.05	1.04	5.32	NA	3.66	1.62	3.68	2.64	0.00	
XOO2847	<i>tsr</i>	chemotaxis protein	-0.96	-2.31	-2.25	1.69	6.75	9.06	7.30	9.55	6.58	4.90	0.00	
XOO2848	<i>tsr</i>	chemotaxis protein	-1.90	-2.65	-3.19	0.14	5.72	8.37	6.29	9.48	5.07	4.93	0.00	
XOO2849	-	hypothetical protein	-3.55	-4.00	-3.29	-3.36	5.54	9.54	7.57	10.86	7.07	10.44	0.00	
XOO2850	<i>cheW</i>	chemotaxis protein	-2.54	-3.18	-1.69	-2.74	5.41	8.59	7.66	9.35	6.68	9.42	0.00	
XOO2854	-	hypothetical protein	1.46	2.50	0.43		7.37	4.87	2.95	2.53	6.15	NA	0.00	
XOO2857	<i>cheR</i>	chemotaxis protein methyltransferase	-4.14	-3.28	-4.14	-4.99	5.55	8.84	5.51	9.66	5.00	9.99	0.00	
XOO2858	<i>cheD</i>	chemoreceptor glutamine deamidase CheD	-3.45	-3.43	-3.48	-3.45	6.92	10.36	8.20	11.69	8.14	11.58	0.00	
XOO2859	<i>cheB</i>	chemotaxis-specific methylesterase	-2.51	-2.28	-2.74	-2.50	6.57	8.85	7.29	10.03	7.37	9.87	0.00	
XOO2860	<i>pdeA</i>	c-di-GMP phosphodiesterase A	-2.27	-1.99	-2.28	-2.54	6.49	8.49	5.84	8.12	6.16	8.70	0.00	
XOO2862	<i>acnB</i>	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.30	0.99	1.33	1.59	8.29	7.30	9.37	8.04	8.85	7.27	0.00	
XOO2863	-	hypothetical protein	0.48	0.45	0.55	0.46	8.28	7.83	9.20	8.65	8.79	8.34	0.00	
XOO2864	-	hypothetical protein	0.77	0.70	0.77	0.83	9.10	8.40	9.44	8.67	9.39	8.56	0.00	
XOO2865	<i>rpfA</i>	aconitate hydratase	-1.17	-1.30	-1.11	-1.10	7.67	8.97	9.47	10.58	9.38	10.47	0.00	
XOO2868	<i>rpfB</i>	long-chain fatty acid-CoA ligase	1.24	1.24	1.39	1.09	9.64	8.41	10.98	9.59	11.09	10.00	0.00	
XOO2869	<i>rpfF</i>	enoyl-CoA hydratase	0.50	0.17	0.42	0.90	6.63	6.46	8.63	8.20	8.48	7.57	0.00	
XOO2870	<i>rpfC</i>	RpfC protein	-0.43	-1.31	-0.04	0.04	6.40	7.71	8.19	8.22	6.59	6.55	0.00	
XOO2871	<i>rpfG</i>	response regulator	0.75	0.78	0.76	0.71	9.58	8.81	10.63	9.87	10.56	9.84	0.00	
XOO2872	<i>lysS</i>	lysyl-tRNA synthetase	1.23	2.94	0.30	0.45	6.79	3.85	9.18	8.88	9.02	8.57	0.00	
XOO2873	<i>prfB</i>	peptide chain release factor 2	-0.30	-0.25	-0.31	-0.34	8.60	8.85	10.05	10.36	9.71	10.05	0.00	
XOO2874	<i>prfD</i>	regulatory protein	2.26	3.90	1.47	1.41	6.02	2.11	7.94	6.47	8.41	7.00	0.00	
XOO2875	-	hypothetical protein	1.29	1.32	1.18	1.39	4.22	2.90	9.73	8.56	9.71	8.31	0.00	
XOO2880	-	hypothetical protein	0.85	-2.25	3.96		1.16	3.41	7.65	3.69	2.85	NA	0.00	
XOO2881	-	hypothetical protein	0.04	0.08	0.08	-0.03	9.67	9.59	10.07	9.99	9.75	9.78	0.00	
XOO2884	<i>recJ</i>	single-stranded-DNA-specific exonuclease	0.32	-1.37	4.27	-1.93	3.01	4.38	7.81	3.55	5.85	7.78	0.00	
XOO2885	<i>rpfE</i>	regulatory protein	-0.86	-0.89	-0.90	-0.80	1.90	2.79	7.81	8.70	6.04	6.84	0.00	
XOO2886	<i>greA</i>	transcription elongation factor GreA	-0.14	0.31	0.42	-1.16	4.29	3.98	9.50	9.08	8.45	9.61	0.00	
XOO2894	-	hypothetical protein	0.97	-0.44	0.55	2.81	5.39	5.84	7.94	7.39	6.51	3.70	0.00	
XOO2895	<i>avtA</i>	valine-pyruvate aminotransferase	0.18	0.39	-0.01	0.15	7.39	7.00	8.82	8.83	8.74	8.59	0.00	
XOO2897	-	hypothetical protein	0.32	-0.15	0.30	0.82	8.97	9.12	8.86	8.56	8.38	7.56	0.00	
XOO2899	<i>feoB</i>	ferrous iron transport protein B	1.63	1.62	1.83	1.42	9.59	7.97	10.51	8.68	10.52	9.10	0.00	
XOO2901	-	enoyl-CoA hydratase	1.44	1.44			4.53	3.09	5.82	NA	4.11	NA	0.00	
XOO2902	-	hypothetical protein	1.37	1.50	1.28	1.35	8.65	7.16	9.13	7.85	8.55	7.20	0.00	
XOO2903	<i>mvaB</i>	hydroxymethylglutaryl-CoA lyase	-0.25	0.25	-1.10	0.10	8.28	8.02	5.66	6.76	6.75	6.65	0.00	
XOO2904	<i>hadH2</i>	3-hydroxyacyl-CoA dehydrogenase	0.69	-0.81	3.03	-0.14	2.79	3.61	6.57	3.55	3.56	3.70	0.00	
XOO2905	<i>yeIP</i>	elongation factor P	0.28	0.23	0.26	0.34	4.13	3.90	9.54	9.28	9.46	9.12	0.00	
XOO2907	-	hypothetical protein	2.63	3.29	0.53	4.08	5.80	2.51	7.73	7.20	7.66	3.59	0.00	
XOO2911	-	D-xylulokinase	0.39	0.46	0.53	0.20	8.24	7.78	9.39	8.86	8.91	8.71	0.00	
XOO2912	-	hypothetical protein	0.33	-0.02	0.69	0.79	0.81	3.18	NA	1.79	1.10	0.01		
XOO2913	-	relaxation protein	1.68	3.41	0.87	0.77	7.10	3.69	8.09	7.22	7.79	7.02	0.00	
XOO2915	-	galactose-binding protein regulator	1.39		0.15	2.63	2.50	NA	5.93	5.79	6.10	3.47	0.00	
XOO2916	<i>gbpR</i>	galactose-binding protein regulator	1.63	0.79	1.16	2.93	7.66	6.87	6.90	5.74	5.79	2.85	0.00	
XOO2917	<i>dgoA</i>	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	-0.61	-0.69	-1.42	0.28	7.06	7.75	6.81	8.23	5.81	5.53	0.00	
XOO2920	<i>dgoK</i>	2-oxo-3-deoxygalactonate kinase	#DIV/0!				NA	NA	4.23	NA	2.64	NA	0.01	
XOO2921	-	ferredoxin	-0.38	-0.57	-0.18	-0.37	7.94	8.51	10.08	10.27</				

XOO2932	-	transcriptional regulator	0.13	0.13	2.29	NA	4.57	4.44	0.50	NA	0.01		
XOO2933	-	hypothetical protein	2.85		2.85	4.08	NA	3.64	5.44	2.59	0.00		
XOO2934	-	endolysin	-0.22	0.02	-0.47	4.11	4.09	3.62	4.09	1.73	NA	0.00	
XOO2936	-	isopentenyl transferase	-2.27	-2.37	-2.26	-2.18	6.61	8.99	7.92	10.18	7.36	9.54	0.00
XOO2937	-	hypothetical protein	-0.64	1.18	-1.29	-1.80	5.13	3.95	7.41	8.70	5.83	7.63	0.00
XOO2938	<i>csrA</i>	carbon storage regulator	-0.20	-0.08	-0.19	-0.33	12.48	12.56	13.78	13.97	13.56	13.89	0.00
XOO2939	<i>aiaS</i>	alanyl-tRNA synthetase	-0.25	-0.22	-0.32	-0.22	10.47	10.69	11.77	12.09	11.17	11.39	0.00
XOO2940	<i>recX</i>	recombination regulator RecX	-1.46	-1.21	-1.66	-1.52	8.30	9.51	9.14	10.80	8.54	10.06	0.00
XOO2941	<i>recA</i>	recombinase A	-0.92	-0.88	-0.98	-0.90	11.21	12.09	12.22	13.19	11.42	12.32	0.00
XOO2942	<i>lexA</i>	LexA repressor	-1.13	-1.19	-1.09	-1.10	8.62	9.81	9.44	10.53	9.52	10.62	0.00
XOO2943	<i>aarF</i>	ubiquinone biosynthesis protein	-0.20	-0.54	0.14	-0.21	10.15	10.69	8.66	8.52	7.37	7.58	0.00
XOO2944	-	hypothetical protein	0.56	-0.22	0.52	1.38	3.25	3.47	7.03	6.50	3.39	2.01	0.00
XOO2945	<i>hflX</i>	GTP-binding protein	-0.37	-0.61	-0.07	-0.45	7.79	8.39	8.65	8.72	7.82	8.27	0.00
XOO2946	<i>hfq</i>	RNA-binding protein Hfq	1.09	-0.07	3.51	-0.18	11.29	11.37	9.93	6.42	11.59	11.77	0.00
XOO2947	<i>miaA</i>	tRNA delta(2)-isopentenylpyrophosphate transferase	-1.65	-1.46	-1.87	-1.62	8.31	9.76	8.70	10.58	7.20	8.82	0.00
XOO2949	<i>hflB</i>	cell division protein	-0.19	-0.12	-0.24	-0.22	9.78	9.90	11.48	11.73	11.03	11.25	0.00
XOO2950	<i>ftsJ</i>	cell division protein	-1.00	-1.01	-0.93	-1.07	10.63	11.64	11.53	12.46	11.59	12.66	0.00
XOO2951	-	hypothetical protein	0.00	0.03	0.01	-0.05	10.78	10.75	11.97	11.96	11.72	11.78	0.00
XOO2952	-	hypothetical protein	-0.73	-0.68	-0.73	-0.77	8.13	8.81	9.72	10.46	8.77	9.55	0.00
XOO2953	<i>nlpD</i>	lipoprotein	0.05	0.07	-0.02	0.08	9.20	9.13	10.38	10.40	9.90	9.82	0.00
XOO2954	-	hypothetical protein	-0.38	-0.42	-0.33	-0.37	10.71	11.13	11.61	11.95	11.40	11.78	0.00
XOO2955	<i>pcm</i>	L-isospartate protein carboxylmethyltransferase type II	-0.62	-1.51	-0.22	-0.14	5.80	7.30	9.23	9.45	8.55	8.69	0.00
XOO2956	<i>surE</i>	stationary phase survival protein SurE	-0.11	-0.07	-0.11	-0.16	9.86	9.93	10.71	10.82	9.97	10.12	0.00
XOO2960	<i>ispF</i>	2-C-methyl-D-erythritol 2,4-cyclo diphosphate synthase	-1.08	-0.69	-0.75	-1.80	7.68	8.37	8.16	8.91	6.37	8.18	0.00
XOO2961	<i>ispD</i>	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	0.18	-0.34	0.10	0.79	5.53	5.87	5.51	5.40	5.28	4.50	0.00
XOO2962	<i>ftsB</i>	cell division protein FtsB	-0.33	-0.38	-0.27	-0.32	10.91	11.29	12.52	12.80	11.81	12.13	0.00
XOO2963	<i>eno</i>	phosphopyruvate hydratase	0.43	0.46	0.40	0.42	10.06	9.60	11.68	11.28	11.08	10.66	0.00
XOO2969	<i>parE</i>	DNA topoisomerase IV subunit B	0.02	-0.02	0.12	-0.03	8.70	8.72	10.06	9.94	9.68	9.71	0.00
XOO2972	-	carboxypeptidase-like protein	1.23	0.97	1.15	1.56	8.39	7.42	9.34	8.19	8.98	7.42	0.00
XOO2973	-	hypothetical protein	0.41	0.51	0.28	0.45	8.64	8.13	8.89	8.61	9.27	8.82	0.00
XOO2974	<i>pitA</i>	transporter	-0.11		0.51	-0.73	5.67	NA	4.25	3.73	3.30	4.03	0.00
XOO2975	-	hypothetical protein	-0.43	-0.36	0.00	-0.93	6.61	6.97	4.50	4.51	6.90	7.82	0.00
XOO2976	<i>tlyC</i>	hemolysin	-1.16	-1.43	-0.63	-1.41	7.52	8.95	8.75	9.38	8.09	9.50	0.00
XOO2977	<i>exoD</i>	ExoD protein	-1.39	-1.20	-1.33	-1.64	8.59	9.79	8.61	9.95	8.56	10.20	0.00
XOO2978	-	general stress protein	-0.42	0.08	-1.04	-0.30	5.73	5.65	6.73	7.78	5.53	5.83	0.00
XOO2980	-	MFS transporter	2.24	2.72	1.76		8.06	5.34	7.31	5.56	4.19	NA	0.00
XOO2981	-	ABC transporter ATP-binding protein	#DIV/0!				2.43	NA	NA	NA	2.81	NA	0.01
XOO2982	-	hypothetical protein	#DIV/0!				2.04	NA	2.20	NA	3.58	NA	0.00
XOO2983	-	Mg-protoporphyrin IX monomethyl ester oxidative cyclase	-0.86	-0.27	-2.31	0.00	6.38	6.64	4.16	6.47	5.17	5.16	0.00
XOO2984	-	hypothetical protein	#DIV/0!				1.40	NA	1.90	NA	2.58	NA	0.01
XOO2985	-	hexosyltransferase	#DIV/0!				2.35	NA	5.44	NA	4.44	NA	0.00
XOO2986	-	glycosyltransferase	0.17	-1.06	-0.47	2.04	7.62	8.68	4.71	5.17	5.27	3.23	0.00
XOO2987	<i>bioC</i>	biotin synthesis protein	#DIV/0!				NA	NA	2.38	NA	NA	NA	0.08
XOO2988	-	hypothetical protein	0.13	-1.35	1.62		1.58	2.94	4.67	3.06	2.29	NA	0.00
XOO2989	-	methyltransferase	0.88	0.09	0.79	1.75	6.99	6.90	7.31	6.51	5.27	3.52	0.00
XOO2990	-	hypothetical protein	2.11	1.08	3.14		5.75	4.67	6.05	2.91	3.75	NA	0.00
XOO2992	-	glycosyl transferase family protein	-0.16		-0.16		2.75	NA	2.52	2.69	2.48	NA	0.00
XOO2993	-	lipopolysaccharide biosynthesis protein	0.06			0.06	4.41	NA	2.84	NA	2.38	2.32	0.00
XOO2994	-	aminotransferase	2.20		2.20		2.16	NA	5.53	3.33	1.66	NA	0.00
XOO2995	-	hypothetical protein	1.01	2.69	0.39	-0.04	6.25	3.56	7.93	7.54	7.02	7.06	0.00
XOO2996	-	hypothetical protein	0.39	1.10	-0.84	0.90	6.00	4.90	3.47	4.30	4.00	3.10	0.00
XOO2997	-	hypothetical protein	0.61			0.61	NA	5.58	NA	2.90	2.29	0.00	
XOO2998	-	hypothetical protein	2.14	1.01	1.45	3.96	6.30	5.29	4.41	2.97	7.94	3.98	0.00
XOO2999	-	cytochrome like B561	#DIV/0!				2.16	NA	2.16	NA	5.59	NA	0.01
XOO3000	-	cytochrome C	0.07	0.36	0.21	-0.35	9.73	9.37	9.52	9.31	8.53	8.88	0.00
XOO3001	<i>cycA</i>	cytochrome C2	0.94		0.94		5.46	NA	3.09	2.16	2.48	NA	0.00
XOO3002	-	hypothetical protein	-0.21			-0.21	NA	NA	5.08	NA	2.70	2.91	0.00
XOO3003	<i>rpoE</i>	RNA polymerase sigma-E factor	1.77	0.90	2.63	1.79	3.01	2.11	5.96	3.33	5.01	3.22	0.00
XOO3006	<i>ccmC</i>	heme exporter protein C; cytochrome C-type biogenesis protein	#DIV/0!				1.50	NA	NA	NA	4.02	NA	0.03
XOO3009	<i>cycK</i>	C-type cytochrome biogenesis membrane protein	0.24	1.39	0.29	-0.97	4.43	3.03	6.78	6.49	2.00	2.97	0.00
XOO3010	<i>dsbE</i>	C-type cytochrome biogenesis protein/thioredoxin	#DIV/0!				2.04	NA	5.44	NA	4.39	NA	0.00
XOO3011	<i>cycL</i>	C-type cytochrome biogenesis protein	0.69		0.69		5.00	NA	6.25	5.57	5.64	NA	0.00
XOO3012	-	hypothetical protein	0.68	-0.41	-1.19	3.63	1.79	2.21	4.07	5.26	5.98	2.34	0.00
XOO3016	-	cation/multidrug efflux pump	0.91	1.19	1.07	0.46	8.04	6.85	8.64	7.57	8.46	7.99	0.00
XOO3018	<i>mexB</i>	multidrug efflux transporter	#DIV/0!				1.85	NA	2.16	NA	NA	NA	0.02
XOO3019	-	hypothetical protein	-0.91	-0.22	-1.01	-1.50	7.52	7.74	7.90	8.91	6.46	7.97	0.00
XOO3020	-	hypothetical protein	-1.06	-0.69	-1.31	-1.18	3.83	4.51	8.46	9.76	8.19	9.37	0.00
XOO3022	-	type III effector HolPsyAE	2.77		2.77		NA	NA	4.43	1.66	NA	NA	0.02
XOO3026	-	IS1404 transposase	-0.03	0.00	-0.08	0.00	8.94	8.95	9.82	9.91	9.71	9.72	0.00
XOO3027	-	IS1404 transposase	0.06	0.23	-0.08	0.05	7.48	7.26	9.27	9.36	8.63	8.59	0.00
XOO3028	-	transposase	-0.13	2.19	-2.09	-0.48	3.78	1.59	1.16	3.25	5.09	5.57	0.00
XOO3029	-	Tn5044 transposase	2.52	4.85	0.35	2.35	5.61	0.77	6.68	6.32	5.74	3.39	0.00
XOO3030	-	VirG-like two component response regulator	1.87		1.87		2.81	NA	3.91	2.03	3.20	NA	0.00
XOO3031	-	cytochrome C peroxidase	0.34	0.72	-1.06	1.35	5.44	4.72	3.58	4.64	6.12	4.78	0.00
XOO3032	<i>virA</i>	two-component VirA-like sensor kinase	#DIV/0!				2.85	NA	2.08	NA	4.17	NA	0.00
XOO3033	-	hypothetical protein	-0.78			-0.78	3.08	NA	2.71	NA	1.66	2.44	0.00
XOO3034	-	hypothetical protein	0.29	0.87	-0.29		2.95	2.09	6.31	6.61	2.70	NA	0.00
XOO3035	-	serine/threonine kinase	0.49	1.66	1.21	-1.41	4.36	2.70	7.09	5.88	4.67	6.08	0.00
XOO3036	<i>ptc1</i>	phosphoprotein phosphatase	#DIV/0!				NA	3.48	1.40	NA	4.48	NA	0.01
XOO3037	-	hypothetical protein	-0.23	-0.01		-0.44	2.68	2.69	1.85	NA	2.43	2.87	0.00
XOO3038	-	hypothetical protein	2.43		2.43		2.73	NA	4.95	2.51	5.20	NA	0.00
XOO3039	-	hypothetical protein	-0.85	-0.85			4.97	5.82	NA	NA	2.08	NA	0.00
XOO3042	-	hypothetical protein	#DIV/0!				1.58	NA	NA	NA	1.66	NA	0.05
XOO3043	-	hypothetical protein	1.19	1.40	-0.26	2.43	2.82	1.42	5.51	5.77	4.95	2.52	0.00
XOO3045	<i>clpB</i>	chaperone ClpB	0.35	0.40	0.27	0.36	3.73	3.33	8.36	8.09	7.99	7.63	0.00
XOO3046	-	hypothetical protein	3.19	1.70	4.68		4.63	2.92	7.16	2.48	3.00	NA	0.00
XOO3047	-	hypothetical protein	-0.94	-0.94			4.90	5.83	2.43	NA	1.29	NA	0.00
XOO3048	-	hypothetical protein	#DIV/0!</										

XOO3051	-	hypothetical protein	0.76	-0.11	0.07	2.33	6.83	6.94	7.62	7.55	6.45	4.13	0.00
XOO3052	-	hypothetical protein	#DIV/0!				2.56	NA	7.13	NA	NA	NA	0.02
XOO3061	-	hypothetical protein	0.34	0.38	0.33	0.31	9.08	8.70	10.63	10.30	10.29	9.98	0.00
XOO3066	-	hypothetical protein	-0.62	-0.62	-0.48	-0.75	8.39	9.01	9.85	10.33	9.58	10.33	0.00
XOO3067	<i>phhB</i>	pterin-4-alpha-carbinolamine dehydratase	0.05	0.09	0.06	-0.01	9.48	9.39	10.97	10.91	10.27	10.28	0.00
XOO3071	-	hypothetical protein	0.17	0.27	0.00	0.24	5.92	5.65	7.77	7.77	7.54	7.30	0.00
XOO3072	<i>rluC</i>	pseudouridylate synthase	0.06	-0.37	0.79	-0.26	7.10	7.47	8.47	7.68	7.89	8.14	0.00
XOO3073	<i>rne</i>	ribonuclease E	0.03	-0.11	0.04	0.16	8.68	8.79	10.43	10.38	10.13	9.97	0.00
XOO3077	<i>gacA</i>	LuxR family transcriptional regulator	0.26	0.31	0.26	0.22	8.10	7.79	9.69	9.43	9.10	8.88	0.00
XOO3078	-	rhodanese superfamily protein	0.07	0.19	0.04	-0.02	9.68	9.49	11.41	11.38	10.87	10.89	0.00
XOO3079	-	hypothetical protein	-0.91	-0.95	-0.61	-1.16	7.80	8.76	8.53	9.14	8.12	9.28	0.00
XOO3080	<i>fkpA</i>	FKBP-type peptidylprolyl isomerase	-0.57	-0.48	-0.75	-0.47	8.22	8.71	8.72	9.47	6.45	6.93	0.00
XOO3081	-	hypothetical protein	0.33	0.28	0.39	5.17	NA	3.55	3.28	2.73	2.34	0.00	
XOO3082	<i>vipA</i>	polysaccharide biosynthetic protein	-0.52	-0.02	-0.19	-1.34	6.91	6.93	7.89	8.08	6.86	8.20	0.00
XOO3083	-	phosphopantetheinyl transferase	0.56	1.33	2.16	-1.82	6.20	4.87	7.61	5.45	5.83	7.64	0.00
XOO3084	-	ISXo8 transposase	-0.62	-1.23	0.74	-1.36	5.40	6.64	7.99	7.25	6.53	7.89	0.00
XOO3088	-	hypothetical protein	0.92	1.08	0.72	0.97	9.90	8.82	11.50	10.77	10.95	9.98	0.00
XOO3102	<i>cysG</i>	siroheme synthase	0.57	0.77	0.09	0.85	7.30	6.53	8.34	8.24	7.79	6.94	0.00
XOO3105	<i>mobA</i>	molybdopterin guanine dinucleotide synthase	0.75	2.34	0.38	-0.48	6.91	4.56	7.82	7.44	7.13	7.61	0.00
XOO3106	<i>moeA</i>	molybdopterin biosynthesis	-0.34	-0.17		-0.51	2.12	2.29	3.18	NA	3.96	4.47	0.00
XOO3107	-	hypothetical protein	1.37		1.37		2.56	NA	4.55	3.18	4.34	NA	0.00
XOO3112	-	hypothetical protein	-0.22	-0.14	-0.14	-0.36	7.32	7.46	7.89	8.03	7.51	7.87	0.00
XOO3119	<i>btuB</i>	TonB-dependent receptor	2.53	2.53			5.01	2.48	5.38	NA	6.21	NA	0.00
XOO3121	<i>xsa</i>	xylosidase	0.63		0.63		NA	NA	3.06	2.43	2.54	NA	0.00
XOO3122	-	hypothetical protein	1.91	2.22	1.60		2.85	0.63	6.33	4.73	5.15	NA	0.00
XOO3123	<i>btuB</i>	TonB-dependent receptor	1.25	2.68	0.57	0.50	6.47	3.79	7.90	7.33	7.65	7.15	0.00
XOO3124	-	hypothetical protein	-0.39		-0.99	0.20	5.14	NA	4.99	5.97	6.31	6.11	0.00
XOO3125	-	peptidase	1.61	1.61			5.24	3.63	2.23	NA	2.16	NA	0.00
XOO3126	-	hypothetical protein	-0.21	3.06	-1.18	-2.51	5.42	2.36	6.16	7.34	1.16	3.67	0.00
XOO3127	-	hypothetical protein	1.11	0.00		2.23	4.97	4.97	2.54	NA	4.76	2.53	0.00
XOO3132	<i>yveA</i>	amino acid permease	0.52	0.82	0.53	0.21	7.41	6.59	7.99	7.46	5.98	5.77	0.00
XOO3133	-	hypothetical protein	2.36		4.70	0.02	1.50	NA	8.41	3.71	6.92	6.90	0.00
XOO3134	-	hypothetical protein	0.57	0.37	1.00	0.35	8.73	8.35	9.74	8.74	9.74	9.39	0.00
XOO3135	<i>pepQ</i>	proline dipeptidase	-0.11	-0.11	-0.08	-0.14	9.53	9.64	10.55	10.64	10.46	10.60	0.00
XOO3137	<i>dapA</i>	dihydronicotinate synthetase	0.30	0.45	0.16	0.29	9.04	8.59	10.96	10.80	10.58	10.29	0.00
XOO3138	-	oxidoreductase	1.18	1.58	0.95	1.02	8.42	6.84	10.54	9.59	10.18	9.16	0.00
XOO3140	-	D-amino acid oxidase	0.74	0.63	0.87	0.71	8.70	8.07	10.10	9.23	9.91	9.20	0.00
XOO3141	-	hypothetical protein	1.20	1.23	1.25	1.11	10.32	9.09	11.12	9.87	10.79	9.68	0.00
XOO3142	-	transcriptional regulator	1.18	1.45	1.08	1.00	8.79	7.34	10.19	9.10	9.92	8.93	0.00
XOO3143	<i>ftsY</i>	cell division protein	-0.96	-0.81	-0.85	-1.23	8.19	9.00	8.45	9.31	8.25	9.48	0.00
XOO3144	<i>mutY</i>	A/G-specific adenine glycosylase	-0.72	-1.03	-0.65	-0.48	4.25	5.29	6.95	7.60	7.31	7.80	0.00
XOO3145	-	hypothetical protein	-0.23	-0.51	-0.09	-0.10	6.11	6.61	9.36	9.45	9.15	9.25	0.00
XOO3147	<i>fixL</i>	sensor histidine kinase	-2.64	-2.57	-2.59	-2.75	8.46	11.03	9.18	11.78	9.30	12.05	0.00
XOO3150	-	hypothetical protein	-0.56		-0.56		2.84	NA	3.59	4.15	5.71	NA	0.00
XOO3152	-	hypothetical protein	0.01	-0.04	-2.69	2.76	4.98	5.02	4.57	7.26	6.12	3.36	0.00
XOO3154	-	hypothetical protein	-0.17	2.22	-1.60	-1.12	5.81	3.60	6.97	8.57	7.24	8.36	0.00
XOO3155	-	hypothetical protein	0.22	1.50	-1.06		6.01	4.51	7.28	8.34	2.56	NA	0.00
XOO3161	<i>blc</i>	outer membrane lipoprotein Blc	-1.48	-1.18	-1.16	-2.10	8.07	9.25	9.38	10.54	8.09	10.19	0.00
XOO3166	<i>gumN</i>	GumN protein	-0.35	-0.90	0.09	-0.25	2.38	3.28	6.99	6.89	6.50	6.75	0.00
XOO3167	-	hypothetical protein	0.60	-0.44	2.04	0.21	7.01	7.46	6.86	4.82	3.80	3.59	0.00
XOO3168	<i>gumM</i>	protein GumM	-1.34	-1.20	-0.86	-1.95	7.53	8.74	8.11	8.97	7.19	9.14	0.00
XOO3169	<i>gumL</i>	GumL protein	-0.26	-0.07	-0.13	-0.57	7.85	7.92	9.69	9.83	8.99	9.56	0.00
XOO3170	<i>gumK</i>	glucuronosyltransferase GumK	-0.83	-0.37	-1.51	-0.61	3.67	4.04	8.34	9.85	9.48	10.08	0.00
XOO3171	<i>gumJ</i>	protein GumJ	-0.17	0.12	-2.76	2.14	5.03	4.91	0.50	3.26	5.71	3.57	0.00
XOO3172	<i>guml</i>	protein GumL	0.26	0.25	0.28	0.24	8.33	8.08	9.31	9.03	9.54	9.30	0.00
XOO3173	<i>gumH</i>	protein GumH	0.89	2.78	-0.34	0.22	5.39	2.61	7.49	7.83	7.28	7.06	0.00
XOO3175	<i>gumF</i>	protein GumF	-0.16	-0.37	-0.15	0.03	7.98	8.35	9.28	9.43	8.39	8.36	0.00
XOO3176	<i>gumE</i>	protein GumE	0.12	0.17	0.06	0.14	10.04	9.87	10.55	10.49	10.60	10.46	0.00
XOO3177	<i>gumD</i>	protein GumD	-0.62	-0.75	-0.47	-0.65	10.00	10.76	10.39	10.86	10.26	10.91	0.00
XOO3178	<i>gumC</i>	protein GumC	-0.92	-0.82	-0.94	-1.01	10.66	11.49	11.32	12.26	11.08	12.09	0.00
XOO3179	<i>gumB</i>	protein GumB	-1.22	-1.31	-0.98	-1.36	8.28	9.59	8.96	9.94	8.13	9.50	0.00
XOO3180	-	hypothetical protein	0.37	0.17	0.59	0.36	10.77	10.60	11.28	10.68	11.42	11.06	0.00
XOO3181	<i>ihfA</i>	integration host factor subunit alpha	1.14	1.28	1.07	1.07	9.21	7.93	11.66	10.60	11.34	10.27	0.00
XOO3182	<i>pheT</i>	phenylalanyl-tRNA synthetase subunit beta	1.03	1.28	0.92	0.88	8.68	7.39	10.33	9.41	10.17	9.30	0.00
XOO3183	<i>pheS</i>	phenylalanyl-tRNA synthetase subunit alpha	0.80	1.67	0.26	0.47	7.29	5.62	8.54	8.28	8.32	7.85	0.00
XOO3184	<i>rplT</i>	50S ribosomal protein L20	0.21	0.32	0.13	0.17	11.18	10.85	12.12	11.99	11.89	11.72	0.00
XOO3186	<i>infC</i>	translation initiation factor IF-3	-0.17	0.00	-0.22	-0.31	11.74	11.74	13.74	13.96	13.23	13.54	0.00
XOO3187	<i>thrS</i>	threonyl-tRNA synthetase	-0.29	-0.29	-0.21	-0.38	12.84	13.13	14.08	14.29	13.61	13.99	0.00
XOO3189	-	IS1404 transposase	0.15	0.28	0.17	-0.01	11.63	11.35	12.48	12.31	12.47	12.47	0.00
XOO3194	<i>fimT</i>	fimbrial biogenesis protein	-0.56	-0.76	-0.36	-0.36	3.53	4.28	5.78	NA	6.75	7.11	0.00
XOO3195	<i>pilE1</i>	type IV pilin	-0.29	-0.15	-0.44	-0.27	9.95	10.10	10.38	10.82	9.47	9.75	0.00
XOO3196	<i>pilY1</i>	protein PilY1	0.20	0.23	0.33	0.04	10.14	9.91	10.58	10.25	9.56	9.52	0.00
XOO3199	<i>pilX</i>	protein PilX	0.40	0.32	0.24	0.63	8.48	8.15	10.27	10.03	9.33	8.70	0.00
XOO3200	-	hypothetical protein	0.24	0.37	0.10	0.25	9.33	8.96	10.84	10.73	10.04	9.79	0.00
XOO3201	<i>pilV</i>	pre-pilin leader sequence	0.43	0.15	1.09	0.05	9.28	9.12	9.73	8.64	10.32	10.27	0.00
XOO3202	<i>fimT</i>	pre-pilin like leader sequence	-0.27	-0.30	-0.51	-0.01	8.85	9.15	9.85	10.36	4.50	4.51	0.00
XOO3203	-	hypothetical protein	0.40	0.45	0.29	0.44	8.08	7.62	9.81	9.52	9.00	8.55	0.00
XOO3204	<i>oar</i>	Oar protein	1.84	2.55	-0.10	3.09	6.49	3.95	7.11	7.22	6.54	3.45	0.00
XOO3205	-	hypothetical protein	-0.40	-1.32	0.04	0.07	7.09	8.41	9.00	8.96	8.90	8.83	0.00
XOO3206	-	short chain dehydrogenase	-1.61		-1.61		2.20	NA	6.12	7.73	3.26	NA	0.00
XOO3207	-	hypothetical protein	-0.22	0.01	-0.34	-0.33	8.66	8.65	9.83	10.17	9.48	9.82	0.00
XOO3208	<i>sodB</i>	iron superoxide dismutase	-0.18	-0.73	-0.12	0.32	8.91	9.64	8.69	8.80	8.51	8.19	0.00
XOO3209	<i>purK</i>	phosphoribosylaminoimidazole carboxylase ATPase subunit	1.31	0.12	0.08	3.74	8.52	8.39	4.83				

XOO3222	<i>nuoN</i>	NADH dehydrogenase subunit N	-0.28	-0.30	-0.29	-0.25	9.73	10.03	10.66	10.95	10.46	10.71	0.00
XOO3223	<i>nuoM</i>	NADH dehydrogenase subunit M	-0.07	-0.01	-0.11	-0.09	11.67	11.68	12.29	12.39	11.76	11.85	0.00
XOO3224	<i>nuoL</i>	NADH dehydrogenase subunit L	-0.01	-0.04	0.02	-0.01	11.70	11.74	6.48	6.46	11.54	11.55	0.00
XOO3225	<i>nuoK</i>	NADH dehydrogenase subunit K	-0.03	-0.06	-0.12	0.08	11.66	11.72	12.01	12.13	11.13	11.05	0.00
XOO3226	<i>nuoJ</i>	NADH dehydrogenase subunit J	0.08	0.26	0.00	-0.01	10.16	9.90	11.56	11.56	10.87	10.88	0.00
XOO3227	<i>nuoI</i>	NADH dehydrogenase subunit I	0.28	0.39	0.16	0.29	8.50	8.11	10.41	10.24	10.23	9.93	0.00
XOO3230	<i>nuoF</i>	NADH-ubiquinone oxidoreductase NQO1 subunit	-0.03	0.03	-0.07	-0.06	10.04	10.01	10.77	10.84	10.19	10.25	0.00
XOO3233	<i>nuoD</i>	NADH dehydrogenase subunit D	-0.01	0.11	-0.06	-0.07	11.46	11.35	12.41	12.48	11.88	11.95	0.00
XOO3234	<i>nuoC</i>	NADH dehydrogenase subunit C	-0.10	-0.06	-0.04	-0.19	10.40	10.47	11.58	11.62	11.45	11.64	0.00
XOO3235	<i>nuoB</i>	NADH dehydrogenase subunit B	-0.30	-0.18	-0.30	-0.43	11.27	11.45	12.61	12.91	12.26	12.68	0.00
XOO3236	<i>nuoA</i>	NADH dehydrogenase subunit A	-0.43	-0.38	-0.43	-0.49	12.46	12.84	13.47	13.90	13.10	13.59	0.00
XOO3237	<i>secG</i>	preprotein translocase subunit SecG	-0.90	-0.68	-1.05	-0.98	10.37	11.05	9.73	10.77	10.54	11.51	0.00
XOO3238	<i>tpiA</i>	triosephosphate isomerase	-0.85	-0.80	-0.81	-0.95	10.93	11.73	10.88	11.69	10.88	11.83	0.00
XOO3239	-	dehydrogenase	0.58	-0.78	0.51	2.00	7.03	7.81	7.38	6.87	6.03	4.02	0.00
XOO3246	-	phosphodiesterase	#DIV/0!				2.35	NA	NA	NA	NA	NA	0.08
XOO3247	-	hypothetical protein	-1.21	0.90	-1.78	-2.74	4.95	4.06	7.34	9.11	4.28	7.01	0.00
XOO3249	<i>glmM</i>	phosphoglucomamine mutase	0.60	1.21	0.21	0.36	8.30	7.08	9.02	8.81	8.45	8.08	0.00
XOO3250	<i>accD</i>	acetyl-CoA carboxylase subunit beta	-0.21	-0.22	-0.30	-0.12	10.09	10.31	11.04	11.34	10.73	10.85	0.00
XOO3251	<i>trpA</i>	tryptophan synthase subunit alpha	-0.68	0.34	-0.62	-1.76	3.72	3.39	7.10	7.72	6.31	8.06	0.00
XOO3253	<i>trpI</i>	transcriptional regulator	0.61		0.61	5.08	NA	2.04	NA	5.66	5.05	0.00	
XOO3254	<i>trpF</i>	N-(5'-phosphoribosyl)anthranilate isomerase	-1.26	-1.25	-1.37	-1.16	8.03	9.29	8.36	9.73	8.90	10.06	0.00
XOO3255	<i>truA</i>	tRNA pseudouridine synthase A	-0.23	-0.54	-0.43	0.28	7.64	8.18	7.16	7.59	8.14	7.86	0.00
XOO3258	-	protein FimV	-0.67	-0.70	-0.60	-0.70	13.49	14.19	13.72	14.32	12.71	13.41	0.00
XOO3259	<i>asd</i>	aspartate-semialdehyde dehydrogenase	0.85	-0.94	0.16	3.33	6.91	7.85	7.65	7.48	7.22	3.89	0.00
XOO3260	-	2-hydroxyacid dehydrogenase	0.37	0.81	-0.02	0.33	8.33	7.52	8.52	8.54	8.55	8.23	0.00
XOO3261	<i>aroC</i>	chorismate synthase	0.52	0.39	0.64	0.52	7.95	7.55	9.62	8.98	9.16	8.65	0.00
XOO3262	<i>yfcB</i>	N5-glutamine S-adenosyl-L-methionine-dependent methyltransfer:	0.25	0.34	0.21	0.19	9.90	9.56	11.29	11.08	10.57	10.38	0.00
XOO3263	-	hypothetical protein	0.66	1.04	0.31	0.64	8.09	7.05	9.09	8.78	8.93	8.29	0.00
XOO3266	<i>dnlR</i>	membrane-bound lytic murein transglycosylase D	-0.47	-0.59	-0.54	-0.28	8.17	8.76	9.35	9.89	8.74	9.02	0.00
XOO3271	<i>greB</i>	transcription elongation factor GreB	0.92	0.48	0.98	1.30	7.86	7.38	9.49	8.50	9.10	7.80	0.00
XOO3272	<i>rimO</i>	30S ribosomal protein S12 methylthiotransferase	0.76	1.06	0.38	0.83	8.68	7.62	4.98	4.60	9.23	8.41	0.00
XOO3278	<i>dcd</i>	deoxycytidine triphosphate deaminase	0.03	0.20	0.04	-0.17	7.89	7.68	8.72	8.68	8.63	8.80	0.00
XOO3281	-	metallopeptidase	0.76	0.72	0.83	0.74	8.89	8.17	9.40	8.57	8.56	7.82	0.00
XOO3282	-	hypothetical protein	-0.83	-0.68	-0.91	-0.91	10.51	11.19	11.50	12.41	11.24	12.15	0.00
XOO3283	-	methylated-DNA-protein-cysteine S-methyltransferase related prot	-0.45	-0.39	-0.98	0.00	4.81	5.19	6.49	7.47	6.98	6.97	0.00
XOO3288	<i>dadA</i>	D-amino acid dehydrogenase subunit	-0.66		-1.16	-0.17	2.99	NA	5.79	6.95	6.24	6.40	0.00
XOO3289	<i>yxaH</i>	transporter	-0.61	-0.72	-0.51	-0.60	8.29	9.01	9.35	9.86	9.24	9.84	0.00
XOO3290	<i>slyD</i>	peptidyl-prolyl cis-trans isomerase	-0.10	-0.22	-0.03	-0.04	8.36	8.59	9.66	9.69	9.14	9.18	0.00
XOO3291	-	lipoprotein	0.10	0.11	0.21	-0.02	8.30	8.19	9.26	9.05	9.18	9.19	0.00
XOO3292	-	hypothetical protein	1.81	1.79	1.98	1.66	9.44	7.64	9.51	7.53	10.39	8.73	0.00
XOO3293	-	acyl-CoA thioester hydrolase	0.64	1.01	0.68	0.23	7.96	6.94	9.07	8.39	8.67	8.44	0.00
XOO3294	-	hypothetical protein	1.99	1.99			7.62	5.62	4.74	NA	2.48	NA	0.00
XOO3295	<i>gltT</i>	glutamate symporter	1.01	0.89	0.97	1.16	8.60	7.70	9.28	8.30	9.01	7.85	0.00
XOO3296	<i>phoA</i>	alkaline phosphatase	-0.27	-0.61	-0.05	-0.14	8.07	8.68	8.52	8.57	8.37	8.50	0.00
XOO3297	<i>mesJ</i>	cell cycle protein	1.59	3.37	0.59	0.81	6.88	3.52	5.23	4.65	2.50	1.69	0.00
XOO3298	<i>xseB</i>	exodeoxyribonuclease VII small subunit	0.39	0.70	0.25	0.21	9.02	8.32	10.90	10.65	10.49	10.28	0.00
XOO3299	<i>ispA</i>	geranyltranstransferase	0.30	0.21	0.29	0.40	8.58	8.36	9.97	9.68	9.69	9.29	0.00
XOO3302	-	hypothetical protein	1.84	1.67	1.69	2.17	9.03	7.37	10.12	8.42	9.88	7.72	0.00
XOO3303	<i>pmbA</i>	hypothetical protein	-0.50	-1.46	-0.78	0.73	4.35	5.81	6.95	7.73	6.68	5.96	0.00
XOO3304	-	hypothetical protein	-0.30	-0.41	-0.16	-0.32	8.37	8.78	9.75	9.91	9.53	9.85	0.00
XOO3305	<i>tldD</i>	hypothetical protein	0.41	0.31	0.51	0.42	9.39	9.08	10.25	9.74	9.97	9.56	0.00
XOO3306	-	hypothetical protein	-0.45	-0.72	-0.60	-0.05	8.09	8.81	7.67	8.27	7.40	7.45	0.00
XOO3313	-	hypothetical protein	0.52		0.52	NA	NA	1.50	NA	4.09	3.56	0.00	
XOO3316	<i>maf</i>	Maf-like protein	-0.46	-0.44	-0.32	-0.62	8.42	8.86	9.43	9.75	9.08	9.70	0.00
XOO3317	<i>bp26</i>	hypothetical protein	-1.68	-1.54	-1.43	-2.09	7.94	9.48	8.57	9.99	7.98	10.07	0.00
XOO3320	<i>oar</i>	Oar protein	0.33	0.35	0.27	0.37	11.88	11.53	12.60	12.32	12.12	11.75	0.00
XOO3321	-	TonB-like protein	0.58	-0.67	1.12	1.29	6.02	6.69	8.98	7.86	8.19	6.90	0.00
XOO3322	-	rRNA large subunit methyltransferase	0.33	1.48	0.33	-0.81	5.39	3.91	7.68	7.36	6.52	7.33	0.00
XOO3324	-	DnaJ domain-containing protein	-0.07	-0.11	-0.04	-0.07	10.60	10.71	12.03	12.07	11.64	11.71	0.00
XOO3325	-	hypothetical protein	-0.11	0.07	-0.27	-0.13	11.37	11.29	12.35	12.62	11.77	11.90	0.00
XOO3327	<i>holA</i>	DNA polymerase III subunit delta	-0.87	-0.84	-0.99	-0.78	7.71	8.55	8.36	9.34	8.42	9.20	0.00
XOO3328	<i>rlpB</i>	lipoprotein	-0.72	-0.91	-0.66	-0.61	8.95	9.85	10.09	10.75	10.00	10.61	0.00
XOO3329	<i>leuS</i>	Ieucyl-tRNA synthetase	-0.26	-0.36	-0.18	-0.24	8.02	8.38	9.19	9.38	8.93	9.17	0.00
XOO3332	<i>trx</i>	thioredoxin	0.13	0.25	0.12	0.02	10.28	10.03	11.58	11.46	11.15	11.13	0.00
XOO3333	-	hypothetical protein	0.81	-0.29	-1.27	4.00	5.53	5.82	5.95	7.23	6.18	2.19	0.00
XOO3339	-	hypothetical protein	0.16	-0.06	0.18	0.35	8.52	8.59	9.40	9.22	8.64	8.29	0.00
XOO3340	-	peptidyl-prolyl cis-trans isomerase	1.45	1.62	1.39	1.33	8.57	6.94	9.11	7.72	8.48	7.14	0.00
XOO3345	-	hypothetical protein	1.43	1.71	1.37	1.21	10.06	8.35	11.82	10.45	11.53	10.32	0.00
XOO3349	<i>glgX</i>	glycogen debranching protein	0.56		-0.22	1.34	NA	NA	2.48	2.69	5.86	4.52	0.00
XOO3363	<i>xrvA</i>	virulence regulator	0.27	0.64	0.20	-0.01	7.82	7.18	9.46	9.27	9.36	9.37	0.00
XOO3364	-	hypothetical protein	-2.16	-2.17	-3.34	-0.97	5.67	7.84	5.63	8.97	3.32	4.29	0.00
XOO3370	<i>estA</i>	lipase/esterase	0.65	0.55	0.67	0.71	10.91	10.36	11.84	11.16	11.64	10.92	0.00
XOO3372	<i>thiG</i>	thiazole synthase	-0.84	-0.92	-0.66	-0.93	8.82	9.74	10.14	10.80	9.58	10.51	0.00
XOO3373	<i>trmB</i>	tRNA (guanine-N(7)-)methyltransferase	-0.28	0.07	-0.37	-0.54	8.52	8.46	9.31	9.68	9.11	9.65	0.00
XOO3374	<i>sac1</i>	sulfur deprivation response regulator	0.23	0.95	-0.06	-0.20	7.12	6.17	8.39	8.46	8.10	8.30	0.00
XOO3375	-	hypothetical protein	-0.22	-0.02	-0.34	-0.30	3.91	3.93	8.71	9.05	9.05	9.35	0.00
XOO3380	-	fumarylacetate hydrolase	-0.81	-0.57	-0.58	-1.27	7.31	7.88	8.40	8.98	7.79	9.06	0.00
XOO3381	<i>mscL</i>	large-conductance mechanosensitive channel	-0.58	-0.44	-0.50	-0.80	10.50	10.95	11.25	11.75	11.07	11.87	0.00
XOO3388	-	tRNA/rRNA methyltransferase	-0.15	1.57	-0.76	-1.25	4.91	3.34	6.95	7.70	4.45	5.71	0.00
XOO3392	-	hypothetical protein	1.25	2.35	0.76	0.63	9.55	7.20	8.72	7.96	8.08	7.45	0.00
XOO3393	<i>pepN</i>												

XOO3405	-	sensor histidine kinase	0.09	0.17	-0.06	0.18	7.87	7.70	9.53	9.59	9.50	9.33	0.00
XOO3406	-	hypothetical protein	-0.56		0.84	-1.97	3.38	NA	6.21	5.36	5.16	7.12	0.00
XOO3407	<i>cysB</i>	transcriptional regulator CysB-like protein	0.98	1.67	0.94	0.32	6.91	5.24	9.64	8.69	9.01	8.69	0.00
XOO3408	<i>cysG</i>	siroheme synthase	1.06	3.67	0.13	-0.61	5.65	1.98	6.34	6.21	2.66	3.27	0.00
XOO3409	<i>cysK</i>	cysteine synthase	-2.05	-1.72	-2.27	-2.18	8.36	10.08	7.33	9.60	6.91	9.09	0.00
XOO3410	-	hypothetical protein	1.24	2.08	1.31	0.32	7.23	5.15	8.13	6.81	6.99	6.66	0.00
XOO3411	-	hypothetical protein	-2.65	-2.89	-2.78	-2.28	4.52	7.41	6.73	9.51	6.85	9.12	0.00
XOO3413	<i>pykA</i>	pyruvate kinase	0.10	0.04	0.10	0.16	7.65	7.61	9.36	9.26	8.59	8.43	0.00
XOO3414	<i>idgB</i>	indigoine synthesis-like protein	-0.25	-0.24	-0.48	-0.04	8.31	8.55	9.60	10.08	8.29	8.33	0.00
XOO3415	<i>pgk</i>	phosphoglycerate kinase	-0.61	-0.49	-0.70	-0.64	7.07	7.56	7.33	8.03	7.42	8.06	0.00
XOO3416	-	hypothetical protein	0.78	0.88	0.54	0.91	8.20	7.32	8.82	8.28	8.37	7.46	0.00
XOO3417	-	hypothetical protein	0.37	0.73	0.42	-0.06	6.89	6.16	8.19	7.77	7.49	7.55	0.00
XOO3423	<i>katE</i>	catalase	-0.65	-0.61	-0.66	-0.69	8.39	8.99	10.44	11.09	9.49	10.18	0.00
XOO3424	-	hypothetical protein	0.56		0.42	0.71	2.58	NA	10.73	10.31	10.24	9.53	0.00
XOO3425	-	hypothetical protein	-0.24		-0.24		2.32	NA	1.85	2.09	2.94	NA	0.00
XOO3427	-	AraC family transcriptional regulator	-0.83	-0.78	-0.70	-1.00	7.44	8.22	8.52	9.22	7.84	8.84	0.00
XOO3428	-	hypothetical protein	-1.11	-1.13	-1.03	-1.16	8.06	9.20	9.36	10.40	8.86	10.02	0.00
XOO3429	-	IS1595 transposase	0.21		0.21		NA	NA	3.20	2.99	1.16	NA	0.01
XOO3434	-	hypothetical protein	#DIV/0!				2.12	NA	4.55	NA	4.13	NA	0.00
XOO3436	-	endopeptidase ArgC	1.57	-0.42	1.79	3.33	6.83	7.25	6.16	4.37	6.04	2.71	0.00
XOO3437	-	hypothetical protein	1.62	2.76	0.86	1.24	6.74	3.98	9.08	8.21	8.85	7.61	0.00
XOO3439	<i>dnaE2</i>	DNA polymerase III subunit alpha	-1.24		-1.24		5.31	NA	1.85	3.09	NA	NA	0.01
XOO3440	-	hypothetical protein	-0.09	-0.62	-0.43	0.78	4.90	5.52	6.66	7.09	4.42	3.64	0.00
XOO3442	<i>lexA</i>	LexA repressor	-0.87	-0.61	-1.00	-0.99	7.99	8.60	8.48	9.47	8.48	9.47	0.00
XOO3444	<i>doc</i>	death-on-curing protein	-1.29		0.24	-2.83	5.86	NA	6.77	6.53	4.46	7.29	0.00
XOO3447	-	hypothetical protein	-0.72	-0.63	-0.62	-0.92	10.20	10.83	11.19	11.80	10.48	11.40	0.00
XOO3448	-	hypothetical protein	4.45		4.45		NA	NA	6.24	1.79	4.51	NA	0.01
XOO3449	<i>uidR</i>	uid family transcriptional regulator	-1.36	-1.27	-1.51	-1.29	7.06	8.33	8.12	9.63	7.93	9.22	0.00
XOO3451	<i>stkXac1</i>	serine/threonine kinase	-0.56	-1.76	0.19	-0.11	1.79	3.56	8.35	8.15	4.96	5.08	0.00
XOO3457	<i>hsdM-1</i>	type I restriction system adenine methylase	0.03	0.26	-0.06	-0.12	8.43	8.17	5.28	5.34	9.84	9.96	0.00
XOO3458	-	hypothetical protein	0.32	0.06	0.58	0.32	8.72	8.66	8.83	8.26	9.10	8.78	0.00
XOO3459	-	hypothetical protein	0.46	0.47	0.54	0.36	9.51	9.04	10.48	9.94	10.65	10.29	0.00
XOO3460	-	hypothetical protein	0.90	0.96	0.95	0.78	11.94	10.99	13.16	12.21	12.65	11.87	0.00
XOO3461	<i>hsdR</i>	type I restriction enzyme EcoKI subunit R	-0.10	-1.01	0.32	0.38	6.61	7.62	8.23	7.91	8.18	7.79	0.00
XOO3462	-	abortive infection bacteriophage resistance protein	-0.34	-0.24	-0.30	-0.47	4.01	4.24	9.29	9.58	8.83	9.31	0.00
XOO3463	<i>hsdM-2</i>	type I restriction-modification system, M subunit	-0.55	-0.07	-1.00	-0.59	2.43	2.50	3.00	4.00	5.44	6.03	0.00
XOO3464	-	Type I restriction enzyme StySPI specificity protein	0.39	0.18	0.35	0.66	8.62	8.44	9.70	9.35	8.95	8.29	0.00
XOO3467	-	hypothetical protein	-0.52	-0.54	-0.52	-0.51	8.85	9.39	10.08	10.60	9.51	10.02	0.00
XOO3468	-	hypothetical protein	-0.55	-0.60	-0.49	-0.57	10.73	11.32	11.43	11.93	10.29	10.87	0.00
XOO3472	-	hypothetical protein	#DIV/0!				NA	NA	5.37	NA	2.12	NA	0.02
XOO3475	<i>clpB</i>	chaperone ClpB	0.47	0.25	0.57	0.58	8.18	7.93	9.70	9.14	9.22	8.63	0.00
XOO3476	-	hypothetical protein	-0.27	-0.06	-0.52	-0.22	8.15	8.21	9.54	10.06	9.93	10.15	0.00
XOO3477	-	hypothetical protein	0.04	0.19	0.07	-0.13	10.51	10.32	11.65	11.58	11.56	11.69	0.00
XOO3478	-	hypothetical protein	-0.85	-0.84	-0.76	-0.96	9.10	9.94	10.20	10.96	9.71	10.67	0.00
XOO3479	<i>hcp</i>	hypothetical protein	-0.33	-0.36	-0.28	-0.34	11.76	12.12	13.15	13.43	12.78	13.12	0.00
XOO3480	-	hypothetical protein	0.13	0.19	0.14	0.07	13.95	13.77	15.73	15.59	15.42	15.35	0.00
XOO3482	-	hypothetical protein	-0.48	-0.50	-0.55	-0.40	11.81	12.31	13.05	13.60	12.52	12.92	0.00
XOO3483	-	transmembrane protein	-0.44	-0.23	-0.60	-0.48	10.09	10.33	11.31	11.91	10.46	10.94	0.00
XOO3487	-	EF hand domain-containing protein	-0.63	-0.72	-0.64	-0.53	8.67	9.38	10.29	10.93	9.35	9.88	0.00
XOO3489	-	hypothetical protein	1.85	1.85			4.11	2.27	2.48	NA	2.26	NA	0.00
XOO3490	-	hypothetical protein	#DIV/0!				0.79	NA	2.35	NA	4.29	NA	0.02
XOO3492	-	hypothetical protein	-0.33		-0.33		5.35	NA	5.53	5.86	3.25	NA	0.00
XOO3499	-	hypothetical protein	-0.13	0.37	-0.31	-0.45	7.91	7.54	8.70	9.01	8.08	8.52	0.00
XOO3500	-	hypothetical protein	#DIV/0!				2.08	NA	NA	NA	3.92	NA	0.01
XOO3505	-	sulfatase modifying factor 1 (C-alpha-formylglycine-generating enz	-0.62	0.23	-0.83	-1.25	6.07	5.84	8.21	9.04	7.67	8.92	0.00
XOO3506	-	DNA repair ATPase	-0.53	-0.54	-0.54	-0.51	7.44	7.98	8.85	9.39	8.68	9.19	0.00
XOO3507	-	hypothetical protein	-0.02		-0.05	0.01	2.38	NA	3.78	3.84	6.67	6.66	0.00
XOO3508	-	hypothetical protein	0.48	0.51	0.50	0.42	8.24	7.72	9.11	8.61	9.00	8.58	0.00
XOO3511	-	hypothetical protein	-0.02	-0.09	0.02	0.00	7.39	7.48	8.52	8.50	7.73	7.73	0.00
XOO3514	-	hypothetical protein	0.94	0.78	1.15	0.88	7.91	7.13	7.89	6.74	4.28	3.40	0.00
XOO3516	-	hypothetical protein	-0.14	0.14	-0.30	-0.25	9.30	9.16	10.91	11.20	10.06	10.31	0.00
XOO3517	-	hypothetical protein	-0.63	-0.58	-0.66	-0.64	9.93	10.51	11.34	12.00	10.47	11.11	0.00
XOO3519	<i>purT</i>	phosphoribosylglycinamide formyltransferase 2	1.56	2.23	-0.14	2.58	5.21	2.99	6.69	6.83	4.90	2.32	0.00
XOO3520	-	hypothetical protein	0.28	2.54	-0.86	-0.83	4.28	1.75	2.89	3.75	6.55	7.38	0.00
XOO3523	-	hypothetical protein	0.01	-0.11	0.07	0.08	9.40	9.51	9.90	9.83	9.15	9.07	0.00
XOO3524	-	DNA-3-methyladenine glycosylase	0.00	-0.23	0.08	0.15	7.84	8.06	8.72	8.64	8.60	8.45	0.00
XOO3525	-	hypothetical protein	-0.33	-0.32	-0.50	-0.16	7.37	7.69	9.22	9.72	8.32	8.48	0.00
XOO3526	-	hypothetical protein	-0.19	-0.13	-0.27	-0.18	10.19	10.32	11.41	11.68	11.01	11.19	0.00
XOO3527	-	two-component system regulatory protein	0.69	1.67	-0.02	0.42	5.54	3.87	8.23	8.25	4.30	3.87	0.00
XOO3528	-	two-component system sensor protein	0.47	0.50	0.30	0.61	8.65	8.15	5.21	4.91	4.69	4.08	0.00
XOO3529	-	hypothetical protein	-0.14	-0.02	-0.18	-0.22	10.74	10.76	11.11	11.29	10.30	10.51	0.00
XOO3530	<i>minC</i>	septum formation inhibitor	-0.63	-0.60	-0.61	-0.67	9.29	9.89	11.19	11.80	10.46	11.13	0.00
XOO3531	<i>minD</i>	septum site-determining protein	-0.58	-0.51	-0.56	-0.65	10.95	11.47	12.84	13.41	12.25	12.91	0.00
XOO3532	<i>minE</i>	cell division topological specificity factor MinE	-0.28	-0.17	-0.34	-0.32	11.44	11.61	12.59	12.93	12.20	12.52	0.00
XOO3533	-	hypothetical protein	-0.61	-0.17	-0.30	-1.37	8.47	8.64	9.74	10.04	7.13	8.50	0.00
XOO3534	<i>colS</i>	two-component system sensor protein	-0.09	-1.59	0.95	0.38	5.17	6.77	8.86	7.90	8.27	7.89	0.00
XOO3535	<i>colS</i>	two-component system regulatory protein	-0.44	-0.76	1.00	-1.56	6.25	7.01	6.55	5.55	5.98	7.54	0.00
XOO3536	-	hypothetical protein	2.80	3.08	2.53	5.46	5.46	2.38	5.58	3.05	2.00	NA	0.00
XOO3537	-	hypothetical protein	0.55	0.41	0.30	0.94	8.79	8.38	10.23	9.93	9.40	8.46	0.00
XOO3538	<i>yjdB</i>	hypothetical protein	-0.10	-1.14	0.36	0.49	6.24	7.38	8.09	7.73	7.65	7.16	0.00
XOO3539	-	dipeptidyl carboxypeptidase	0.23	0.32	0.51	-0.15	4.44	4.12	9.49	8.97	9.05	9.20	0.00
XOO3543	<i>raxB</i>	ABC transporter protein RaxB	1.44		1.44	2.00	NA	2.70	NA	2.32	0.88	0.00	
XOO3544	<i>raxA</i>	membrane fusion protein RaxA	-1.31	-1.13	-0.45	-2.35	5.88	7.01	4.29	4.74	4.96	7.31	0.00
XOO3546	<i>raxST</i>	sulfotransferase RaxST	0.19	-0.25	-0.37	1.20	7.90	8.15	9.26	9.62	6.71	5.51	0.00
XOO3547	<i>gcvP</i>	glycine dehydrogenase											

XOO3559	<i>rpsD</i>	30S ribosomal protein S4	-0.37	-0.34	-0.47	-0.30	11.78	12.12	12.19	12.66	11.64	11.94	0.00
XOO3562	<i>secY</i>	preprotein translocase subunit SecY	-0.37	-0.28	-0.46	-0.36	8.94	9.22	10.31	10.77	9.94	10.31	0.00
XOO3568	<i>rplF</i>	50S ribosomal protein L6	-0.49	-0.45	-0.54	-0.48	12.65	13.10	14.07	14.61	13.60	14.08	0.00
XOO3569	<i>rpsN</i>	30S ribosomal protein S14	-0.07	-0.02	-0.19	-0.01	12.52	12.54	13.92	14.11	12.84	12.85	0.00
XOO3570	<i>rplE</i>	50S ribosomal protein L5	0.11	0.10	0.13	0.11	14.55	14.46	15.81	15.68	15.40	15.29	0.00
XOO3571	<i>rplX</i>	50S ribosomal protein L24	-0.38	-0.32	-0.30	-0.53	14.64	14.96	15.57	15.88	15.19	15.71	0.00
XOO3576	<i>rplP</i>	50S ribosomal protein L16	0.16	0.25	0.07	0.15	13.55	13.30	14.75	14.67	14.49	14.34	0.00
XOO3577	<i>rpsC</i>	30S ribosomal protein S3	0.32	0.36	0.30	0.31	13.68	13.32	14.88	14.58	14.67	14.36	0.00
XOO3578	<i>rplV</i>	50S ribosomal protein L22	0.28	0.36	0.15	0.33	13.76	13.40	7.83	7.68	14.52	14.18	0.00
XOO3579	<i>rpsS</i>	30S ribosomal protein S19	0.01	0.09	0.22	-0.27	13.14	13.05	13.11	12.89	14.01	14.28	0.00
XOO3580	<i>rplB</i>	50S ribosomal protein L2	0.30	0.41	0.22	0.28	13.09	12.68	13.64	13.41	13.05	12.77	0.00
XOO3590	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'	-0.75	-0.63	-0.82	-0.80	11.70	12.33	12.66	13.48	12.24	13.04	0.00
XOO3591	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	-0.19	-0.11	-0.23	-0.24	12.23	12.34	13.66	13.88	13.26	13.50	0.00
XOO3592	<i>rplL</i>	50S ribosomal protein L7/L12	1.57	0.67	3.46	0.59	13.75	13.08	10.95	7.49	14.96	14.37	0.00
XOO3593	<i>rplJ</i>	50S ribosomal protein L10	-0.21	-0.06	-0.15	-0.42	11.32	11.38	12.69	12.84	12.97	13.39	0.00
XOO3594	<i>rplA</i>	50S ribosomal protein L1	-0.20	-0.07	-0.32	-0.19	10.54	10.61	11.00	11.32	10.91	11.10	0.00
XOO3597	<i>nusG</i>	transcription antitermination protein NusG	-0.77	-0.71	-0.83	-0.76	11.02	11.73	11.58	12.42	10.61	11.37	0.00
XOO3598	<i>secE</i>	preprotein translocase subunit SecE	-0.66	-0.53	-0.73	-0.72	12.48	13.01	13.60	14.32	13.13	13.85	0.00
XOO3600	<i>ychF</i>	GTP-dependent nucleic acid-binding protein EngD	-0.24	-0.17	-0.26	-0.29	8.15	8.32	10.37	10.63	9.79	10.08	0.00
XOO3602	<i>rplY</i>	50S ribosomal protein L25	0.09	0.05	0.09	0.13	11.62	11.57	12.86	12.77	12.20	12.07	0.00
XOO3603	-	ribose-phosphate pyrophosphokinase	-1.48	-1.49	-1.46	-1.48	8.65	10.14	9.84	11.30	9.25	10.73	0.00
XOO3604	<i>ipk</i>	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	-0.49	-0.48	-0.45	-0.54	11.91	12.38	12.91	13.36	12.52	13.07	0.00
XOO3606	-	hypothetical protein	-0.77	-0.98	-0.71	-0.62	7.93	8.90	9.35	10.06	9.12	9.74	0.00
XOO3607	<i>hemA</i>	glutamyl-tRNA reductase	0.30	0.37	0.25	0.26	8.44	8.06	5.03	4.78	9.13	8.87	0.00
XOO3608	<i>prfA</i>	peptide chain release factor 1	-0.14	-0.23	-0.22	0.02	8.36	8.58	9.69	9.91	9.42	9.40	0.00
XOO3609	-	hypothetical protein	-0.37	-0.12	-0.88	-0.09	7.53	7.65	8.85	9.74	8.45	8.55	0.00
XOO3610	<i>moaB</i>	molybdopterin biosynthesis protein B	0.11	-0.04	0.08	0.30	9.41	9.45	10.06	9.98	9.45	9.16	0.00
XOO3611	-	transcriptional regulator	-2.87	-2.25	-3.44	-2.91	7.57	9.82	7.27	10.72	6.70	9.61	0.00
XOO3612	-	hypothetical protein	-0.53	0.88	-1.66	-0.80	5.79	4.91	5.98	7.65	8.73	9.53	0.00
XOO3614	<i>yneN</i>	thioredoxin	-0.95	-1.01	-0.88	-0.94	7.18	8.19	9.16	10.05	8.67	9.62	0.00
XOO3615	<i>rbn</i>	ribonuclease BN/hypothetical protein	-0.72	-0.81	-0.53	-0.82	10.05	10.87	10.77	11.30	10.30	11.12	0.00
XOO3618	-	xylanase	0.16	0.24	0.09	1.73	1.49	2.75	2.66	4.02	NA	0.00	
XOO3619	<i>aspG</i>	asparaginase	-0.31	-0.45	-0.36	-0.11	7.15	7.60	7.86	8.22	7.66	7.77	0.00
XOO3620	-	transcriptional regulator	-0.28	-0.42	-0.10	-0.32	6.23	6.65	7.28	7.38	7.25	7.57	0.00
XOO3624	<i>ilvE</i>	branched-chain amino acid aminotransferase	-0.39	-0.44	-0.35	-0.37	9.92	10.36	10.68	11.03	10.67	11.04	0.00
XOO3629	<i>pntB</i>	pyridine nucleotide transhydrogenase subunit beta	0.73	0.28	1.26	0.66	7.82	7.54	7.63	6.37	8.20	7.54	0.00
XOO3630	<i>pntA</i>	pyridine nucleotide transhydrogenase subunit alpha	2.11	1.59	0.74	3.98	8.30	6.71	9.01	8.27	7.42	3.44	0.00
XOO3631	-	RNA polymerase factor sigma-70	0.05	-0.72	0.82	3.75	NA	7.24	7.95	4.69	3.87	0.00	
XOO3633	<i>pntA</i>	pyridine nucleotide transhydrogenase	2.36	2.36	4.96	2.60	2.00	NA	2.26	NA	0.00		
XOO3637	-	hypothetical protein	-0.45	-0.48	-0.60	-0.28	8.24	8.72	10.19	10.79	9.81	10.10	0.00
XOO3638	<i>exo</i>	exodeoxyribonuclease IX	-0.47	-1.19	0.25	2.35	3.54	7.45	7.20	4.29	NA	0.00	
XOO3639	-	MutT-like protein	-0.89	-0.89	-0.86	-0.91	6.98	7.87	8.92	9.78	8.63	9.54	0.00
XOO3640	-	hypothetical protein	-0.80	-1.41	-0.55	-0.44	1.90	3.31	7.63	8.18	6.33	6.77	0.00
XOO3643	-	hypothetical protein	2.45	2.45	1.58	3.33	5.52	3.08	8.57	6.99	7.02	3.69	0.00
XOO3644	<i>hemK</i>	protoporphyrinogen oxidase	0.23	-0.33	0.31	0.72	7.73	8.07	8.41	8.10	8.58	7.86	0.00
XOO3645	<i>ahpC</i>	alkyl hydroperoxide reductase	0.21	0.19	0.14	0.29	9.91	9.72	11.33	11.19	10.54	10.24	0.00
XOO3646	<i>ahpF</i>	alkyl hydroperoxide reductase	2.12	-	1.49	2.75	2.23	NA	6.73	5.24	5.78	3.03	0.00
XOO3647	<i>oxyR</i>	oxidative stress transcriptional regulator	0.04	-	0.30	-0.23	6.09	NA	7.86	7.56	9.25	9.48	0.00
XOO3648	<i>rnk</i>	regulator of nucleoside diphosphate kinase	-1.02	-2.51	-0.23	-0.33	6.29	8.81	8.15	8.37	7.71	8.04	0.00
XOO3649	<i>talB</i>	transaldolase B	0.33	0.45	0.13	0.40	9.07	8.62	9.63	9.50	9.05	8.65	0.00
XOO3656	-	hypothetical protein	0.02	-0.05	0.10	2.04	2.09	4.88	4.79	1.40	NA	0.00	
XOO3657	<i>pms</i>	methionine sulfoxide reductase A	0.47	0.39	0.40	0.63	9.43	9.04	9.37	8.98	8.99	8.36	0.00
XOO3658	-	hypothetical protein	1.64	0.80	1.21	2.91	3.73	2.93	8.15	6.94	6.82	3.91	0.00
XOO3663	-	hypothetical protein	-0.77	-0.04	-0.55	-1.72	7.17	7.21	8.92	9.47	7.04	8.76	0.00
XOO3664	<i>grxC</i>	glutaredoxin	-0.40	-0.47	-0.27	-0.45	7.95	8.42	9.39	9.66	9.29	9.74	0.00
XOO3665	-	hypothetical protein	-0.69	-1.28	-0.38	-0.40	6.80	8.08	7.71	8.09	6.48	6.89	0.00
XOO3666	<i>phoB</i>	two-component system regulatory protein	-0.44	-0.69	-0.20	-0.45	8.65	9.33	9.80	10.00	10.02	10.46	0.00
XOO3667	<i>phoR</i>	two-component system sensor protein	-1.54	-2.12	-1.30	-1.20	6.04	8.15	7.89	9.18	7.72	8.92	0.00
XOO3668	<i>ppk</i>	polyphosphate kinase	-0.92	-1.70	-0.66	-0.41	5.89	7.59	8.43	9.09	3.55	3.96	0.00
XOO3669	<i>ppx</i>	exopolyphosphatase	-1.23	-1.42	-1.06	-1.22	7.33	8.75	8.48	9.54	8.25	9.47	0.00
XOO3670	<i>gtrB</i>	glycosyl transferase family protein	1.56	-0.12	2.73	2.05	3.45	3.57	6.11	3.38	4.65	2.60	0.00
XOO3671	-	hypothetical protein	-0.75	-0.35	-1.08	-0.82	7.88	8.23	7.79	8.87	7.70	8.52	0.00
XOO3672	-	UDP-2,3-diacylglicosamine hydrolase	0.08	0.71	-0.28	-0.18	7.54	6.83	8.37	8.66	8.41	8.59	0.00
XOO3674	-	hypothetical protein	0.38	-	0.67	0.10	2.64	NA	4.04	3.37	5.59	5.49	0.00
XOO3675	<i>purF</i>	amidophosphoribosyltransferase	-0.09	0.01	0.00	-0.28	9.08	9.06	10.44	10.45	10.33	10.61	0.00
XOO3677	<i>cvpA</i>	colicin V production protein	-0.77	-0.60	-0.78	-0.92	10.49	11.09	11.15	11.93	10.73	11.65	0.00
XOO3678	-	hypothetical protein	-1.05	-1.07	-1.00	-1.09	8.59	9.65	9.77	10.77	9.13	10.22	0.00
XOO3679	<i>folC</i>	bifunctional folylpolyglutamate synthase/dihydrofolate synthase	-0.16	-0.14	-0.31	-0.02	9.12	9.26	10.05	10.36	9.88	9.90	0.00
XOO3680	<i>pgmA</i>	phosphoglycerate mutase	-0.30	-0.44	-0.17	-0.28	8.01	8.45	9.59	9.76	9.11	9.39	0.00
XOO3681	-	hypothetical protein	1.81	1.69	1.68	2.07	9.33	7.63	10.61	8.93	10.33	8.26	0.00
XOO3682	-	non-hemolytic phospholipase C	0.85	-	0.85	1.29	NA	4.44	3.59	NA	NA	0.01	
XOO3683	<i>fecA</i>	TonB-dependent receptor	#DIV/0!	-	-	-	4.05	NA	NA	5.26	NA	0.00	
XOO3684	<i>tdh</i>	L-threonine 3-dehydrogenase	0.08	-	0.26	-0.09	6.97	6.71	6.87	6.96	1.66	NA	0.00
XOO3685	-	hypothetical protein	1.50	2.84	0.51	1.13	7.46	4.62	9.28	8.77	9.10	7.96	0.00
XOO3688	<i>cysW</i>	sulfate ABC transporter permease	-1.64	-1.96	-1.17	-1.80	2.68	4.64	7.78	8.95	7.04	8.85	0.00
XOO3689	<i>cysU</i>	sulfate ABC transporter permease	0.30	1.53	-0.30	-0.32	5.60	4.06	8.84	9.14	9.04	9.36	0.00
XOO3690	<i>sbp</i>	sulfate ABC transporter substrate-binding protein	0.14	2.75	-1.09	-1.24	5.75	3.00	8.31	9.40	8.37	9.61	0.00
XOO3691	<i>kbl</i>	2-amino-3-ketobutyrate CoA ligase	-0.99	-	-0.99	-	2.92	NA	5.55	6.54	4.46	NA	0.00
XOO3693	-	pseudouridylate synthase	-0.38	-0.40	-0.30	-0.43	9.99	10.38	10.86	11.16	9.95	10.38	0.00
XOO3696	<i>mopB</i>	hypothetical protein	-0.20	-0.10	-0.19	-0.31	13.59	13.69	15.04	15.24	14.82	15.14	0.00
XOO369													

XOO3722	<i>gfo</i>	glucose-fructose oxidoreductase	1.25	4.55	-0.50	-0.31	5.35	0.81	5.38	5.88	5.43	5.74	0.00	
XOO3723	-	gluconolactonase	-0.62	-0.60	0.04	-1.29	4.69	5.29	7.32	7.28	6.23	7.53	0.00	
XOO3725	-	hypothetical protein	-1.24	-3.48	1.00		3.32	6.80	5.92	4.92	4.80	NA	0.00	
XOO3726	-	hypothetical protein	-0.52	-0.16	-0.68	-0.71	7.72	7.88	9.03	9.71	8.42	9.13	0.00	
XOO3728	<i>fadB</i>	p-hydroxycinnamoyl CoA hydratase/lyase	1.24	1.28	0.91	1.54	9.91	8.63	11.01	10.10	10.42	8.89	0.00	
XOO3729	<i>badH</i>	aldehyde dehydrogenase	2.69	4.24	3.08	0.77	6.38	2.14	6.81	3.73	3.66	2.89	0.00	
XOO3730	-	acyl-CoA synthetase	1.52	-0.14		3.18	2.62	2.77	3.21	NA	5.95	2.77	0.00	
XOO3731	<i>pcaQ</i>	transcriptional regulator	0.74	-1.09	2.57		4.03	5.13	5.89	3.32	6.01	NA	0.00	
XOO3734	<i>pcaH</i>	protocatechuate 4,5-dioxygenase subunit beta	1.62	4.30	0.65	-0.09	6.31	2.01	8.45	7.81	7.32	7.41	0.00	
XOO3735	<i>vanR</i>	GntR family transcriptional regulator	-0.08	0.40	-0.43	-0.20	8.07	7.68	7.87	8.30	7.54	7.74	0.00	
XOO3739	-	hydrolase	-0.98	-0.77	-0.76	-1.41	2.38	3.15	6.56	7.32	5.64	7.05	0.00	
XOO3740	<i>visC</i>	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase	-0.41	-0.51	-0.33	-0.39	7.91	8.42	9.56	9.88	9.29	9.67	0.00	
XOO3741	<i>ubiH</i>	2-octaprenyl-6-methoxyphenyl hydroxylase	-0.94	-1.32	-0.84	-0.67	6.40	7.72	8.37	9.21	8.01	8.68	0.00	
XOO3742	-	hypothetical protein	-0.59	-1.41	-0.33	-0.03	6.81	8.22	8.97	9.31	8.58	8.61	0.00	
XOO3743	-	hypothetical protein	-0.23	-0.14	-0.24	-0.29	10.41	10.55	11.16	11.41	10.46	10.75	0.00	
XOO3744	-	acetoin utilization family protein	0.11	0.09	-0.04	0.29	8.56	8.47	9.63	9.67	8.77	8.48	0.00	
XOO3745	<i>ostA</i>	organic solvent tolerance protein	-0.17	-0.27	-0.19	-0.04	11.93	12.20	12.33	12.52	11.84	11.88	0.00	
XOO3746	<i>surA</i>	peptidyl-prolyl cis-trans isomerase	-0.52	-0.46	-0.48	-0.61	9.38	9.84	11.19	11.67	10.86	11.47	0.00	
XOO3747	<i>pdxA</i>	4-hydroxythreonine-4-phosphate dehydrogenase	-0.20	-0.09	-0.27	-0.24	7.22	7.31	8.80	9.07	8.48	8.72	0.00	
XOO3748	<i>ksgA</i>	dimeThylenadenosine transferase	-0.44	-0.25	-0.43	-0.66	8.20	8.45	9.46	9.89	9.42	10.08	0.00	
XOO3750	<i>apaH</i>	diadenosine tetraphosphatase	-1.05	-1.29	-0.84	-1.02	7.46	8.75	9.11	9.95	9.19	10.21	0.00	
XOO3752	<i>thyA</i>	thymidylate synthase	-0.88	-0.58	-0.78	-1.28	7.27	7.85	8.25	9.03	7.95	9.23	0.00	
XOO3753	<i>lgt</i>	prolipoprotein diacylglycerol transferase	-1.36	-1.32	-1.37	-1.37	8.37	9.69	9.70	11.07	9.42	10.80	0.00	
XOO3754	-	hypothetical protein	-0.89	-0.49	0.10	-2.27	5.35	5.84	6.35	6.25	6.36	8.63	0.00	
XOO3755	-	glycine rich protein	-0.43		-1.71	0.85	1.90	NA	6.47	8.18	5.27	4.42	0.00	
XOO3756	-	hypothetical protein	-0.86	-0.82	-0.85	-0.91	8.83	9.65	10.32	11.17	9.63	10.54	0.00	
XOO3757	<i>dgkA</i>	diacylglycerol kinase	-0.14	0.31	0.03	-0.76	6.96	6.65	8.50	8.47	7.71	8.47	0.00	
XOO3758	-	hypothetical protein	3.13		3.25	3.01	5.73	NA	5.98	2.74	5.40	2.39	0.00	
XOO3762	<i>colS</i>	two-component system sensor protein	-1.65	-1.42	-1.89	-1.64	6.97	8.39	6.96	8.85	5.90	7.54	0.00	
XOO3763	<i>colR</i>	two-component system regulatory protein	-2.70	-2.71	-2.63	-2.76	8.51	11.22	9.60	12.23	9.37	12.12	0.00	
XOO3764	<i>tesA</i>	acyl-CoA thioesterase	-0.87	-0.96	-0.78	-0.86	6.69	7.65	8.49	9.27	7.84	8.70	0.00	
XOO3766	-	oxidoreductase	-0.10	0.35	0.27	-0.94	9.16	8.81	10.23	9.96	8.71	9.64	0.00	
XOO3767	<i>tauD</i>	taurine dioxygenase	#DIV/0!					3.79	NA	NA	NA	5.81	NA	0.00
XOO3774	-	hypothetical protein	-0.82	-0.90	-0.74	-0.82	9.03	9.93	10.08	10.82	9.51	10.33	0.00	
XOO3775	-	hypothetical protein	5.33		5.37	5.30	2.73	NA	7.91	2.54	7.56	2.26	0.00	
XOO3782	-	voltage-gated potassium channel subunit beta	0.42	0.34	0.51	0.41	7.74	7.40	8.81	8.31	7.96	7.55	0.00	
XOO3785	<i>rbsK</i>	ribokinase	-0.14	-0.23	-0.11	-0.08	9.89	10.12	10.57	10.68	9.39	9.47	0.00	
XOO3786	-	hypothetical protein	#DIV/0!					5.20	NA	4.39	NA	1.95	NA	0.00
XOO3787	-	hypothetical protein	-0.35	-0.08	-0.26	-0.70	2.89	2.97	7.93	8.19	7.38	8.08	0.00	
XOO3788	-	methyltransferase	0.69	2.83	-0.36	-0.41	7.10	4.27	9.10	9.46	8.71	9.12	0.00	
XOO3791	<i>metK</i>	S-adenosylmethionine synthetase	-0.39	-0.49	-0.44	-0.24	8.74	9.23	9.89	10.33	9.42	9.66	0.00	
XOO3792	<i>appA</i>	phosphoanhydride phosphohydrolase	1.59	3.57	0.54	0.66	6.97	3.40	8.71	8.17	8.59	7.93	0.00	
XOO3793	<i>cirA</i>	TonB-dependent receptor	-1.21	-0.67	-1.49	-1.48	5.71	6.37	6.92	8.40	6.65	8.13	0.00	
XOO3795	-	TetR/AcrF family transcriptional regulator	1.75	3.47	1.40	0.38	7.15	3.68	8.18	6.78	7.31	6.94	0.00	
XOO3796	<i>ppc</i>	phosphoenolpyruvate carboxylase	0.37		0.62	0.13	2.58	NA	4.84	4.22	6.86	6.73	0.00	
XOO3797	-	hypothetical protein	#DIV/0!					3.89	NA	3.25	NA	NA	NA	0.00
XOO3798	<i>sahH</i>	S-adenosyl-L-homocysteine hydrolase	-0.31	-0.15	-0.47	-0.31	9.80	9.95	10.53	11.00	9.83	10.13	0.00	
XOO3799	-	methyltransferase	0.32	0.53	0.58	-0.15	8.50	7.97	4.12	3.54	6.36	6.50	0.00	
XOO3800	-	sulfotransferase	0.53		0.53		NA	NA	3.20	2.67	2.48	NA	0.00	
XOO3801	-	hypothetical protein	-0.19	-0.20	0.62	-0.98	6.72	6.91	8.69	8.07	6.24	7.21	0.00	
XOO3802	-	hypothetical protein	1.19	3.08	-1.18	1.67	7.11	4.03	5.78	6.96	5.28	3.61	0.00	
XOO3803	-	hypothetical protein	-0.22	-0.66	-0.09	0.08	6.38	7.04	7.99	8.08	7.91	7.82	0.00	
XOO3804	<i>dgd</i>	D-galactose 1-dehydrogenase	0.19	0.02	0.34	0.22	7.75	7.73	9.07	8.73	8.17	7.95	0.00	
XOO3805	-	hypothetical protein	1.70	1.28	2.01	1.81	7.40	6.12	8.45	6.43	8.00	6.19	0.00	
XOO3806	<i>xcp</i>	protease	-1.09	-0.36		-1.81	0.79	1.16	4.31	NA	2.29	4.10	0.00	
XOO3807	-	quinone reductase	-2.61	-2.17	-4.65	-1.01	5.36	7.53	4.54	9.19	2.99	4.00	0.00	
XOO3808	-	hypothetical protein	#DIV/0!					3.58	NA	NA	2.12	NA	0.01	
XOO3809	-	hypothetical protein	1.37	3.15	0.01	0.97	7.00	3.85	3.91	3.91	4.97	4.00	0.00	
XOO3810	<i>metF</i>	5,10-methylenetetrahydrofolate reductase	1.25	0.36	2.91	0.48	3.03	2.68	5.86	2.95	4.14	3.66	0.00	
XOO3812	-	hypothetical protein	-1.66	-1.87	-1.44	-1.67	7.65	9.52	9.80	11.25	9.24	10.90	0.00	
XOO3816	-	hypothetical protein	1.60	3.67	0.40	0.74	6.92	3.26	8.84	8.43	8.50	7.77	0.00	
XOO3817	-	hypothetical protein	1.25	4.23	-0.19	-0.29	7.33	3.10	8.21	8.40	7.67	7.95	0.00	
XOO3819	-	peptidase	-1.42	-1.46	-1.33	-1.49	9.53	10.99	10.75	12.08	10.11	11.60	0.00	
XOO3820	-	hypothetical protein	0.30	-0.03	0.56	0.37	7.21	7.24	8.25	7.69	7.93	7.56	0.00	
XOO3823	<i>ftsA</i>	cell division protein	0.10	0.12	-0.11	0.30	10.14	10.02	11.34	11.46	10.83	10.53	0.00	
XOO3824	<i>ddl</i>	D-alanine--D-alanine ligase	0.37		0.47	0.26	1.85	NA	8.87	8.40	7.91	7.65	0.00	
XOO3825	<i>murC</i>	UDP-N-acetylMuramate-L-alanine ligase	-0.11	0.26	-0.77	0.20	9.28	9.02	7.97	8.74	8.42	8.22	0.00	
XOO3826	<i>murG</i>	undecaprenylidiphospho-Muramoylpentapeptide beta-N-acetylgluc	0.69	0.54	0.57	0.97	10.59	10.05	10.96	10.39	9.40	8.43	0.00	
XOO3827	<i>ftsW</i>	cell division protein	0.30	0.33	0.30	0.27	9.37	9.04	10.83	10.52	9.91	9.64	0.00	
XOO3828	<i>mraY</i>	phospho-N-acetylMuramoylpentapeptide-transferase	0.21	0.41	0.13	0.08	8.58	8.17	10.18	10.05	9.76	9.68	0.00	
XOO3829	<i>murF</i>	UDP-N-acetylMuramyl tripeptide synthetase	0.73	0.56	0.93	0.69	8.67	8.11	9.73	8.79	9.44	8.75	0.00	
XOO3830	<i>murE</i>	UDP-N-acetylMuramylalanyl-D-glutamate-2,6-diaminopimelate II	0.84	1.31	0.54	0.66	5.30	4.00	9.45	8.91	8.20	7.54	0.00	
XOO3831	<i>ftsI</i>	penicillin-binding protein 3	0.32	0.29	0.17	0.49	8.74	8.45	9.96	9.79	9.00	8.51	0.00	
XOO3832	<i>ftsL</i>	cell division protein	-0.08	-0.12	-0.08	-0.04	9.92	10.04	10.83	10.91	10.49	10.53	0.00	
XOO3833	<i>mraW</i>	S-adenosyl-methyltransferase MraW	-0.35	-0.31	-0.35	-0.40	11.25	11.55	12.07	12.42	11.41	11.81	0.00	
XOO3834	-	cell division protein MraZ	1.04	0.95	0.81	1.38	9.78	8.83	10.80	9.99	9.36	7.98	0.00	
XOO3835	-	hypothetical protein	-0.40	-0.34	-0.44	-0.41	10.58	10.91	11.63	12.07	10.25	10.65	0.00	
XOO3836	-	hypothetical protein	-0.22	-1.27	0.82	5.49	6.76	NA	NA	4.32	3.50	0.00		
XOO3837	-	hypothetical protein	1.10	2.65	0.70	-0.04	6.79	4.15	8.73	8.03	3.29	3.33	0.00	
XOO3838	-	hypothetical protein	0.25	0.48	-0.02	0.28	9.15	8.66	9.88	9.90	8.47	8.19	0.00	
XOO3840	-	hypothetical protein	0.29	1.86	-0.91	-0.09	8.20	6.34	2.90	3.81	6.73	6.82	0.00	
XOO3841	<i>dld</i>	D-lactate dehydrogenase	-1.30	-1.81	-1.12	-0.98	1.40	3.21	5.80	6.92	5.38	6.36	0.00	
XOO3842	<i>kdpE</i>													

XOO3853	<i>ribA</i>	GTP cyclohydrolase II	0.02	-0.03	-0.12	0.22	8.42	8.45	8.39	8.51	8.26	8.04	0.00
XOO3855	-	hypothetical protein	-0.13	0.13	-0.22	-0.28	9.12	9.00	10.93	11.15	10.13	10.41	0.00
XOO3856	<i>ribD</i>	bifunctional riboflavin-specific deaminase/5-amino-6-uracil reducta	0.00	0.20	-0.15	-0.04	5.99	5.79	8.77	8.92	8.32	8.36	0.00
XOO3857	-	acetyltransferase	-0.05	-0.10	0.01	-0.07	8.38	8.48	10.26	10.26	10.45	10.52	0.00
XOO3859	-	hypothetical protein	-0.21	0.00	-0.13	-0.52	8.71	8.71	9.39	9.52	7.09	7.61	0.00
XOO3860	<i>glyA</i>	serine hydroxymethyltransferase	-0.24	-0.27	-0.28	-0.17	9.92	10.20	11.08	11.36	10.48	10.65	0.00
XOO3861	-	TonB-dependent receptor	0.93	0.53	1.32	3.01	NA	8.17	7.64	8.39	7.07	0.00	
XOO3862	-	hypothetical protein	-0.27	0.00	-0.27	0.00	2.86	NA	3.48	3.75	4.64	NA	0.00
XOO3863	<i>yjjK</i>	ABC transporter ATP-binding protein	0.09	-0.09	0.59	-0.22	9.51	9.61	10.89	10.30	10.32	10.53	0.00
XOO3865	<i>sll7047</i>	hypothetical protein	#DIV/0!		NA	NA	2.48	NA	NA	NA	NA	0.07	
XOO3866	-	esterase	1.60	2.89	1.00	0.92	6.77	3.88	8.23	7.23	7.97	7.05	0.00
XOO3867	-	alcohol dehydrogenase	-1.63	-1.97	-2.10	-0.82	7.21	9.18	7.03	9.13	7.15	7.97	0.00
XOO3868	-	hypothetical protein	1.34	0.26	2.42	1.95	NA	6.90	6.64	6.13	3.71	0.00	
XOO3869	-	hypothetical protein	0.93	0.30	1.21	1.27	3.89	3.58	9.28	8.06	8.95	7.67	0.00
XOO3870	-	two-component system regulatory protein	0.81	0.00	-0.28	1.89	3.05	NA	8.48	8.75	7.20	5.30	0.00
XOO3871	-	two-component system sensor protein	0.34	2.91	-1.99	0.10	5.47	2.56	5.57	7.56	3.95	3.85	0.00
XOO3872	-	hypothetical protein	0.88	0.14	1.02	1.47	3.76	3.62	8.83	7.81	8.27	6.80	0.00
XOO3873	<i>gsh1</i>	glutamate–cysteine ligase	#DIV/0!		1.95	NA	1.40	NA	2.58	NA	0.01		
XOO3875	-	two-component system sensor protein	1.98	0.00	1.73	2.24	4.78	NA	3.60	1.87	4.38	2.14	0.00
XOO3877	<i>gsh1</i>	glutamate–cysteine ligase	-0.72	-3.29	1.66	-0.54	5.03	8.33	5.89	4.22	7.98	8.52	0.00
XOO3878	<i>dr161</i>	nodulin 21-like protein	-1.43	-0.36	-2.37	-1.56	3.02	3.38	7.08	9.45	3.09	4.65	0.00
XOO3881	<i>engB</i>	ribosome biogenesis GTP-binding protein YsxC	-1.32	-0.81	-1.50	-1.66	7.99	8.80	7.43	8.93	4.49	6.15	0.00
XOO3882	<i>cycA</i>	cytochrome C4	-0.31	-0.22	-0.14	-0.58	9.94	10.16	10.73	10.87	10.07	10.65	0.00
XOO3884	<i>dsbA</i>	thiol:disulfide interchange protein	-0.91	-0.71	-0.79	-1.23	7.09	7.80	8.48	9.28	7.86	9.09	0.00
XOO3885	-	hypothetical protein	-0.24	-0.93	-0.44	0.65	4.42	5.35	7.92	8.36	7.62	6.97	0.00
XOO3893	<i>metC</i>	cystathione gamma-synthase	-0.94	-1.26	-0.48	-1.08	6.24	7.50	8.95	9.43	9.07	10.14	0.00
XOO3895	<i>tnp</i>	transposase	0.18	-0.88	0.37	1.04	6.30	7.18	7.79	7.42	7.60	6.57	0.00
XOO3909	<i>fyuA</i>	TonB-dependent receptor	-0.65	0.00	-0.43	-0.86	1.79	NA	2.62	3.05	5.54	6.40	0.00
XOO3911	<i>hmsH</i>	protein Hmsprotein H	-1.41	-1.35	-1.51	-1.37	6.93	8.28	9.07	10.58	8.52	9.89	0.00
XOO3912	<i>hmsF</i>	protein HmsF	-0.65	-0.48	-0.59	-0.88	7.71	8.19	8.79	7.50	8.38	0.00	
XOO3913	<i>hmsR</i>	N-glycosyltransferase	-0.04	-0.14	-0.11	0.13	9.80	9.94	10.33	10.44	9.72	9.59	0.00
XOO3914	-	hypothetical protein	-0.13	-0.21	-0.19	0.02	7.61	7.82	8.92	9.11	8.92	8.91	0.00
XOO3917	<i>glmS</i>	glucosamine-fructose-6-phosphate aminotransferase	-0.71	-0.26	-0.94	-0.93	8.47	8.73	8.95	9.89	8.45	9.38	0.00
XOO3918	-	LacI family transcriptional regulator	-0.89	-0.97	-0.77	-0.94	7.62	8.59	9.77	10.54	9.42	10.36	0.00
XOO3919	<i>gluP</i>	glucose-galactose transporter	-1.40	0.00	-2.02	-0.78	NA	NA	7.02	9.05	8.00	8.78	0.00
XOO3920	-	GntR family transcriptional regulator	0.10	0.29	0.13	-0.12	8.74	8.45	10.05	9.92	9.57	9.69	0.00
XOO3921	-	hypothetical protein	-2.04	-1.27	-3.08	-1.76	7.31	8.59	5.68	8.76	6.35	8.11	0.00
XOO3922	-	N-acetylglucosaminidase	-0.59	0.00	-0.59	0.00	2.84	NA	1.00	1.59	2.32	NA	0.00
XOO3923	<i>lacZ</i>	hypothetical protein	0.30	0.00	0.12	0.49	3.67	NA	2.76	2.64	2.66	2.17	0.00
XOO3932	<i>ptr1</i>	pteridine reductase	-0.11	0.84	-0.48	-0.69	6.06	5.22	6.45	6.93	5.77	6.46	0.00
XOO3933	<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophospho	-0.29	-0.24	-0.39	-0.24	8.36	8.61	9.14	9.53	8.82	9.05	0.00
XOO3934	-	histidine kinase-response regulator hybrid protein	-0.67	-0.55	-0.71	-0.73	8.81	9.36	9.66	10.37	9.54	10.27	0.00
XOO3935	-	two-component system regulatory protein	-0.87	-0.85	-0.91	-0.85	9.57	10.41	11.79	12.70	11.25	12.10	0.00
XOO3936	-	two-component system sensor protein	-0.11	1.81	-0.97	-1.16	6.41	4.60	10.47	11.44	10.27	11.43	0.00
XOO3937	-	hypothetical protein	-1.64	-1.67	-1.56	-1.69	9.11	10.78	10.75	12.31	10.40	12.08	0.00
XOO3938	<i>ydgJ</i>	oxidoreductase	-1.20	-1.29	-1.43	-0.87	7.36	8.65	7.36	8.79	7.11	7.98	0.00
XOO3939	<i>gndA</i>	6-phosphogluconate dehydrogenase	-1.71	-1.53	-1.43	-2.16	2.08	3.62	5.20	6.64	5.55	7.70	0.00
XOO3940	-	hypothetical protein	-1.65	-2.08	-2.02	-0.84	2.68	4.76	6.66	8.68	7.49	8.33	0.00
XOO3941	-	hypothetical protein	-1.57	-1.64	-1.50	-1.55	9.21	10.86	10.66	12.16	10.30	11.85	0.00
XOO3946	-	hypothetical protein	0.50	0.00	1.35	-0.36	NA	3.36	5.19	3.84	3.98	4.34	0.00
XOO3947	<i>pbeF</i>	nicotinate phosphoribosyltransferase	0.08	0.12	-0.02	0.13	8.05	7.93	8.36	8.38	8.03	7.90	0.00
XOO3948	-	bifunctional nicotinamide mononucleotide adenylyltransferase/ADF	1.13	1.03	0.83	1.53	9.70	8.67	10.33	9.50	9.87	8.34	0.00
XOO3949	-	hypothetical protein	-0.69	-0.23	-0.89	-0.95	8.28	8.51	7.74	8.63	7.78	8.73	0.00
XOO3950	<i>prc</i>	tail-specific protease	-0.33	-0.26	-0.43	-0.32	8.44	8.70	10.31	10.74	9.73	10.04	0.00
XOO3952	<i>lipA</i>	lipoyl synthase	-0.15	-0.06	-0.14	-0.25	10.46	10.52	11.71	11.85	11.60	11.84	0.00
XOO3953	<i>lipB</i>	lipoate-protein ligase B	-0.03	-0.20	0.14	-0.02	8.12	8.32	9.36	9.23	9.39	9.41	0.00
XOO3956	<i>dacC</i>	penicillin-binding protein 6	0.19	0.13	0.31	0.14	8.82	8.69	10.42	10.11	10.17	10.03	0.00
XOO3957	<i>rlpA</i>	rare lipoprotein A	1.19	0.99	0.95	1.64	8.30	7.31	9.79	8.83	8.99	7.36	0.00
XOO3958	<i>mltB</i>	membrane-bound lytic transglycosylase	0.75	0.90	0.61	0.74	11.08	10.18	12.01	11.40	11.53	10.79	0.00
XOO3964	-	hypothetical protein	0.57	0.85	0.66	0.21	4.47	3.62	8.63	7.96	9.09	8.88	0.00
XOO3966	-	hypothetical protein	-0.72	-0.91	-0.64	-0.62	8.21	9.12	10.30	10.94	9.86	10.48	0.00
XOO3967	<i>mrdB</i>	rod shape-determining protein	0.18	0.00	0.15	0.21	2.23	NA	1.95	1.80	4.01	3.79	0.00
XOO3968	<i>mrdA</i>	penicillin-binding protein 2	1.72	2.55	0.70	1.92	6.20	3.65	7.68	6.98	8.11	6.19	0.00
XOO3969	<i>mreD</i>	rod shape-determining protein	-0.17	-0.22	-0.25	-0.04	9.01	9.22	9.79	10.04	9.12	9.15	0.00
XOO3970	<i>mreB</i>	rod shape-determining protein MreB	0.91	0.92	0.89	0.94	10.01	9.09	11.38	10.50	11.14	10.20	0.00
XOO3971	-	sugar kinase	0.58	0.52	0.74	0.47	3.73	3.21	9.04	8.30	8.67	8.19	0.00
XOO3979	<i>codA</i>	cytosine deaminase	0.89	0.44	1.21	1.02	6.83	6.38	8.42	7.21	4.41	3.39	0.00
XOO3980	-	hypothetical protein	0.47	1.60	-0.67	0.00	4.06	2.46	5.53	6.20	2.81	NA	0.00
XOO3987	<i>ubiE</i>	ubiquinone/menaquinone biosynthesis methyltransferase	-0.08	-0.14	-0.17	0.06	9.09	9.22	9.64	9.80	8.97	8.91	0.00
XOO3988	-	response regulator	0.88	3.09	-1.08	0.62	5.57	2.48	3.08	4.17	4.75	4.13	0.00
XOO3989	<i>pepN</i>	aminopeptidase	0.47	0.43	0.47	0.52	9.86	9.44	11.82	11.35	11.31	10.79	0.00
XOO3990	-	hypothetical protein	0.10	0.02	0.02	0.27	4.12	4.10	9.12	9.10	9.24	8.97	0.00
XOO3992	<i>hsfU</i>	ATP-dependent protease ATP-binding subunit HsfU	-0.41	-1.01	0.01	-0.23	5.93	6.94	8.67	8.67	8.34	8.57	0.00
XOO3994	<i>xerC</i>	site-specific tyrosine recombinase XerC	0.51	-0.37	-1.36	3.26	6.40	6.77	6.95	8.31	6.25	2.99	0.00
XOO3998	-	hypothetical protein	-0.01	-0.05	0.05	-0.04	7.72	7.77	9.40	9.36	9.11	9.15	0.00
XOO3999	<i>ptrB</i>	oligopeptidase B	0.43	0.41	0.41	0.47	8.57	8.16	10.21	9.80	9.29	8.82	0.00
XOO4000	<i>aspC</i>	hypothetical protein	0.52	0.66	0.50	0.40	9.12	8.47	10.08	9.58	9.68	9.27	0.00
XOO4002	-	prolyl oligopeptidase	0.53	0.52	0.53	0.54	8.96	8.44	9.90	9.37	9.81	9.27	0.00
XOO4004	-	outer membrane lipoprotein	-1.83	-1.68	-1.93	-1.86	9.14	10.82	9.95	11.89	9.37	11.23	0.00
XOO4005	-	hypothetical protein	0.13	-0.07	0.11	0.34	7.74	7.80	9.57	9.46	9.36	9.02	0.00
XOO4006	-	hypothetical protein	1.25	2.77	0.65	0.33	5.57	2.80	8.47	7.82	7.82	7.49	0.00
XOO4007	<i>hemC</i>	porphobilinogen deaminase	0.03	0.27	-0.20	0							

XOO4024	-	hypothetical protein	#DIV/0!		3.25	NA	NA	3.80	NA	3.27	0.00			
XOO4030	<i>treA</i>	trehalase		-0.62	-0.45	-0.54	-0.88	4.12	4.56	8.72	9.27	8.23	9.11	0.00
XOO4032	<i>corA</i>	magnesium and cobalt transport protein		-0.22	-0.23	-0.11	-0.32	9.45	9.67	10.25	10.37	10.19	10.51	0.00
XOO4033	-	hypothetical protein		0.05	0.36	-0.15	-0.08	6.96	6.60	7.92	8.07	7.42	7.50	0.00
XOO4035	-	1,4-beta-celllobiosidase		-0.05	0.47	-0.37	-0.26	7.85	7.37	8.82	9.19	8.28	8.54	0.00
XOO4036	-	cellulase		-0.79	-0.68	-0.15	-1.52	7.53	8.21	8.36	8.52	4.96	6.48	0.00
XOO4037	-	hypothetical protein		-0.13	-0.58	0.31	-0.12	7.80	8.38	9.03	8.72	8.84	8.96	0.00
XOO4038	-	hypothetical protein		3.58		3.58		2.26	NA	6.23	2.65	4.78	NA	0.00
XOO4043	-	dipeptidyl peptidase IV		0.40	0.23	0.14	0.83	7.46	7.23	8.59	8.45	8.16	7.33	0.00
XOO4044	-	prolyl oligopeptidase		-0.11	-0.23	0.04	-0.13	9.75	9.99	10.11	10.08	8.98	9.11	0.00
XOO4045	-	hypothetical protein		2.37		3.02	1.72	NA	NA	6.71	3.69	5.01	3.29	0.00
XOO4046	-	oxidoreductase		2.44		2.87	2.01	2.90	NA	6.38	3.50	5.72	3.71	0.00
XOO4048	-	threonine aldolase		1.83	3.82	2.29	-0.63	5.76	1.93	5.36	3.07	4.62	5.25	0.00
XOO4049	<i>trpE</i>	anthranilate synthase component I		0.48	0.35	0.58	0.50	9.64	9.29	10.40	9.82	10.69	10.19	0.00
XOO4050	-	lipid kinase		-1.24	-1.11	-1.02	-1.59	7.16	8.27	8.51	9.54	7.88	9.47	0.00
XOO4051	-	N-acetyltransferase		0.16	-0.01	0.16	0.35	7.78	7.79	8.99	8.83	8.84	8.54	0.00
XOO4054	<i>purC</i>	phosphoribosylaminoimidazolesuccinocarboxamide synthase		0.03	-0.05	-0.19	0.32	9.04	9.09	10.14	10.33	9.59	9.26	0.00
XOO4058	-	hypothetical protein		0.18	0.23	-0.01	0.32	3.96	3.72	7.72	7.73	8.58	8.26	0.00
XOO4059	-	lytic enzyme		0.69		-2.66	4.05	2.71	NA	0.79	3.45	7.13	3.08	0.00
XOO4062	-	hypothetical protein		0.57	0.62	0.69	0.41	8.97	8.35	9.72	9.03	9.58	9.17	0.00
XOO4064	<i>ndhF</i>	monovalent cation/H <sup>+</sup> antiporter subunit A		2.02		3.49	0.56	6.44	NA	7.32	3.83	6.76	6.20	0.00
XOO4065	<i>phaC</i>	monovalent cation/H <sup>+</sup> antiporter subunit C		2.45	0.39		4.51	2.89	2.50	5.99	NA	5.85	1.34	0.00
XOO4066	<i>phaD</i>	monovalent cation/H <sup>+</sup> antiporter subunit D		0.69	-0.07	2.19	-0.05	6.59	6.66	8.52	6.33	7.41	7.46	0.00
XOO4067	<i>phaE</i>	monovalent cation/H <sup>+</sup> antiporter subunit E		0.00	-0.44	0.15	0.30	6.92	7.36	7.98	7.83	8.04	7.74	0.00
XOO4069	-	monovalent cation/H <sup>+</sup> antiporter subunit G		0.81	0.90	0.55	1.00	7.84	6.95	8.98	8.43	8.82	7.82	0.00
XOO4070	<i>hmgA</i>	homogenitate 1,2-dioxygenase		0.89	-0.02	0.82	1.89	3.13	3.15	7.48	6.66	8.15	6.27	0.00
XOO4071	-	4-hydroxyphenylpyruvate dioxygenase		1.77	1.61	2.00	1.70	8.55	6.94	9.73	7.73	9.96	8.26	0.00
XOO4072	-	MarR family transcriptional regulator		-0.63	-0.23	-1.17	-0.48	8.09	8.32	8.63	9.80	8.67	9.14	0.00
XOO4073	-	hypothetical protein		0.35	0.54	0.53	-0.02	5.65	5.10	7.82	7.29	7.15	7.18	0.00
XOO4074	<i>yhiP</i>	di-tripeptide transporter		0.63	0.58	0.57	0.74	9.99	9.41	10.59	10.01	10.07	9.33	0.00
XOO4076	<i>nucH</i>	nuclease		-0.22		-0.20	-0.24	NA	NA	3.42	3.62	2.71	2.95	0.00
XOO4077	<i>pdhA</i>	Pyruvate dehydrogenase e1 component subunit alpha	#DIV/0!				4.31	NA	2.45	NA	3.89	NA	0.00	
XOO4078	<i>pdhB</i>	Pyruvate dehydrogenase E1 component subunit beta		0.45	0.56	-0.27	1.06	2.76	2.20	1.95	2.22	2.64	1.59	0.00
XOO4081	<i>pdhB</i>	Pyruvate dehydrogenase E1 component subunit beta		0.57		-1.84	2.99	2.68	NA	3.92	5.77	5.29	2.30	0.00
XOO4083	-	hypothetical protein		-1.58	-1.72	-1.33	-1.68	7.51	9.23	8.79	10.11	8.56	10.24	0.00
XOO4084	<i>yfcY</i>	acetyl-CoA acetyltransferase		-0.46	-0.64	-0.35	-0.40	8.24	8.87	9.22	9.57	8.79	9.19	0.00
XOO4085	-	hypothetical protein		0.72	0.60	0.77	0.79	9.21	8.61	10.13	9.36	9.29	8.51	0.00
XOO4086	<i>hemY</i>	porphyrin biosynthesis protein		-0.14	0.33	-0.50	-0.26	6.87	6.53	7.73	8.23	7.23	7.49	0.00
XOO4087	-	hypothetical protein		-0.63	-0.16	-1.75	0.01	7.20	7.36	7.54	9.29	6.54	6.53	0.00
XOO4088	<i>hemD</i>	uroporphyrinogen-III synthase		1.70		0.65	2.74	5.39	NA	6.89	6.24	5.81	3.07	0.00
XOO4089	<i>lgtB</i>	glycosyltransferase		-0.20		0.80	-1.19	NA	NA	3.54	2.75	5.47	6.66	0.00
XOO4092	-	hypothetical protein		0.88	0.68	0.74	1.21	9.17	8.48	9.40	8.66	8.66	7.44	0.00
XOO4093	-	hypothetical protein		0.89		0.89		1.29	NA	4.13	3.24	5.91	NA	0.00
XOO4094	-	HAD superfamily hydrolase		-0.14	-0.04	-0.16	-0.22	8.92	8.97	10.40	10.56	9.92	10.14	0.00
XOO4095	-	hypothetical protein		-2.14		-2.03	-2.25	NA	NA	4.88	6.91	0.50	2.75	0.01
XOO4096	-	hypothetical protein		-0.86	-0.89	-0.89	-0.79	8.59	9.49	9.65	10.54	8.66	9.45	0.00
XOO4097	-	hypothetical protein		1.16	0.89	-0.29	2.87	2.99	2.09	3.30	3.59	6.21	3.34	0.00
XOO4099	-	D-alanyl-D-alanine dipeptidase		1.24	-0.02	0.38	3.37	2.38	2.39	3.76	3.39	6.39	3.02	0.00
XOO4101	-	hypothetical protein		4.07		2.76	5.39	2.58	NA	5.61	2.84	7.85	2.46	0.00
XOO4102	<i>tcbD</i>	chloromuconate cycloisomerase		1.29	2.01	-0.25	2.12	4.65	2.64	3.42	3.67	6.54	4.43	0.00
XOO4108	-	hypothetical protein		1.82	-0.24	2.48	3.22	7.43	7.68	6.70	4.22	6.45	3.23	0.00
XOO4109	-	cationic amino acid transporter		1.43	2.83	0.04		5.44	2.61	3.54	3.50	3.29	NA	0.00
XOO4112	-	hypothetical protein		2.07		1.07	3.07	3.67	NA	3.81	2.74	7.38	4.31	0.00
XOO4113	-	hypothetical protein		1.03		2.52	-0.45	2.45	NA	5.92	3.40	2.98	3.43	0.00
XOO4114	<i>yiaA</i>	hypothetical protein		0.32	-0.30	0.73	0.53	7.24	7.54	9.57	8.85	9.05	8.52	0.00
XOO4115	<i>yliI</i>	dehydrogenase		2.66	3.67	1.64		4.68	1.01	6.10	4.46	2.16	NA	0.00
XOO4123	<i>bgfX</i>	beta-glucosidase		-0.18	-0.05	-0.21	-0.30	8.22	8.26	10.17	10.38	9.80	10.10	0.00
XOO4124	<i>folB</i>	dihydronopterin aldolase		0.00	0.10	-0.12	0.03	8.97	8.88	9.95	10.07	9.77	9.74	0.00
XOO4125	<i>gcp</i>	DNA-binding/iron metalloprotein/AP endonuclease		-0.43	-0.46	-0.51	-0.31	8.44	8.90	9.56	10.07	8.48	8.79	0.00
XOO4126	-	hypothetical protein		-0.38	-1.07	-0.13	0.06	6.49	7.56	8.70	8.83	8.31	8.24	0.00
XOO4127	<i>rnb</i>	ribonuclease BN		0.52	2.72	-0.66	-0.50	6.47	3.75	8.10	8.76	3.44	3.93	0.00
XOO4128	<i>dnaG</i>	DNA primase		1.64	4.08	-0.31	1.17	7.32	3.24	4.11	4.42	7.01	5.84	0.00
XOO4130	-	hypothetical protein		0.90	0.35	-0.18	2.54	7.97	7.62	8.06	8.24	6.84	4.30	0.00
XOO4131	-	disulfide-isomerase		0.06	0.09	-0.41	0.51	7.16	7.08	7.86	8.27	4.02	3.51	0.00
XOO4132	<i>coxD</i>	protoheme IX farnesyltransferase		-0.57	-0.68	-0.44	-0.58	7.92	8.60	8.71	9.15	8.22	8.80	0.00
XOO4133	-	hypothetical protein		-0.20	-0.18	-0.18	-0.22	11.43	11.61	12.68	12.86	11.84	12.06	0.00
XOO4134	-	hypothetical protein		-0.66	-0.12	-0.86	-1.01	6.56	6.68	8.55	9.41	7.73	8.74	0.00
XOO4135	-	hypothetical protein		1.38	3.63	0.19	0.32	4.88	1.25	6.06	5.88	3.55	3.23	0.00
XOO4136	-	hypothetical protein		0.49	1.33	0.99	-0.86	7.16	5.83	7.65	6.66	3.39	4.25	0.00
XOO4137	<i>cox3</i>	cytochrome C oxidase subunit III		0.09	-0.30	1.04	-0.48	6.53	6.84	7.50	6.46	7.22	7.69	0.00
XOO4138	<i>cox11</i>	cytochrome C oxidase assembly protein		1.27	1.21	1.29	1.30	9.93	8.72	10.82	9.53	10.57	9.27	0.00
XOO4140	<i>ctaD</i>	cytochrome C oxidase subunit I		0.85	0.68	0.65	1.21	8.40	7.72	10.08	9.43	8.71	7.50	0.00
XOO4141	<i>ctaC</i>	cytochrome C oxidase subunit II		1.93	1.85	1.65	2.29	7.58	5.73	5.32	3.68	9.50	7.20	0.00
XOO4142	-	hypothetical protein		1.08	1.11	1.11	1.02	8.60	7.49	9.85	8.74	9.65	8.64	0.00
XOO4145	<i>putA</i>	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydr		-0.92	-0.83	-1.00	-0.92	10.55	11.38	11.26	12.26	10.74	11.66	0.00
XOO4149	<i>bfr</i>	bacterioferritin		-2.96	-2.96	-2.95	-2.97	9.66	12.62	10.74	13.69	9.11	12.08	0.00
XOO4150	-	bacterioferritin-associated ferredoxin		1.76	2.11	1.41	1.76	12.21	10.10	13.79	12.38	13.06	11.30	0.00
XOO4151	<i>nudH</i>	dinucleoside polyphosphate hydrolase		0.45	0.58	0.43	0.34	8.26	7.68	10.15	9.71	9.54	9.20	0.00
XOO4152	<i>rpsI</i>	30S ribosomal protein S9		0.21	0.19	0.09	0.36	11.36	11.17	12.63	12.54	12.03	11.66	0.00
XOO4153	<i>rplM</i>	50S ribosomal protein L13		-0.21	-0.28	-0.24	-0.12	10.95	11.23	12.24	12.48	11.68	11.80	0.00
XOO4154	-	ubiquinone biosynthesis protein		-0.16	-0.21	-0.34	0.06	8						

XOO4168	-	hypothetical protein	1.37	2.47	0.87	0.77	5.18	2.71	7.56	6.70	8.42	7.65	0.00
XOO4185	<i>queF</i>	7-cyano-7-deazaguanine reductase	-1.46	-1.66	-1.50	-1.20	7.81	9.48	8.91	10.42	7.97	9.17	0.00
XOO4186	-	transposase	0.40	-0.19	0.74	0.65	7.27	7.47	8.36	7.61	8.20	7.55	0.00
XOO4187	<i>amaA</i>	N-acyl-L-amino acid amidohydrolase	0.59	0.65	1.05	0.08	6.63	5.98	7.51	6.46	5.81	5.73	0.00
XOO4188	<i>mtrC</i>	membrane fusion protein	2.45	4.41	2.28	0.66	7.47	3.06	6.28	4.00	7.26	6.60	0.00
XOO4189	<i>acrD</i>	acriflavin resistance protein	0.03	-0.56	0.15	0.51	7.62	8.18	8.73	8.58	9.05	8.54	0.00
XOO4190	<i>acrA</i>	acriflavin resistance protein	-0.14	-0.09	-0.28	-0.06	8.32	8.41	9.35	9.63	8.54	8.60	0.00
XOO4191	-	hypothetical protein	-0.84	-0.11	-1.56		5.74	5.85	5.27	6.83	6.42	NA	0.00
XOO4194	-	hypothetical protein	0.56	0.30	0.41	0.97	9.08	8.78	10.02	9.61	8.94	7.97	0.00
XOO4195	-	hypothetical protein	0.58	1.82	-0.01	-0.07	5.55	3.73	6.88	6.89	6.95	7.02	0.00
XOO4196	-	hypothetical protein	-0.96	-1.02	-0.97	-0.90	8.59	9.61	10.54	11.52	10.03	10.94	0.00
XOO4197	<i>secB</i>	preprotein translocase subunit SecB	0.33	0.38	0.33	0.28	5.03	4.65	12.01	11.68	11.71	11.43	0.00
XOO4198	<i>gpsA</i>	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	0.14	-0.10	0.16	0.35	8.17	8.26	9.97	9.81	9.16	8.80	0.00
XOO4199	-	hypothetical protein	-0.59	-0.60	-0.62	-0.55	12.79	13.39	14.03	14.65	13.20	13.75	0.00
XOO4200	<i>poxB</i>	pyruvate dehydrogenase	-1.08	-1.22	-0.89	-1.13	7.79	9.01	9.20	10.09	8.76	9.90	0.00
XOO4201	-	two-component system sensor protein	-0.46	-0.63	-0.23	-0.51	7.45	8.08	9.11	9.35	8.75	9.26	0.00
XOO4202	<i>ntrC</i>	two-component system regulatory protein	-0.02		-0.02		NA	NA	6.95	6.97	6.01	NA	0.00
XOO4203	-	hypothetical protein	4.15	4.15			5.91	1.76	3.08	NA	3.39	NA	0.00
XOO4205	-	MFS transporter	0.22	-0.38	-1.01	2.04	6.04	6.41	8.59	9.60	6.01	3.97	0.00
XOO4206	-	tRNA/rRNA methyltransferase	0.00	2.19	-0.61	-1.56	6.23	4.04	7.43	8.04	6.44	8.01	0.00
XOO4208	-	hypothetical protein	-0.13	-0.22	-0.23	0.06	9.08	9.30	10.11	10.34	9.37	9.31	0.00
XOO4209	<i>fabH</i>	3-oxoacyl-ACP synthase	-0.46	-0.45	-0.54	-0.39	7.17	7.61	9.11	9.66	9.10	9.49	0.00
XOO4210	-	hypothetical protein	0.34	0.54	0.23	0.27	8.28	7.74	10.39	10.16	9.89	9.62	0.00
XOO4211	-	methyltransferase	0.28	0.79	0.05	-0.01	5.33	4.54	10.93	10.89	10.67	10.68	0.00
XOO4212	-	hypothetical protein	-0.11	-0.15	-0.10	-0.08	9.48	9.63	10.60	10.71	10.30	10.38	0.00
XOO4213	<i>dhaA</i>	haloalkane dehalogenase	-0.02	0.15	-0.18	-0.03	7.59	7.43	8.64	8.82	8.47	8.50	0.00
XOO4214	<i>ykgJ</i>	ferredoxin	-0.10	-0.07	-0.13	-0.10	8.42	8.49	9.13	9.26	8.72	8.83	0.00
XOO4215	-	peptide synthase	-0.74	-0.69	-0.81	-0.73	8.37	9.06	9.59	10.40	9.36	10.09	0.00
XOO4216	<i>cdh</i>	NAD(P)H steroid dehydrogenase	0.74	1.14	0.76	0.32	6.81	5.67	7.85	7.08	7.01	6.69	0.00
XOO4219	-	MarR family transcriptional regulator	1.68	0.26	3.10	4.03	NA	6.34	6.08	6.51	3.42	0.00	
XOO4220	-	hypothetical protein	1.60	0.65	2.54	NA	NA	4.90	4.25	6.01	3.46	0.00	
XOO4228	-	transferase	0.62	0.64	0.73	0.49	8.81	8.17	9.78	9.05	9.06	8.57	0.00
XOO4231	<i>ilvD</i>	dihydroxy-acid dehydratase	-0.23	-0.18	-0.37	-0.14	7.16	7.34	9.59	9.96	9.36	9.50	0.00
XOO4232	-	site-specific recombinase	1.93		1.93		4.04	NA	5.11	3.18	2.00	NA	0.00
XOO4240	<i>polA</i>	DNA polymerase I	0.49	2.75	-1.86	0.57	5.51	2.76	6.31	8.17	6.30	5.73	0.00
XOO4241	-	hypothetical protein	-1.31	-1.32	-1.37	-1.24	10.00	11.32	11.60	12.97	10.90	12.14	0.00
XOO4247	<i>dgt</i>	deoxyguanosinetriphosphate triphosphohydrolase	0.63	1.83	-0.57	7.46	5.63	2.73	NA	4.77	5.34	0.00	
XOO4251	-	arabinogalactan endo-1,4-beta-galactosidase	0.97		0.24	1.71	NA	NA	7.99	7.75	7.37	5.66	0.00
XOO4252	-	hypothetical protein	3.15	4.25	2.34	2.87	5.97	1.71	5.33	2.99	6.31	3.44	0.00
XOO4253	-	hypothetical protein	#DIV/0!				5.61	NA	2.45	NA	NA	0.01	
XOO4262	-	hypothetical protein	0.82		1.18	0.46	2.99	NA	8.75	7.57	7.77	7.31	0.00
XOO4263	<i>icfG</i>	IcfG protein	-1.07	-1.06	-1.07	-1.07	11.88	12.95	13.83	14.89	13.28	14.34	0.00
XOO4266	-	hypothetical protein	1.78	2.14	1.51	1.69	9.73	7.59	11.49	9.98	11.22	9.53	0.00
XOO4268	-	hypothetical protein	0.27	0.49	0.24	0.07	15.99	15.50	15.99	15.75	15.99	15.93	0.00
XOO4269	-	hypothetical protein	-0.47	-0.29	-0.49	-0.62	7.92	8.21	8.84	9.33	8.69	9.31	0.00
XOO4270	-	hypothetical protein	-0.39	1.46	-1.57	-1.07	4.73	3.26	6.82	8.38	6.42	7.49	0.00
XOO4271	-	proteinase	0.07	2.78	-2.65		5.19	2.41	0.50	3.15	2.58	NA	0.00
XOO4272	-	proteinase	0.76		0.76		4.92	NA	6.97	6.20	4.80	NA	0.00
XOO4273	-	hypothetical protein	1.55	1.05	0.54	3.05	6.64	5.59	3.85	3.31	7.22	4.17	0.00
XOO4275	-	hypothetical protein	2.39		2.39		1.73	NA	4.73	2.34	2.20	NA	0.00
XOO4276	<i>gnl</i>	gluconolactonase	0.73	-0.53	2.00	2.00	2.78	NA	2.04	2.58	4.89	2.88	0.00
XOO4277	-	hypothetical protein	#DIV/0!				1.73	NA	1.58	NA	2.64	NA	0.01
XOO4279	-	hypothetical protein	-1.51	-0.30	-1.85	-2.37	3.39	3.69	6.88	8.74	1.66	4.03	0.00
XOO4280	-	hypothetical protein	#DIV/0!				3.66	NA	2.82	NA	4.14	NA	0.00
XOO4285	-	hypothetical protein	1.41		1.41		2.35	NA	4.15	2.74	2.50	NA	0.00
XOO4286	-	hypothetical protein	#DIV/0!				5.10	NA	1.73	NA	2.04	NA	0.01
XOO4287	-	hypothetical protein	-0.99	-1.02	-0.69	-1.27	0.50	1.52	7.71	8.40	6.70	7.97	0.00
XOO4288	<i>groEL</i>	molecular chaperone GroEL	-0.01	-0.02	-0.15	0.15	12.79	12.82	13.98	14.13	13.48	13.33	0.00
XOO4292	-	hypothetical protein	-0.54	-1.39	0.58	-0.82	2.64	4.03	6.44	5.87	2.75	3.57	0.00
XOO4294	<i>ndh</i>	NADH dehydrogenase	-0.14	-0.16	0.03	-0.30	8.27	8.43	8.77	8.74	8.09	8.39	0.00
XOO4296	<i>rpoH</i>	RNA polymerase factor sigma-32	-0.13	-0.09	-0.21	-0.09	9.49	9.58	11.54	11.75	10.85	10.94	0.00
XOO4297	<i>ung</i>	uracil-DNA glycosylase	-0.43	-0.12	-0.53	-0.65	7.62	7.74	9.22	9.75	8.77	9.41	0.00
XOO4298	-	response regulator protein	-0.66	-1.10	-0.34	-0.53	8.09	9.19	10.06	10.40	9.65	10.18	0.00
XOO4299	<i>ftsX</i>	cell division protein	0.08	0.07	0.08	0.10	11.02	10.95	12.11	12.03	11.75	11.66	0.00
XOO4300	<i>ftsE</i>	ABC transporter ATP-binding protein	0.59	1.81	-0.16	0.12	5.93	4.12	8.09	8.25	7.58	7.46	0.00
XOO4302	<i>trxA</i>	thioredoxin	-0.34	-0.29	-0.35	-0.38	11.65	11.94	13.15	13.49	12.60	12.98	0.00
XOO4303	<i>rho</i>	transcription termination factor Rho	-1.21	-1.19	-1.14	-1.29	10.63	11.82	12.17	13.31	11.86	13.15	0.00
XOO4305	-	hypothetical protein	1.31	0.74	0.07	3.11	8.02	7.28	9.53	9.46	7.67	4.57	0.00
XOO4306	-	hypothetical protein	-0.79	-0.53	-1.14	-0.72	6.02	6.55	8.10	9.24	7.97	8.69	0.00
XOO4307	-	hypothetical protein	-0.42	-0.25	-0.43	-0.58	12.37	12.61	13.22	13.64	12.83	13.41	0.00
XOO4312	-	hypothetical protein	-1.33	-1.21	-1.31	-1.49	8.43	9.64	9.15	10.46	8.44	9.93	0.00
XOO4319	-	ketosynthase	-1.17	-1.10	-1.20	-1.19	8.55	9.66	9.18	10.38	8.63	9.82	0.00
XOO4321	-	hydroxylase	-0.26	-0.35	-0.19	-0.25	10.11	10.47	11.26	11.44	11.26	11.51	0.00
XOO4322	<i>rapK</i>	pteridine-dependent deoxygenase like protein	-0.06		-0.69	0.56	5.37	NA	2.81	3.49	4.74	4.18	0.00
XOO4323	-	5'-nucleotidase	0.81	0.80	0.97	0.68	8.59	7.79	9.73	8.77	9.20	8.52	0.00
XOO4324	-	AMP-ligase	-0.51	-0.04	-0.61	-0.90	5.91	5.95	8.20	8.81	8.87	9.77	0.00
XOO4325	-	dipeptidyl peptidase	1.13	1.51	0.95	0.93	8.25	6.74	9.55	8.60	9.35	8.42	0.00
XOO4326	-	hypothetical protein	-1.01	-2.12	-0.69	-0.23	4.33	6.46	6.74	7.43	6.72	6.95	0.00
XOO4327	-	hypothetical protein	0.03	0.16	-0.02	-0.04	8.92	8.75	10.33	10.35	9.67	9.71	0.00
XOO4328	-	hypothetical protein	1.88	3.50	1.28	0.85	6.18	2.68	9.22	7.94	8.77	7.92	0.00
XOO4329	-	oxidoreductase	0.75	0.87	0.66	0.72	6.84	5.97	8.39	7.73	8.64	7.92	0.00
XOO4332	<i>kdgT</i>	2-keto-3-deoxygluconate permease	#DIV/0!				5.58	NA	5.07	NA	5.57	NA	0.00
XOO4333	<i>metE</i>	5-methyltetrahydropteroyltriglutamate/homocysteine S-methyltrans	0.41		0.41		NA	NA	2.40	1.99	5.53	NA	0.01
XOO4334	-	hypothetical protein	0.11	-0.03	0.22	0.14	4.54	4.57	8.28	8.06	8.12	7.99	0.00
XOO4335	<i>sflA</i>	NADH-dependent FMN reductase	3.50	3.49	3.51		5.77	2.28	6.				

XOO4349	<i>ynfM</i>	MFS transporter	-0.05	-0.05	0.13	-0.21	3.59	3.64	6.80	6.68	7.45	7.66	0.00
XOO4350	-	LysR family transcriptional regulator	0.81	3.10	-1.49	7.48	4.38	1.73	NA	2.32	3.81	0.00	
XOO4354	<i>gvpU</i>	gas vesicle protein	1.32	1.45	1.23	1.27	11.90	10.45	13.01	11.78	12.92	11.65	0.00
XOO4356	-	alpha/beta hydrolase	0.67	0.67			2.08	1.41	1.66	NA	2.52	NA	0.00
XOO4358	-	LysR family transcriptional regulator	-0.31	0.21	-0.36	-0.78	3.62	3.41	7.39	7.75	7.43	8.21	0.00
XOO4362	-	serine-pyruvate aminotransferase					5.49	NA	4.55	NA	NA	NA	0.00
XOO4363	-	hypothetical protein	1.81	0.73	2.90		5.46	4.73	6.94	4.04	NA	NA	0.00
XOO4367	-	ISxac1 transposase	-0.06	-0.09	0.07	-0.16	7.97	8.07	9.40	9.34	9.32	9.48	0.00
XOO4376	-	dipeptidyl aminopeptidase	0.84	0.91	0.99	0.63	9.66	8.75	10.29	9.30	10.49	9.86	0.00
XOO4377	<i>accC</i>	biotin carboxylase	-1.22	-1.47	-1.03	-1.16	6.06	7.52	7.45	8.48	7.30	8.46	0.00
XOO4378	<i>accD</i>	acyl-CoA carboxyltransferase subunit beta	-0.38	-0.41	-0.50	-0.22	8.19	8.60	9.23	9.73	9.24	9.46	0.00
XOO4379	<i>acdA</i>	acyl-CoA dehydrogenase	0.31	0.33	0.27	0.33	9.75	9.42	10.95	10.68	10.87	10.54	0.00
XOO4382	-	hypothetical protein	1.78	3.01	-0.20	2.52	6.42	3.40	7.40	7.60	5.84	3.33	0.00
XOO4383	-	hypothetical protein	-0.03		-0.03		1.79	NA	3.77	3.80	NA	NA	0.00
XOO4384	-	hypothetical protein	1.16	1.16			3.95	2.80	NA	NA	5.06	NA	0.00
XOO4386	-	hypothetical protein	0.74	0.74			4.50	3.76	NA	NA	1.95	NA	0.00
XOO4387	-	cytochrome C5	1.18	1.52	0.91	1.11	8.42	6.90	10.31	9.40	9.46	8.35	0.00
XOO4388	-	nuclease	0.28	0.30	0.26	0.29	9.15	8.85	10.43	10.18	9.40	9.11	0.00
XOO4389	-	hypothetical protein	1.86	1.95	1.74	1.87	9.30	7.35	10.19	8.45	9.61	7.73	0.00
XOO4390	-	nitrile hydratase activator	2.84	2.28	3.14	3.11	8.35	6.07	9.81	6.67	9.36	6.26	0.00
XOO4392	-	hypothetical protein	0.37	2.10		-1.36	4.52	2.43	6.02	NA	2.29	3.65	0.00
XOO4393	-	hypothetical protein	1.13	-0.13	-0.16	3.69	7.49	7.63	4.23	4.39	7.90	4.21	0.00
XOO4394	-	ATPase	-0.16	-0.04	-0.23	-0.21	7.64	7.67	8.71	8.94	8.76	8.96	0.00
XOO4396	-	TonB-dependent receptor	-0.07	0.34	0.27	-0.81	7.02	6.68	7.39	7.13	7.32	8.13	0.00
XOO4397	-	hypothetical protein	-0.17	0.12	-0.23	-0.41	7.07	6.95	8.59	8.82	7.64	8.06	0.00
XOO4398	<i>glyS</i>	glycyl-tRNA synthetase subunit beta	0.89	-0.59	-0.04	3.31	7.01	7.60	4.08	4.12	7.37	4.06	0.00
XOO4399	<i>glyQ</i>	glycyl-tRNA synthetase subunit alpha	-0.78	-0.96	-0.36	-1.02	8.14	9.10	8.80	9.16	7.80	8.82	0.00
XOO4400	<i>gspE</i>	general secretory pathway related protein	0.13	0.05	0.17	0.17	3.66	3.60	7.59	7.42	7.08	6.91	0.00
XOO4401	-	hypothetical protein	1.71	3.25	0.80	1.07	6.55	3.30	9.17	8.37	8.87	7.80	0.00
XOO4404	<i>guaA</i>	glutamine amidotransferase	1.29	1.26	1.14	1.47	9.38	8.12	10.80	9.65	10.12	8.65	0.00
XOO4406	<i>tatC</i>	sec-independent protein translocase	-0.01	-0.11	-0.01	0.09	8.43	8.54	9.58	9.58	9.07	8.97	0.00
XOO4407	<i>tatB</i>	sec-independent translocase	-0.24	-0.09	-0.34	-0.30	10.49	10.58	11.85	12.19	11.52	11.82	0.00
XOO4409	-	hypothetical protein	-0.60	-0.63	-0.68	-0.49	8.52	9.15	8.96	9.64	8.74	9.24	0.00
XOO4410	<i>hemH</i>	ferrochelatase	-0.29	-0.09	-0.27	-0.50	8.04	8.13	8.58	8.84	8.04	8.54	0.00
XOO4412	-	hydrolase	-1.09	-3.68	0.22	0.18	4.54	8.22	3.50	3.28	6.26	6.09	0.00
XOO4413	-	hypothetical protein	-1.56	-1.03	-0.55	-3.11	6.21	7.23	8.36	8.90	5.61	8.72	0.00
XOO4414	-	hypothetical protein	0.26	0.85	-0.20	0.11	7.36	6.51	8.52	8.72	7.46	7.35	0.00
XOO4415	<i>rdgC</i>	recombination associated protein	-1.08	-1.18	-1.20	-0.87	8.50	9.68	8.45	9.65	8.51	9.39	0.00
XOO4416	-	C32 tRNA thiolase	-1.42	-1.48	-1.30	-1.48	7.73	9.21	8.35	9.66	7.68	9.17	0.00
XOO4419	<i>aguA</i>	alpha-glucuronidase	0.35	-1.02	-1.37	3.46	3.38	4.40	6.76	8.13	6.77	3.31	0.00
XOO4420	-	sialic acid-specific 9-O-acetyl esterase	3.82	3.82			5.03	1.20	2.26	NA	2.26	NA	0.01
XOO4421	<i>rspA</i>	starvation sensing protein	-0.44	-2.18	1.29		1.16	3.34	2.29	1.00	4.74	NA	0.00
XOO4422	<i>xyI/B</i>	xylosidase	1.11	0.46	1.98	0.89	3.26	2.80	5.72	3.74	4.85	3.97	0.00
XOO4423	-	glucan 1,4-beta-glucosidase					3.40	NA	2.43	NA	2.68	NA	0.00
XOO4424	<i>mtlD</i>	mannitol dehydrogenase	1.97		1.97		2.93	NA	5.18	3.21	5.89	NA	0.00
XOO4426	-	hypothetical protein	-0.34	-0.82	-0.25	0.04	5.91	6.73	7.53	7.78	7.53	7.49	0.00
XOO4428	-	secreted xylanase	-0.92		-2.52	0.67	3.66	NA	5.25	7.77	4.80	4.13	0.00
XOO4430	<i>exuT</i>	hexuronate transporter	0.90	-0.02	-0.02	2.74	7.85	7.87	7.04	7.06	6.36	3.62	0.00
XOO4431	<i>cirA</i>	TonB-dependent receptor	-0.67		-1.40	0.06	NA	NA	6.34	7.74	2.43	2.37	0.00
XOO4432	<i>xylP</i>	transporter	0.08	-0.04	0.32	-0.05	8.19	8.23	8.43	8.11	7.76	7.80	0.00
XOO4433	<i>xsa</i>	xylosidase	0.46	0.46			2.75	NA	7.50	7.05	5.55	NA	0.00
XOO4442	-	hypothetical protein	0.28	0.61	0.37	-0.16	7.59	6.98	8.51	8.14	7.80	7.96	0.00
XOO4445	-	hypothetical protein	0.24	0.14	0.03	0.56	7.45	7.31	8.41	8.38	8.06	7.50	0.00
XOO4446	-	hypothetical protein	0.76	0.88	0.72	0.67	8.54	7.66	8.88	8.17	8.53	7.86	0.00
XOO4447	-	oxidoreductase	1.56	1.76	1.32	1.61	9.85	8.10	10.98	9.66	10.45	8.84	0.00
XOO4448	-	TetR family transcriptional regulator	-0.34	-0.65	-0.05	-0.34	7.86	8.51	4.82	4.86	8.21	8.55	0.00
XOO4453	-	hypothetical protein	0.73	0.41	1.77	0.02	8.51	8.10	6.30	4.53	8.17	8.16	0.00
XOO4454	-	hypothetical protein	0.98	-0.03	2.31	0.66	8.02	8.05	5.93	3.62	4.43	3.77	0.00
XOO4455	-	MarR family transcriptional regulator	-0.11	-0.06	-0.11	-0.17	10.43	10.50	11.39	11.50	10.40	10.56	0.00
XOO4456	<i>ohr</i>	organic hydroperoxide resistance protein	0.19	0.40	0.06	0.11	12.69	12.29	14.89	14.82	14.13	14.03	0.00
XOO4457	-	hypothetical protein	-0.56	-1.00	-0.25	-0.44	6.41	7.41	7.77	8.02	7.31	7.75	0.00
XOO4460	-	hypothetical protein	-0.45	-0.11	-0.53	-0.70	6.75	6.86	8.62	9.15	8.57	9.27	0.00
XOO4461	-	DNA-binding protein	-0.38	-0.47	-0.40	-0.26	10.72	11.19	11.64	12.03	10.92	11.18	0.00
XOO4462	-	hypothetical protein	1.83	3.72	1.38	0.40	6.73	3.01	8.32	6.94	8.22	7.82	0.00
XOO4463	-	hypothetical protein	0.44	0.31	0.53	0.47	8.89	8.57	10.03	9.51	9.78	9.31	0.00
XOO4464	-	hypothetical protein	-1.73	-1.80	-1.67	-1.72	10.77	12.58	11.25	12.92	11.43	13.15	0.00
XOO4468	-	hypothetical protein	-0.24	-0.03	-0.65	-0.05	9.31	9.34	9.26	9.91	10.05	10.09	0.00
XOO4469	<i>recD</i>	exodeoxyribonuclease V subunit alpha	-0.75	-1.95	-0.23	-0.06	6.70	8.65	8.58	8.82	8.11	8.16	0.00
XOO4470	<i>recB</i>	exodeoxyribonuclease V subunit beta	0.43	3.14	-1.27	-0.59	6.38	3.23	5.14	6.41	5.99	6.58	0.00
XOO4471	<i>recC</i>	exodeoxyribonuclease V subunit gamma	-0.65	-0.69	-0.87	-0.39	7.27	7.96	8.56	7.23	7.61	0.00	
XOO4472	-	hypothetical protein	-0.07	-0.21	0.01	-0.02	7.38	7.59	8.67	8.66	8.08	8.10	0.00
XOO4475	-	hemagglutinin	-0.23		-0.23		1.16	NA	1.40	1.63	2.50	NA	0.00
XOO4481	<i>sodC2</i>	superoxide dismutase	-2.04	-2.79	-1.30		4.42	7.21	7.72	9.01	5.95	NA	0.00
XOO4482	<i>yojM</i>	superoxide dismutase like protein	-0.97	-1.19	-0.76	-0.97	8.24	9.42	9.56	10.32	8.33	9.30	0.00
XOO4483	<i>ntrC</i>	two-component system regulatory protein	-0.11	0.06	-0.16	-0.24	7.71	7.64	9.23	9.39	9.20	9.44	0.00
XOO4484	<i>ntrB</i>	two-component system sensor protein	0.03	0.01	0.01	0.07	8.59	8.58	9.54	9.54	9.27	9.20	0.00
XOO4488	<i>glnA</i>	glutamine synthetase	2.28	1.71	3.73	1.39	8.35	6.63	8.31	4.58	9.18	7.79	0.00
XOO4489	<i>uppP</i>	undecaprenyl pyrophosphate phosphatase	-0.77	-0.99	-0.55	-0.78	7.95	8.93	8.94	9.50	8.46	9.24	0.00
XOO4493	-	hypothetical protein	1.92	0.60	0.43	4.74	8.66	8.06	9.22	8.78	8.71	3.97	0.00
XOO4494	-	hypothetical protein	-0.80	-0.71	-0.90	-0.81	5.56	6.27	7.79	8.69	7.51	8.32	0.00
XOO4495	-	hypothetical protein	-0.54	-0.58	-0.47	-0.56	8.58	9.16	10.28	10.75	9.12	9.68	0.00
XOO4496	-	acetyltransferase	0.36	1.61	-0.39	-0.14	5.95	4.34	10.44	10.84	10.01	10.15	0.00
XOO4498	<i>cls</i>	cardiolipin synthase	-0.81	-0.80	-0.83	-0.80	10.08	10.88	11.15	11.99	10.63	11.43	0.00
XOO4499	-	hypothetical protein	-0.43	-0.38	-0.41	-0.51	10.95	11.33	12.13	12.54	11.94	12.44	0.00
XOO4500	-	hyp											

XOO4507	<i>hipA</i>	serine kinase HipA	3.93	3.86	4.01	3.09	NA	7.40	3.54	7.18	3.18	0.00	
XOO4509	-	hypothetical protein	-1.66	-1.48	-1.65	-1.85	9.03	10.51	10.36	12.01	9.63	11.47	0.00
XOO4510	-	hypothetical protein	-1.43	-1.44	-1.43	2.40	3.84	7.00	8.43	5.19	NA	0.00	
XOO4511	<i>yehZ</i>	ABC transporter amino acid permease	-1.09	-0.96	-1.27	-1.05	7.03	7.99	7.58	8.85	6.82	7.88	0.00
XOO4512	<i>yehX</i>	ABC transporter ATP-binding protein	-1.44	-0.98	-1.72	-1.61	2.75	3.73	6.71	8.43	6.62	8.23	0.00
XOO4513	-	hypothetical protein	0.40	0.44	0.26	0.48	5.97	5.52	8.66	8.40	8.14	7.66	0.00
XOO4515	<i>yimA</i>	ABC transporter ATP-binding protein	0.11	0.15	0.14	0.03	9.33	9.18	9.85	9.71	8.77	8.74	0.00
XOO4518	-	hypothetical protein	-1.47	-1.32	-0.18	-2.92	1.66	2.98	4.02	4.20	4.98	7.90	0.00
XOO4526	-	hypothetical protein	-0.45	-0.28	-0.76	-0.31	7.63	7.91	8.24	9.00	7.91	8.22	0.00
XOO4529	<i>mocA</i>	oxidoreductase	-0.29	-0.48	-0.26	-0.14	7.97	8.45	9.98	10.25	9.37	9.51	0.00
XOO4530	-	hypothetical protein	0.34	0.46	0.24	0.31	7.83	7.37	10.21	9.97	9.82	9.51	0.00
XOO4531	-	pseudouridylate synthase	-0.44	0.55	-1.43	0.50	NA	7.64	7.09	5.25	6.68	0.00	
XOO4533	<i>hrpB</i>	ATP-dependent RNA helicase	-0.32	-0.45	-0.16	-0.34	8.10	8.55	9.67	9.83	9.24	9.59	0.00
XOO4534	-	hypothetical protein	-1.53	-1.73	-1.44	-1.43	6.95	8.68	8.09	9.53	7.81	9.24	0.00
XOO4535	-	RTS beta protein	0.51	0.40	0.48	0.64	9.78	9.38	11.00	10.52	10.67	10.03	0.00
XOO4536	-	2-hydroxyhepta-2,4-diene-1, 7-dioate isomerase	1.80	2.18	1.58	1.64	12.48	10.30	13.31	11.73	13.01	11.37	0.00
XOO4537	<i>ucpA</i>	oxidoreductase	0.29	0.31	0.34	0.23	8.45	8.14	9.92	9.58	9.49	9.26	0.00
XOO4538	-	hypothetical protein	0.75	0.85	0.81	0.58	8.63	7.78	9.36	8.55	9.10	8.52	0.00
XOO4539	-	oxidoreductase	1.17	1.35	0.89	1.28	10.16	8.81	10.80	9.92	10.49	9.20	0.00
XOO4543	<i>tcsR</i>	two-component system regulatory protein	-1.79	-1.89	-1.56	-1.91	2.12	4.01	7.09	8.65	6.81	8.72	0.00
XOO4544	<i>acs</i>	acetyl-CoA synthetase	-1.68	-1.87	-1.38	-1.80	5.86	7.72	8.95	10.33	7.91	9.71	0.00
XOO4545	-	hypothetical protein	-0.34	1.83	-1.42	-1.44	6.31	4.47	8.81	10.23	8.58	10.02	0.00
XOO4546	-	hypothetical protein	-0.77	-0.89	-0.47	-0.96	7.56	8.45	8.86	9.33	7.85	8.81	0.00
XOO4547	-	hypothetical protein	0.42	-0.08	0.37	0.98	7.05	7.13	8.21	7.84	8.04	7.06	0.00
XOO4548	<i>actP</i>	acetate permease	0.32	0.29	0.11	0.56	7.42	7.13	8.74	8.63	8.54	7.98	0.00
XOO4549	-	transcriptional regulator	3.25	3.25	3.47	NA	1.50	NA	6.90	3.65	0.00		
XOO4550	<i>xthA1</i>	exodeoxyribonuclease III	-0.25	-0.37	-0.21	-0.18	8.21	8.58	9.24	9.45	8.48	8.66	0.00
XOO4551	-	hypothetical protein	-0.08	-0.23	-0.12	0.11	9.01	9.24	10.20	10.32	9.51	9.40	0.00
XOO4552	<i>mltA</i>	transglycosylase associated protein	-1.44	-1.56	-1.30	-1.45	8.05	9.61	8.88	10.19	8.98	10.42	0.00
XOO4553	<i>hetl</i>	hypothetical protein	-1.56	-1.26	-1.87	NA	NA	7.32	8.58	5.77	7.64	0.00	
XOO4554	-	hypothetical protein	1.04	3.58	-0.37	-0.10	7.27	3.69	6.34	6.72	2.40	2.50	0.00
XOO4556	<i>gidB</i>	16S rRNA methyltransferase GidB	-0.70	-0.13	-0.94	-1.03	4.93	5.05	7.73	8.67	7.27	8.30	0.00
XOO4559	<i>fldW</i>	4-oxalomesaconate hydratase	-0.78	-0.65	-0.80	-0.90	8.36	9.01	9.84	10.64	9.67	10.57	0.00
XOO4565	<i>fldZ</i>	hypothetical protein	3.79	4.52	3.06	7.74	NA	9.12	4.60	8.73	5.67	0.00	
XOO4566	<i>fldY</i>	transcriptional regulator	0.58	0.76	0.22	0.75	7.43	6.66	8.51	8.28	8.01	7.26	0.00
XOO4567	<i>cls</i>	cardiolipin synthase	0.40	0.65	0.09	0.47	7.22	6.57	8.99	8.91	8.46	7.99	0.00
XOO4568	-	lactoylglutathione lyase and related lyase	-1.10	-1.32	-1.04	-0.92	9.48	10.81	10.80	11.84	9.89	10.81	0.00
XOO4569	-	hypothetical protein	-0.93	-0.41	-0.92	-1.46	7.24	7.66	8.57	9.49	7.72	9.18	0.00
XOO4570	<i>uvrD</i>	DNA-dependent helicase II	-0.53	-0.50	-0.43	-0.67	8.74	9.24	9.44	9.87	9.32	9.98	0.00
XOO4573	-	hypothetical protein	-0.01	0.44	-0.52	0.04	7.15	6.70	8.00	8.51	8.26	8.23	0.00
XOO4574	-	hypothetical protein	0.19	-0.75	-0.11	1.43	4.10	4.85	6.58	6.69	5.94	4.50	0.00
XOO4580	-	hypothetical protein	#DIV/0!				4.72	NA	3.25	NA	5.21	NA	0.00
XOO4582	<i>ompP1</i>	hypothetical protein	0.55	0.49	0.46	0.72	9.78	9.29	11.44	10.99	11.02	10.30	0.00
XOO4583	-	hypothetical protein	0.40	0.71	0.58	-0.09	6.87	6.17	7.35	6.77	6.72	6.81	0.00
XOO4584	-	hypothetical protein	-0.47	-0.46	-0.64	-0.32	9.08	9.53	10.58	11.21	10.22	10.53	0.00
XOO4585	<i>serA</i>	D-3-phosphoglycerate dehydrogenase	0.03	0.04	0.05	0.02	7.01	6.97	8.50	8.45	7.99	7.97	0.00
XOO4586	<i>ctp</i>	carboxyl-terminal protease	-0.54	-0.65	-0.59	-0.38	8.30	8.96	9.56	10.16	8.98	9.35	0.00
XOO4587	-	hypothetical protein	-1.80	-3.16	-0.76	-1.49	4.87	8.03	7.18	7.94	6.26	7.75	0.00
XOO4588	-	hypothetical protein	0.96	1.31	0.56	1.02	4.75	3.44	8.23	7.67	7.98	6.96	0.00
XOO4589	-	hypothetical protein	-0.13	-1.42	-1.33	2.36	6.93	8.35	7.16	8.49	6.74	4.38	0.00
XOO4590	-	hypothetical protein	0.56	1.47	-0.22	0.42	5.42	3.94	7.34	7.56	6.87	6.46	0.00
XOO4594	-	hypothetical protein	-0.25	0.15	-0.51	-0.40	6.49	6.34	8.42	8.93	7.85	8.24	0.00
XOO4595	-	hypothetical protein	-0.36	-0.31	-0.49	-0.29	9.52	9.83	10.44	10.93	10.00	10.29	0.00
XOO4596	-	hypothetical protein	0.59	2.83	-1.02	-0.05	4.85	2.01	5.83	6.85	5.49	5.54	0.00
XOO4597	-	hypothetical protein	1.36	0.66	0.86	2.55	7.80	7.15	8.14	7.27	6.46	3.91	0.00
XOO4599	-	hypothetical protein	0.66	0.72	0.52	0.73	10.00	9.28	11.28	10.76	11.17	10.44	0.00
XOO4600	<i>folE</i>	GTP cyclohydrolase I	-0.01	0.06	-0.11	0.01	6.33	6.28	7.97	8.08	7.77	7.75	0.00
XOO4603	-	hypothetical protein	0.86	0.84	0.93	0.80	9.29	8.44	10.21	9.28	9.95	9.15	0.00
XOO4604	<i>kgtP</i>	dicarboxylate transport protein	-0.90	-0.79	-1.05	-0.87	8.39	9.17	9.12	10.17	9.28	10.15	0.00
XOO4610	-	hypothetical protein	-0.74	-0.37	-1.11	2.68	NA	7.99	8.36	6.77	7.88	0.00	
XOO4615	-	hypothetical protein	-0.40	-0.37	-0.44	-0.40	8.35	8.72	9.46	9.90	9.01	9.41	0.00
XOO4620	<i>glnK</i>	glycerate kinase	-1.13	-1.01	-1.11	-1.27	9.34	10.35	10.06	11.17	10.41	11.67	0.00
XOO4621	<i>ttuB</i>	MFS transporter	-0.49	-0.45	-0.47	-0.54	11.82	12.27	12.77	13.25	12.15	12.69	0.00
XOO4624	-	hypothetical protein	0.30	2.04	-0.42	-0.72	7.73	5.68	3.58	4.00	6.86	7.58	0.00
XOO4625	-	oxidoreductase	-0.30	-0.20	-0.32	-0.37	9.24	9.43	10.15	10.47	10.03	10.40	0.00
XOO4626	<i>ygiT</i>	export protein	-0.50	-0.56	-0.49	-0.45	7.82	8.38	8.99	9.49	8.03	8.48	0.00
XOO4627	-	hypothetical protein	1.10	1.15	0.95	1.18	9.31	8.16	10.29	9.34	9.36	8.18	0.00
XOO4628	<i>glpQ</i>	glycerophosphoryl diester phosphodiesterase	2.32	3.10	2.49	1.38	6.17	3.07	6.28	3.79	7.25	5.87	0.00
XOO4635	-	polysaccharide deacetylase	-0.33	-0.45	-0.49	-0.06	9.04	9.48	8.51	9.00	8.47	8.53	0.00
XOO4636	-	inner membrane protein translocase component YidC	-0.25	-0.44	-0.11	-0.20	9.90	10.35	11.42	11.54	11.20	11.40	0.00
XOO4637	<i>rmpA</i>	ribonuclease P	-1.22	-1.15	-1.30	-1.20	8.79	9.94	10.24	11.54	9.91	11.12	0.00
XOO4733	-	glycosyltransferase	0.76	0.32	0.69	1.25	8.96	8.64	9.31	8.62	7.79	6.54	0.00
XOO4787	<i>mtgA</i>	monofunctional biosynthetic peptidoglycan transglycosylase	-1.07	0.08	-3.51	0.20	3.72	3.64	4.19	7.70	6.86	6.66	0.00

Table S2. Functional categorization of the upregulated and downregulated genes in opsX mutant based on GO annotation

Expression level	Level	GO ID	Term	Type	NodeScore	%Seq	#Seqs	Sequences
4	GO:0070727	cellular macromolecule localization	Biological Process	0.22	2.94	1	XOO2619	
6	GO:0015031	protein transport	Biological Process	0.36	2.94	1	XOO2619	
4	GO:0008104	protein localization	Biological Process	0.22	2.94	1	XOO2619	
3	GO:0044710	single-organism metabolic process	Biological Process	0.16	5.88	2	XOO3409, XOO2685	
4	GO:0044281	small molecule metabolic process	Biological Process	0.26	5.88	2	XOO3409, XOO2685	
4	GO:0050794	regulation of cellular process	Biological Process	1.8	8.82	3	XOO2787, XOO3763, XOO1721	
3	GO:0051641	cellular localization	Biological Process	0.13	2.94	1	XOO2619	
4	GO:0051649	establishment of localization in cell	Biological Process	0.22	2.94	1	XOO2619	
2	GO:0065007	biological regulation	Biological Process	1.01	11.76	4	XOO2787, XOO3763, XOO4149, XOO1721	
3	GO:0065008	regulation of biological quality	Biological Process	0.6	2.94	1	XOO4149	
5	GO:0046907	intracellular transport	Biological Process	0.36	2.94	1	XOO2619	
5	GO:0048646	anatomical structure formation involved in mor	Biological Process	1	2.94	1	XOO2621	
8	GO:0006605	protein targeting	Biological Process	1	2.94	1	XOO2619	
2	GO:0023052	signaling	Biological Process	1.08	8.82	3	XOO2787, XOO3763, XOO1721	
7	GO:0019752	carboxylic acid metabolic process	Biological Process	1.2	5.88	2	XOO3409, XOO2685	
5	GO:0034613	cellular protein localization	Biological Process	0.36	2.94	1	XOO2619	
2	GO:0040011	locomotion	Biological Process	10.8	26.47	9	XOO2572, XOO2836, XOO2858, XOO2859, XOO2607, XOO2849, XOO2568, XOO2833, XOO2850	
3	GO:1902578	single-organism localization	Biological Process	0.22	2.94	1	XOO2619	
4	GO:0009653	anatomical structure morphogenesis	Biological Process	0.6	2.94	1	XOO2621	
2	GO:0044699	single-organism process	Biological Process	2.32	29.41	10	XOO2849, XOO2787, XOO2685, XOO3763, XOO1721, XOO2621	
6	GO:1902582	single-organism intracellular transport	Biological Process	0.6	2.94	1	XOO2619	
4	GO:0006790	sulfur compound metabolic process	Biological Process	1	2.94	1	XOO3409	
5	GO:0043412	macromolecule modification	Biological Process	1.44	11.76	4	XOO1207, XOO2857, XOO2836, XOO2228	
3	GO:0006950	response to stress	Biological Process	1	2.94	1	XOO4481	
4	GO:0005975	carbohydrate metabolic process	Biological Process	2	5.88	2	XOO1603, XOO1781	
3	GO:0051674	localization of cell	Biological Process	1.8	8.82	3	XOO2572, XOO2607, XOO2849	
3	GO:0051716	cellular response to stimulus	Biological Process	1.8	8.82	3	XOO2787, XOO3763, XOO1721	
3	GO:0071704	organic substance metabolic process	Biological Process	2.44	23.53	8	XOO1603, XOO1207, XOO1781, XOO2857, XOO2836, XOO3409, XOO2685, XOO2228	
5	GO:0071702	organic substance transport	Biological Process	0.22	2.94	1	XOO2619	
5	GO:0006082	organic acid metabolic process	Biological Process	0.43	5.88	2	XOO3409, XOO2685	
6	GO:0036211	protein modification process	Biological Process	2.4	11.76	4	XOO1207, XOO2857, XOO2836, XOO2228	
8	GO:0006520	cellular amino acid metabolic process	Biological Process	2	5.88	2	XOO3409, XOO2685	
3	GO:0044238	primary metabolic process	Biological Process	3.26	23.53	8	XOO1603, XOO1207, XOO1781, XOO2857, XOO2836, XOO3409, XOO2685, XOO2228	
7	GO:0006886	intracellular protein transport	Biological Process	0.6	2.94	1	XOO2619	
3	GO:0044237	cellular metabolic process	Biological Process	3.52	26.47	9	XOO1207, XOO2857, XOO2836, XOO3409, XOO2685, XOO2228, XOO3763, XOO2566, XOO2621	
1	GO:0008150	biological_process	Biological Process	40.39	79.41	27	XOO2619, XOO1603, XOO1207, XOO2857, XOO2836, XOO2858, XOO2859, XOO3409, XOO2936, XOO4481, XOO2787, XOO2568, XOO2685, XOO2228, XOO4149, XOO2621, XOO2566, XOO2607, XOO2114, XOO2572, XOO1781, XOO2230, XOO2114, XOO2833, XOO2850, XOO3763, XOO1721	
2	GO:0008152	metabolic process	Biological Process	7	35.29	12	XOO1603, XOO1207, XOO2857, XOO1781, XOO2836, XOO3409, XOO2936, XOO2685, XOO2228, XOO3763, XOO2566, XOO2621	
3	GO:0044763	single-organism cellular process	Biological Process	2.78	26.47	9	XOO2572, XOO3409, XOO2607, XOO2849, XOO2787, XOO2685, XOO3763, XOO1721, XOO2621	
4	GO:0006810	transport	Biological Process	3.22	8.82	3	XOO2619, XOO2114, XOO4149	
5	GO:0044765	single-organism transport	Biological Process	0.36	2.94	1	XOO2619	
3	GO:0044767	single-organism developmental process	Biological Process	0.36	2.94	1	XOO2621	
6	GO:0043436	oxoacid metabolic process	Biological Process	0.72	5.88	2	XOO3409, XOO2685	
5	GO:0045184	establishment of protein localization	Biological Process	0.22	2.94	1	XOO2619	
2	GO:0051179	localization	Biological Process	2.29	17.65	6	XOO2619, XOO2572, XOO2607, XOO2849, XOO2114, XOO4149	
3	GO:0006807	nitrogen compound metabolic process	Biological Process	2.52	14.71	5	XOO3409, XOO2685, XOO3763, XOO2566, XOO2621	
4	GO:0006928	movement of cell or subcellular component	Biological Process	1.8	8.82	3	XOO2572, XOO2607, XOO2849	
4	GO:0042592	homeostatic process	Biological Process	1	2.94	1	XOO4149	
3	GO:0016043	cellular component organization	Biological Process	0.6	2.94	1	XOO2619	
2	GO:0071840	cellular component organization or biogenesis	Biological Process	0.36	2.94	1	XOO2619	
5	GO:0019538	protein metabolic process	Biological Process	1.44	11.76	4	XOO1207, XOO2857, XOO2836, XOO2228	
4	GO:0007154	cell communication	Biological Process	1.8	8.82	3	XOO2787, XOO3763, XOO1721	
7	GO:0006464	cellular protein modification process	Biological Process	4	11.76	4	XOO1207, XOO2857, XOO2836, XOO2228	
3	GO:0048856	anatomical structure development	Biological Process	0.36	2.94	1	XOO2621	
4	GO:1901564	organonitrogen compound metabolic process	Biological Process	1.2	5.88	2	XOO3409, XOO2685	
3	GO:0009058	biosynthetic process	Biological Process	6	17.65	6	XOO1603, XOO2936, XOO3409, XOO3763, XOO2566, XOO2621	
4	GO:0043170	macromolecule metabolic process	Biological Process	0.86	11.76	4	XOO1207, XOO2857, XOO2836, XOO2228	
5	GO:0044260	cellular macromolecule metabolic process	Biological Process	1.44	11.76	4	XOO1207, XOO2857, XOO2836, XOO2228	

downregulation	3	GO:0033036	macromolecule localization	Biological Process	0.13	2.94	1	XOO2619
	4	GO:0034641	cellular nitrogen compound metabolic process	Biological Process	3	8.82	3	XOO3763, XOO2566, XOO2621
	2	GO:0032502	developmental process	Biological Process	0.82	2.94	1	XOO2621
	2	GO:0050896	response to stimulus	Biological Process	1.68	11.76	4	XOO4481, XOO2787, XOO3763, XOO1721
	4	GO:0061024	membrane organization	Biological Process	1	2.94	1	XOO2619
	5	GO:0007165	signal transduction	Biological Process	3	8.82	3	XOO2787, XOO3763, XOO1721
	6	GO:0044267	cellular protein metabolic process	Biological Process	2.4	11.76	4	XOO1207, XOO2857, XOO2836, XOO2228
	3	GO:0044700	single organism signaling	Biological Process	1.8	8.82	3	XOO2787, XOO3763, XOO1721
								XOO2619, XOO1207, XOO2857, XOO2836,
	2	GO:0009987	cellular process	Biological Process	4.42	44.12	15	XOO3409, XOO2607, XOO2849, XOO2572,
								XOO2787, XOO2685, XOO2228, XOO3763,
								XOO3763, XOO2566, XOO2621
	4	GO:0048869	cellular developmental process	Biological Process	0.6	2.94	1	XOO2621
	5	GO:0048870	cell motility	Biological Process	3	8.82	3	XOO2572, XOO2607, XOO2849
	3	GO:0051234	establishment of localization	Biological Process	1.93	8.82	3	XOO2619, XOO2114, XOO4149
	5	GO:0030154	cell differentiation	Biological Process	1	2.94	1	XOO2621
	3	GO:0050789	regulation of biological process	Biological Process	1.08	8.82	3	XOO2787, XOO3763, XOO1721
	6	GO:0043229	intracellular organelle	Cellular Component	0.36	2.94	1	XOO1473
	2	GO:0043226	organelle	Cellular Component	5.22	14.71	5	XOO2572, XOO2583, XOO1473, XOO2607,
								XOO2849
	3	GO:0043228	non-membrane-bounded organelle	Cellular Component	0.36	2.94	1	XOO1473
								XOO2619, XOO1847, XOO1207, XOO2836,
	2	GO:0005623	cell	Cellular Component	24.75	52.94	18	XOO2859, XOO2607, XOO2849, XOO2583,
								XOO2572, XOO2463, XOO1473, XOO2787,
								XOO2568, XOO2228, XOO3763, XOO4149,
								XOO1721, XOO2621
	7	GO:0043232	intracellular non-membrane-bounded organelle	Cellular Component	0.6	2.94	1	XOO1473
	7	GO:0044444	cytoplasmic part	Cellular Component	0.6	2.94	1	XOO1473
	5	GO:0005886	plasma membrane	Cellular Component	3	8.82	3	XOO2619, XOO1847, XOO2463
								XOO2619, XOO1847, XOO1207, XOO2836,
								XOO2859, XOO2607, XOO2849, XOO2572,
	1	GO:0005575	cellular_component	Cellular Component	41.64	61.76	21	XOO2583, XOO2463, XOO1473, XOO2230,
								XOO2787, XOO2568, XOO2558, XOO2228,
								XOO3763, XOO4149, XOO1721, XOO2830,
								XOO2621
	6	GO:0030529	ribonucleoprotein complex	Cellular Component	0.6	2.94	1	XOO1473
								XOO2619, XOO1847, XOO1207, XOO2836,
	3	GO:0044464	cell part	Cellular Component	11.26	47.06	16	XOO2859, XOO2607, XOO2849, XOO2572,
								XOO2463, XOO1473, XOO2787, XOO2568,
								XOO2228, XOO3763, XOO1721, XOO2621
	4	GO:0005622	intracellular	Cellular Component	14.66	38.24	13	XOO1207, XOO2836, XOO2859, XOO2607,
								XOO2849, XOO2572, XOO1473, XOO2787,
								XOO2568, XOO2228, XOO3763, XOO1721, XOO2621
	6	GO:0005737	cytoplasm	Cellular Component	4.36	11.76	4	XOO1473, XOO2836, XOO2859, XOO2621
	4	GO:0071944	cell periphery	Cellular Component	1.8	8.82	3	XOO2619, XOO1847, XOO2463
	8	GO:0005840	ribosome	Cellular Component	1	2.94	1	XOO1473
	2	GO:0032991	macromolecular complex	Cellular Component	0.36	2.94	1	XOO1473
	5	GO:0044424	intracellular part	Cellular Component	2.76	11.76	4	XOO1473, XOO2836, XOO2859, XOO2621
	2	GO:0016020	membrane	Cellular Component	1.8	8.82	3	XOO2619, XOO1847, XOO2463
								XOO1207, XOO2836, XOO2859, XOO2568,
								XOO2558, XOO2833, XOO2860, XOO2228,
								XOO2850, XOO3147
	2	GO:0060089	molecular transducer activity	Molecular Function	6	29.41	10	XOO2830
								XOO3807, XOO2593, XOO4481, XOO2849,
	3	GO:0022892	substrate-specific transporter activity	Molecular Function	0.6	2.94	1	XOO4149
	3	GO:0016491	oxidoreductase activity	Molecular Function	5	14.71	5	XOO3807, XOO2593, XOO4481, XOO2849,
	4	GO:0016772	transferase activity, transferring phosphorus- $\alpha$	Molecular Function	4.2	20.59	7	XOO1207, XOO2836, XOO2860, XOO2228,
	2	GO:0000988	protein binding transcription factor activity	Molecular Function	1	2.94	1	XOO3147, XOO2621, XOO3611
								XOO2621
								XOO2619, XOO3807, XOO1207, XOO1603,
	2	GO:0005488	binding	Molecular Function	6.65	38.24	13	XOO2836, XOO2849, XOO4095, XOO4481,
								XOO3763, XOO2228, XOO1721, XOO4149,
								XOO2621
	4	GO:0016765	transferase activity, transferring alkyl or aryl (o	Molecular Function	1	2.94	1	XOO2936
	4	GO:0016746	transferase activity, transferring acyl groups	Molecular Function	2	5.88	2	XOO1473, XOO2597
	3	GO:1901363	heterocyclic compound binding	Molecular Function	1.08	8.82	3	XOO3763, XOO1721, XOO2621
	4	GO:0008565	protein transporter activity	Molecular Function	1	2.94	1	XOO2830
	5	GO:0008168	methyltransferase activity	Molecular Function	1	2.94	1	XOO2857
								XOO3807, XOO2619, XOO1847, XOO1207,
								XOO1603, XOO2857, XOO2836, XOO2858,
								XOO2936, XOO2859, XOO3409, XOO1473,
								XOO2463, XOO4481, XOO2568, XOO2860,
	1	GO:0003674	molecular_function	Molecular Function	48.44	100	34	XOO2228, XOO2685, XOO4149, XOO2621,
								XOO3611, XOO2849, XOO2593, XOO4095,
								XOO1781, XOO2230, XOO2558, XOO2833,
								XOO2597, XOO3763, XOO2850, XOO3147,
								XOO1721, XOO2830
	2	GO:0005215	transporter activity	Molecular Function	1.56	8.82	3	XOO1847, XOO2463, XOO2830

2	GO:0003824	catalytic activity	Molecular Function	7.86	61.76	21	XOO3807, XOO1603, XOO1207, XOO2857, XOO2858, XOO2836, XOO2936, XOO3409, XOO2849, XOO2593, XOO1473, XOO1781, XOO4481, XOO2860, XOO2597, XOO2685, XOO2228, XOO3147, XOO4149, XOO2621, XOO3611
3	GO:0022857	transmembrane transporter activity	Molecular Function	2	5.88	2	XOO1847, XOO2463
4	GO:0003676	nucleic acid binding	Molecular Function	1.8	8.82	3	XOO3763, XOO1721, XOO2621
5	GO:0003677	DNA binding	Molecular Function	3	8.82	3	XOO3763, XOO1721, XOO2621
3	GO:0016740	transferase activity	Molecular Function	4.68	32.35	11	XOO1207, XOO1473, XOO2857, XOO2836, XOO2936, XOO2860, XOO2597, XOO2228, XOO3147, XOO2621, XOO3611
4	GO:0016741	transferase activity, transferring one-carbon group	Molecular Function	0.6	2.94	1	XOO2857
5	GO:0042578	phosphoric ester hydrolase activity	Molecular Function	0.6	2.94	1	XOO1603
2	GO:0001071	nucleic acid binding transcription factor activity	Molecular Function	1	2.94	1	XOO2621
3	GO:0004871	signal transducer activity	Molecular Function	10	29.41	10	XOO1207, XOO2836, XOO2859, XOO2568, XOO2558, XOO2833, XOO2860, XOO2228, XOO2850, XOO3147
4	GO:0016788	hydrolase activity, acting on ester bonds	Molecular Function	0.36	2.94	1	XOO1603
3	GO:0043167	ion binding	Molecular Function	10	29.41	10	XOO4095, XOO2836, XOO4481, XOO2849, XOO2228, XOO4149
3	GO:0016829	lyase activity	Molecular Function	2	5.88	2	XOO3409, XOO2685
6	GO:0016791	phosphatase activity	Molecular Function	1	2.94	1	XOO1603
4	GO:0016798	hydrolase activity, acting on glycosyl bonds	Molecular Function	1	2.94	1	XOO1781
4	GO:0016810	hydrolase activity, acting on carbon-nitrogen (t)	Molecular Function	1	2.94	1	XOO2858
5	GO:0016779	nucleotidyltransferase activity	Molecular Function	1	2.94	1	XOO2621
3	GO:0097159	organic cyclic compound binding	Molecular Function	1.08	8.82	3	XOO3763, XOO1721, XOO2621
5	GO:0016301	kinase activity	Molecular Function	6	17.65	6	XOO1207, XOO2836, XOO2860, XOO2228, XOO3147, XOO3611
3	GO:0016787	hydrolase activity	Molecular Function	1.42	8.82	3	XOO1603, XOO1781, XOO2858
3	GO:0044710	single-organism metabolic process	Biological Process	16.82	19.13	22	XOO1848, XOO0878, XOO4628, XOO0937, XOO2290, XOO1370, XOO2990, XOO2093, XOO0482, XOO4065, XOO2434, XOO0453, XOO0892, XOO0694, XOO1734, XOO4488, XOO0512, XOO1018, XOO1733, XOO0435, XOO0831, XOO2424
4	GO:0044281	small molecule metabolic process	Biological Process	22.04	18.26	21	XOO1848, XOO0878, XOO4628, XOO0937, XOO2290, XOO1370, XOO2093, XOO0482, XOO4065, XOO2434, XOO0453, XOO0892, XOO0694, XOO1734, XOO4488, XOO0512, XOO1018, XOO1733, XOO0435, XOO0831, XOO2424
4	GO:0050794	regulation of cellular process	Biological Process	2.4	3.48	4	XOO1559, XOO1188, XOO0643, XOO0951
2	GO:0065007	biological regulation	Biological Process	1.22	4.35	5	XOO1559, XOO3646, XOO1188, XOO0643, XOO0951
3	GO:0065008	regulation of biological quality	Biological Process	0.6	0.87	1	XOO3646
2	GO:0002376	immune system process	Biological Process	1	0.87	1	XOO0867
4	GO:0006725	cellular aromatic compound metabolic process	Biological Process	1.6	6.09	7	XOO0867, XOO0609, XOO2737, XOO2710, XOO3029, XOO0831, XOO0567
2	GO:0023052	signaling	Biological Process	1.44	3.48	4	XOO1559, XOO1188, XOO0643, XOO0951
7	GO:0019752	carboxylic acid metabolic process	Biological Process	4.8	6.96	8	XOO2093, XOO0937, XOO0694, XOO2290, XOO4488, XOO0435, XOO0831, XOO2424
5	GO:1901361	organic cyclic compound catabolic process	Biological Process	0.6	0.87	1	XOO2737
4	GO:1901360	organic cyclic compound metabolic process	Biological Process	1.6	6.09	7	XOO0867, XOO0609, XOO2737, XOO2710, XOO3029, XOO0831, XOO0567
2	GO:0040011	locomotion	Biological Process	6.2	4.35	5	XOO2605, XOO2838, XOO2842, XOO2579, XOO0644
3	GO:1902578	single-organism localization	Biological Process	2.16	5.22	6	XOO0847, XOO4188, XOO0745, XOO0849, XOO2644, XOO0336
2	GO:0044699	single-organism process	Biological Process	14.73	30.43	35	XOO1848, XOO0878, XOO0937, XOO1370, XOO4188, XOO0482, XOO4065, XOO2644, XOO1734, XOO4488, XOO1018, XOO1733, XOO0643, XOO2424, XOO0847, XOO0847, XOO0745, XOO0849, XOO2605, XOO0849, XOO2290, XOO2990, XOO2093, XOO2434, XOO3029, XOO0453, XOO2579, XOO0892, XOO0694, XOO1188, XOO0512, XOO0336, XOO0435, XOO0831, XOO0951
4	GO:0046483	heterocycle metabolic process	Biological Process	1.6	6.09	7	XOO0867, XOO0609, XOO2737, XOO2710, XOO3029, XOO0831, XOO0567
7	GO:0016070	RNA metabolic process	Biological Process	0.72	1.74	2	XOO2710, XOO0831
3	GO:0071554	cell wall organization or biogenesis	Biological Process	1	0.87	1	XOO1371
2	GO:0051704	multi-organism process	Biological Process	0.36	0.87	1	XOO1713
6	GO:0055085	transmembrane transport	Biological Process	6	5.22	6	XOO0847, XOO4188, XOO0745, XOO0849, XOO2644, XOO0336
4	GO:0006790	sulfur compound metabolic process	Biological Process	1	0.87	1	XOO2093
9	GO:0006399	tRNA metabolic process	Biological Process	2	1.74	2	XOO2710, XOO0831
5	GO:0043412	macromolecule modification	Biological Process	1.8	4.35	5	XOO4009, XOO0682, XOO1734, XOO1733, XOO0642
3	GO:0006950	response to stress	Biological Process	4	3.48	4	XOO0867, XOO0690, XOO3646, XOO2339

4	GO:0005975	carbohydrate metabolic process	Biological Process	8	6.96	8	XOO2990, XOO4420, XOO4628, XOO1371, XOO1078, XOO0512, XOO1018, XOO4115
3	GO:0051674	localization of cell	Biological Process	1.2	1.74	2	XOO2605, XOO2579
5	GO:0051276	chromosome organization	Biological Process	2	1.74	2	XOO0867, XOO0567
3	GO:0051716	cellular response to stimulus	Biological Process	2.4	3.48	4	XOO1559, XOO1188, XOO0643, XOO0951
4	GO:0071941	nitrogen cycle metabolic process	Biological Process	1	0.87	1	XOO4488
							XOO1848, XOO0878, XOO2737, XOO0937, XOO4420, XOO1371, XOO4009, XOO1078, XOO0682, XOO4488, XOO1734, XOO1018, XOO0567, XOO1733, XOO2424, XOO0642, XOO0867, XOO4628, XOO0609, XOO2290, XOO2990, XOO2093, XOO2710, XOO3029, XOO0694, XOO0892, XOO0831, XOO0512, XOO4115, XOO0435
3	GO:0071704	organic substance metabolic process	Biological Process	13.6	26.09	30	
5	GO:0006082	organic acid metabolic process	Biological Process	1.73	6.96	8	XOO2093, XOO0937, XOO0694, XOO2290, XOO4488, XOO0435, XOO0831, XOO2424
6	GO:0036211	protein modification process	Biological Process	3	4.35	5	XOO4009, XOO0682, XOO1734, XOO1733, XOO0642
5	GO:0019439	aromatic compound catabolic process	Biological Process	0.6	0.87	1	XOO2737
4	GO:0022607	cellular component assembly	Biological Process	2	1.74	2	XOO1713, XOO2579
8	GO:0006520	cellular amino acid metabolic process	Biological Process	8	6.96	8	XOO2093, XOO0937, XOO0694, XOO2290, XOO4488, XOO0435, XOO0831, XOO2424
							XOO1848, XOO0878, XOO2737, XOO0937, XOO4420, XOO1371, XOO4009, XOO1078, XOO0682, XOO4488, XOO1734, XOO1018, XOO0567, XOO1733, XOO2424, XOO0642, XOO0867, XOO4628, XOO0609, XOO2290, XOO2990, XOO2093, XOO2710, XOO3029, XOO0694, XOO0892, XOO0831, XOO0512, XOO4115, XOO0435
3	GO:0044238	primary metabolic process	Biological Process	16.09	26.09	30	
							XOO0935, XOO0917, XOO2737, XOO0937, XOO1370, XOO4065, XOO1510, XOO4009, XOO2367, XOO0682, XOO1870, XOO4488, XOO1734, XOO0567, XOO1733, XOO2029,
3	GO:0044237	cellular metabolic process	Biological Process	24.41	31.3	36	XOO2424, XOO0642, XOO0268, XOO0867, XOO0448, XOO1559, XOO0609, XOO2290, XOO1380, XOO2093, XOO0692, XOO2710, XOO3029, XOO2434, XOO0453, XOO0694, XOO1188, XOO0831, XOO0435, XOO1369
3	GO:0044085	cellular component biogenesis	Biological Process	1.2	1.74	2	XOO1713, XOO2579
6	GO:0090304	nucleic acid metabolic process	Biological Process	3.43	6.09	7	XOO0867, XOO0609, XOO2737, XOO2710, XOO3029, XOO0831, XOO0567
							XOO0935, XOO0855, XOO0937, XOO2838, XOO4188, XOO4101, XOO4420, XOO4065, XOO2765, XOO2842, XOO2644, XOO0861, XOO2368, XOO1510, XOO1432, XOO1993, XOO2367, XOO1992, XOO1078, XOO1870, XOO1359, XOO0268, XOO0847, XOO1419, XOO0448, XOO0609, XOO0849, XOO1260, XOO1380, XOO2990, XOO0692, XOO0690, XOO2434, XOO2710, XOO1345, XOO0970, XOO0453, XOO3646, XOO0892, XOO0694, XOO1188, XOO0336, XOO2994, XOO1848,
1	GO:0008150	biological_process	Biological Process	135.39	79.13	91	XOO0878, XOO0917, XOO2737, XOO1370, XOO0482, XOO1371, XOO0761, XOO4009, XOO3119, XOO0682, XOO1734, XOO4488, XOO1018, XOO1733, XOO0644, XOO0567, XOO2029, XOO0643, XOO1335, XOO2424, XOO0642, XOO0884, XOO0704, XOO0867, XOO0745, XOO1713, XOO1559, XOO4628, XOO2605, XOO2290, XOO2093, XOO2452, XOO0394, XOO0590, XOO1360, XOO3029, XOO2579, XOO2612, XOO2733, XOO2339, XOO0512, XOO0831, XOO4115, XOO0435, XOO1369, XOO0951, XOO0950
4	GO:0006091	generation of precursor metabolites and energ	Biological Process	1	0.87	1	XOO4065
8	GO:0034660	ncRNA metabolic process	Biological Process	1.2	1.74	2	XOO2710, XOO0831
							XOO0935, XOO0937, XOO4420, XOO4065, XOO2368, XOO1510, XOO1432, XOO1993, XOO2367, XOO1078, XOO1870, XOO0268, XOO0448, XOO0609, XOO1380, XOO2990, XOO0692, XOO2434, XOO2710, XOO0453, XOO0694, XOO1188, XOO1848, XOO0892, XOO0694, XOO1188, XOO1848,
2	GO:0008152	metabolic process	Biological Process	51.55	46.09	53	XOO0878, XOO0917, XOO2737, XOO1370, XOO0482, XOO1371, XOO4009, XOO0682, XOO1734, XOO4488, XOO1018, XOO1733, XOO0567, XOO2029, XOO2424, XOO0642, XOO0884, XOO0867, XOO1559, XOO4628, XOO2290, XOO2093, XOO3029, XOO2733, XOO0512, XOO0831, XOO4115, XOO0435, XOO1369

5	GO:0046700	heterocycle catabolic process	Biological Process	0.6	0.87	1	XOO2737 XOO0847, XOO0745, XOO1559, XOO2605, XOO0849, XOO0937, XOO2290, XOO4188, XOO2093, XOO2644, XOO3029, XOO2579, XOO0694, XOO1188, XOO4488, XOO0336, XOO0435, XOO0831, XOO0643, XOO0951, XOO2424
3	GO:0044763	single-organism cellular process	Biological Process	7.4	18.26	21	
7	GO:0006259	DNA metabolic process	Biological Process	5	4.35	5	XOO0867, XOO0609, XOO2737, XOO3029, XOO0567
4	GO:0044249	cellular biosynthetic process	Biological Process	0.36	0.87	1	XOO0831
4	GO:0044403	symbiosis, encompassing mutualism through parasitism	Biological Process	1	0.87	1	XOO1713
5	GO:0044765	single-organism transport	Biological Process	3.6	5.22	6	XOO0847, XOO4188, XOO0745, XOO0849, XOO2644, XOO0336 XOO1419, XOO0847, XOO0855, XOO0745, XOO0849, XOO1260, XOO4188, XOO0394, XOO2644, XOO0336 XOO1992, XOO3119, XOO1359, XOO0336, XOO0950
4	GO:0006810	transport	Biological Process	19.16	14.78	17	XOO0861, XOO1345, XOO2644, XOO2612, XOO1992, XOO3119, XOO1359, XOO0336, XOO0950
5	GO:0006139	nucleobase-containing compound metabolic process	Biological Process	2.66	6.09	7	XOO0867, XOO0609, XOO2737, XOO2710, XOO3029, XOO0831, XOO0567
4	GO:0044248	cellular catabolic process	Biological Process	0.36	0.87	1	XOO2737
6	GO:0043436	oxoacid metabolic process	Biological Process	2.88	6.96	8	XOO2093, XOO0937, XOO0694, XOO2290, XOO4488, XOO0435, XOO0831, XOO2424
7	GO:0006412	translation	Biological Process	1	0.87	1	XOO0831 XOO0847, XOO1419, XOO0745, XOO0855, XOO2605, XOO0849, XOO1260, XOO4188, XOO0394, XOO2644, XOO0336, XOO1992, XOO3119, XOO1359, XOO0336, XOO0950
2	GO:0051179	localization	Biological Process	8.14	16.52	19	
3	GO:0006807	nitrogen compound metabolic process	Biological Process	20.04	27.83	32	XOO0935, XOO0917, XOO2737, XOO0937, XOO1370, XOO4065, XOO1510, XOO2367, XOO1870, XOO4488, XOO1734, XOO0567, XOO1733, XOO2029, XOO2424, XOO0268, XOO0867, XOO0448, XOO1559, XOO0609, XOO2290, XOO1380, XOO2093, XOO0692, XOO2710, XOO3029, XOO2434, XOO0694, XOO1188, XOO0831, XOO0435, XOO1369
4	GO:0006928	movement of cell or subcellular component	Biological Process	1.2	1.74	2	XOO2605, XOO2579
4	GO:0042592	homeostatic process	Biological Process	1	0.87	1	XOO3646
3	GO:0016043	cellular component organization	Biological Process	1.92	3.48	4	XOO0867, XOO1713, XOO2579, XOO0567
6	GO:0034655	nucleobase-containing compound catabolic process	Biological Process	1	0.87	1	XOO2737
5	GO:0010467	gene expression	Biological Process	0.6	0.87	1	XOO0831
2	GO:0071840	cellular component organization or biogenesis	Biological Process	1.15	3.48	4	XOO0867, XOO1713, XOO2579, XOO0567
5	GO:0019538	protein metabolic process	Biological Process	2.16	5.22	6	XOO0409, XOO0682, XOO1734, XOO0831, XOO1733, XOO0642
3	GO:0044419	interspecies interaction between organisms	Biological Process	0.6	0.87	1	XOO1713 XOO1370, XOO0482, XOO2737, XOO1371, XOO2368, XOO2733, XOO0892, XOO0512, XOO2424
3	GO:0009056	catabolic process	Biological Process	9.22	7.83	9	
4	GO:0007154	cell communication	Biological Process	2.4	3.48	4	XOO1559, XOO1188, XOO0643, XOO0951
4	GO:0032196	transposition	Biological Process	1	0.87	1	XOO3029
7	GO:0006464	cellular protein modification process	Biological Process	5	4.35	5	XOO0409, XOO0682, XOO1734, XOO1733, XOO0642
4	GO:1901564	organonitrogen compound metabolic process	Biological Process	4.8	6.96	8	XOO2093, XOO0937, XOO0694, XOO2290, XOO4488, XOO0435, XOO0831, XOO2424
5	GO:0009059	macromolecule biosynthetic process	Biological Process	0.36	0.87	1	XOO0831 XOO0935, XOO0878, XOO0937, XOO1510, XOO1432, XOO1993, XOO2367, XOO1870, XOO1734, XOO4488, XOO0567, XOO1733, XOO0642
3	GO:0009058	biosynthetic process	Biological Process	27.22	23.48	27	XOO2029, XOO0268, XOO0884, XOO2424, XOO0448, XOO1559, XOO1380, XOO2990, XOO2093, XOO0692, XOO0453, XOO0694, XOO1188, XOO0831, XOO1369
4	GO:0043170	macromolecule metabolic process	Biological Process	3.5	10.43	12	XOO0867, XOO0609, XOO2737, XOO2710, XOO3029, XOO0409, XOO0682, XOO1734, XOO0831, XOO0567, XOO1733, XOO0642
5	GO:0044260	cellular macromolecule metabolic process	Biological Process	5.59	10.43	12	XOO0867, XOO0609, XOO2737, XOO2710, XOO3029, XOO0409, XOO0682, XOO1734, XOO0831, XOO0567, XOO1733, XOO0642
4	GO:0051186	cofactor metabolic process	Biological Process	5	4.35	5	XOO0453, XOO2367, XOO1734, XOO1733, XOO2424
4	GO:0034641	cellular nitrogen compound metabolic process	Biological Process	27.6	22.61	26	XOO0268, XOO2424, XOO0867, XOO0448, XOO1559, XOO0609, XOO1380, XOO0692, XOO2434, XOO2710, XOO3029, XOO1188, XOO0831, XOO1369
2	GO:0050896	response to stimulus	Biological Process	3.84	6.96	8	XOO0867, XOO1559, XOO0690, XOO3646, XOO1188, XOO2339, XOO0643, XOO0951
6	GO:0034645	cellular macromolecule biosynthetic process	Biological Process	0.6	0.87	1	XOO0831

5	GO:0007165	signal transduction	Biological Process	4	3.48	4	XOO1559, XOO1188, XOO0643, XOO0951
6	GO:0044267	cellular protein metabolic process	Biological Process	3.6	5.22	6	XOO4009, XOO0682, XOO1734, XOO0831, XOO1733, XOO0642
4	GO:1901576	organic substance biosynthetic process	Biological Process	0.22	0.87	1	XOO0831
4	GO:1901575	organic substance catabolic process	Biological Process	0.36	0.87	1	XOO2737
4	GO:0006996	organelle organization	Biological Process	1.2	1.74	2	XOO0867, XOO0567
3	GO:0044700	single organism signaling	Biological Process	2.4	3.48	4	XOO1559, XOO1188, XOO0643, XOO0951
							XOO0935, XOO0917, XOO2737, XOO0937, XOO1370, XOO4188, XOO4065, XOO1371, XOO2644, XOO1510, XOO2367, XOO4009, XOO1870, XOO0682, XOO4488, XOO1734, XOO0567, XOO1733, XOO2029, XOO0643,
2	GO:0009987	cellular process	Biological Process	21.08	41.74	48	XOO0268, XOO2424, XOO0642, XOO0847, XOO0867, XOO0448, XOO0745, XOO1713, XOO1559, XOO0609, XOO2605, XOO0849, XOO2290, XOO1380, XOO2093, XOO0692, XOO2710, XOO2434, XOO3029, XOO0453, XOO2579, XOO0694, XOO1188, XOO0336, XOO0831, XOO0435, XOO1369, XOO0951
<b>upregulation</b>							
5	GO:0048870	cell motility	Biological Process	2	1.74	2	XOO2605, XOO2579
5	GO:0044270	cellular nitrogen compound catabolic process	Biological Process	0.6	0.87	1	XOO2737
3	GO:0051234	establishment of localization	Biological Process	11.5	14.78	17	XOO0847, XOO1419, XOO0745, XOO0855, XOO0849, XOO1260, XOO4188, XOO0394, XOO2644, XOO0861, XOO1345, XOO2612, XOO1992, XOO3119, XOO0336, XOO1359, XOO0950
4	GO:0006629	lipid metabolic process	Biological Process	6	5.22	6	XOO1848, XOO0878, XOO2990, XOO4628, XOO0892, XOO1018
3	GO:0050789	regulation of biological process	Biological Process	1.44	3.48	4	XOO1559, XOO1188, XOO0643, XOO0951
6	GO:0043229	intracellular organelle	Cellular Component	0.36	0.87	1	XOO0567
2	GO:0043226	organelle	Cellular Component	3.22	2.61	3	XOO2605, XOO2579, XOO0567
3	GO:0043228	non-membrane-bounded organelle	Cellular Component	0.36	0.87	1	XOO0567
							XOO0834, XOO0917, XOO2737, XOO0937, XOO1510, XOO0861, XOO4009, XOO1992, XOO0682, XOO1870, XOO4488, XOO0567, XOO0644, XOO1359, XOO0643, XOO0268, XOO0642, XOO0847, XOO1559, XOO2605, XOO0849, XOO1260, XOO2093, XOO0692, XOO2710, XOO1345, XOO3646, XOO0453, XOO2579, XOO3846, XOO1188, XOO0876, XOO0831, XOO0951, XOO0950
2	GO:0005623	cell	Cellular Component	51.9	32.17	37	
7	GO:0043232	intracellular non-membrane-bounded organelle	Cellular Component	0.6	0.87	1	XOO0567
3	GO:0043234	protein complex	Cellular Component	5	4.35	5	XOO0847, XOO2737, XOO0849, XOO0937, XOO0567
7	GO:0044444	cytoplasmic part	Cellular Component	0.6	0.87	1	XOO0937
5	GO:0005886	plasma membrane	Cellular Component	2	1.74	2	XOO0453, XOO3846
8	GO:0005694	chromosome	Cellular Component	1	0.87	1	XOO0567
2	GO:0005576	extracellular region	Cellular Component	1	0.87	1	XOO0855
							XOO0855, XOO0937, XOO2838, XOO4188, XOO4064, XOO2644, XOO2842, XOO1510, XOO0861, XOO1992, XOO1870, XOO0469, XOO2762, XOO1359, XOO0268, XOO0847, XOO0449, XOO0849, XOO1260, XOO2990, XOO0692, XOO2434, XOO2710, XOO1345, XOO3646, XOO0453, XOO3846, XOO1188, XOO0336, XOO0955, XOO0834, XOO0917, XOO2737, XOO2980, XOO2788, XOO4009, XOO3119, XOO0682, XOO4488, XOO0567, XOO0644, XOO1359, XOO0643, XOO0642, XOO0745, XOO1559, XOO2605, XOO2093, XOO0394, XOO2710, XOO1345, XOO0453, XOO2579, XOO3846, XOO1188, XOO0876, XOO0831, XOO0951, XOO0950
1	GO:0005575	cellular_component	Cellular Component	97.35	48.7	56	
3	GO:0044464	cell part	Cellular Component	24.83	28.7	33	XOO0834, XOO0917, XOO2737, XOO0937, XOO1510, XOO0861, XOO4009, XOO1992, XOO0682, XOO1870, XOO4488, XOO0567, XOO0644, XOO1359, XOO0643, XOO0268, XOO0642, XOO1559, XOO1260, XOO2093, XOO0692, XOO0394, XOO2434, XOO2710, XOO1345, XOO0453, XOO2579, XOO3846, XOO1188, XOO0876, XOO0831, XOO0951, XOO0950
4	GO:0005622	intracellular	Cellular Component	29.03	20.87	24	XOO0834, XOO1559, XOO0917, XOO2737, XOO0937, XOO2093, XOO0692, XOO1510, XOO2434, XOO2710, XOO2579, XOO4009, XOO0682, XOO1188, XOO1870, XOO0876, XOO4488, XOO0567, XOO0644, XOO0831, XOO0951, XOO0950

6	GO:0005737	cytoplasm	Cellular Component	13.36	11.3	13	XOO0834, XOO0917, XOO2737, XOO0937, XOO2093, XOO1510, XOO2434, XOO2710, XOO1870, XOO0876, XOO4488, XOO0644, XOO0831
4	GO:0071944	cell periphery	Cellular Component	5.4	7.83	9	XOO1260, XOO0394, XOO0861, XOO1345, XOO0453, XOO1992, XOO3846, XOO1359, XOO0950
8	GO:0005829	cytosol	Cellular Component	1	0.87	1	XOO0937
2	GO:0032991	macromolecular complex	Cellular Component	3	4.35	5	XOO0847, XOO2737, XOO0849, XOO0937, XOO0567
5	GO:0044424	intracellular part	Cellular Component	8.38	12.17	14	XOO0834, XOO0917, XOO2737, XOO0937, XOO2093, XOO1510, XOO2434, XOO2710, XOO1870, XOO0876, XOO4488, XOO0567, XOO0644, XOO0831
2	GO:0016020	membrane	Cellular Component	1.2	1.74	2	XOO0453, XOO3846
5	GO:0030312	external encapsulating structure	Cellular Component	7	6.09	7	XOO1260, XOO0394, XOO0861, XOO1345, XOO1992, XOO1359, XOO0950
8	GO:0016887	ATPase activity	Molecular Function	5	4.35	5	XOO2062, XOO1071, XOO0388, XOO3846, XOO0567
2	GO:0060089	molecular transducer activity	Molecular Function	4.8	6.96	8	XOO1828, XOO2838, XOO2842, XOO4009, XOO0682, XOO0336, XOO0644, XOO0642
2	GO:0005198	structural molecule activity	Molecular Function	1	0.87	1	XOO2579
8	GO:0004386	helicase activity	Molecular Function	1	0.87	1	XOO0567
3	GO:0022892	substrate-specific transporter activity	Molecular Function	1.2	1.74	2	XOO0847, XOO0849
5	GO:0003723	RNA binding	Molecular Function	2	1.74	2	XOO0917, XOO2710
							XOO1848, XOO3729, XOO2290, XOO4046, XOO0482, XOO0690, XOO4065, XOO0486, XOO3646, XOO1734, XOO2218, XOO2339, XOO2338, XOO2762, XOO4115, XOO4335, XOO2424, XOO3633
3	GO:0016491	oxidoreductase activity	Molecular Function	18	15.65	18	XOO1828, XOO4009, XOO4549, XOO0682, XOO0336, XOO0512, XOO0642
4	GO:0016772	transferase activity, transferring phosphorus-alpha	Molecular Function	4.2	6.09	7	XOO1056
2	GO:0000988	protein binding transcription factor activity	Molecular Function	1	0.87	1	XOO0448
4	GO:0008233	peptidase activity	Molecular Function	2	1.74	2	XOO0834, XOO0444
							XOO0935, XOO0834, XOO0917, XOO2062, XOO1071, XOO0482, XOO1510, XOO0388, XOO0861, XOO1992, XOO1870, XOO0682, XOO4488, XOO0567, XOO1359, XOO1733, XOO2762, XOO2029, XOO1358, XOO0268,
2	GO:0005488	binding	Molecular Function	21.07	38.26	44	XOO2424, XOO0847, XOO1419, XOO0867, XOO0448, XOO1559, XOO0609, XOO1380, XOO0692, XOO0692, XOO0690, XOO1360, XOO2710, XOO2434, XOO3646, XOO2377, XOO0694, XOO1188, XOO3846, XOO0435, XOO0512, XOO0831, XOO1369, XOO2994, XOO2874
4	GO:0016765	transferase activity, transferring alkyl or aryl (o	Molecular Function	1	0.87	1	XOO0453
4	GO:0016746	transferase activity, transferring acyl groups	Molecular Function	5	4.35	5	XOO0878, XOO2093, XOO0596, XOO0595, XOO1881
							XOO0935, XOO0867, XOO0448, XOO1559, XOO0917, XOO0609, XOO1380, XOO0692, XOO2710, XOO1510, XOO1188, XOO1870, XOO0567, XOO1369, XOO2029, XOO0268, XOO2874
3	GO:1901363	heterocyclic compound binding	Molecular Function	6.12	14.78	17	XOO0847, XOO0849
4	GO:0008565	protein transporter activity	Molecular Function	2	1.74	2	XOO0702, XOO0826, XOO2710, XOO4565, XOO0644, XOO4038
5	GO:0008168	methyltransferase activity	Molecular Function	6	5.22	6	XOO0829
3	GO:0008289	lipid binding	Molecular Function	1	0.87	1	XOO2377

1	GO:0003674	molecular_function	Molecular Function	153.48	100	115	XOO0935, XOO0937, XOO2838, XOO4101, XOO1071, XOO4065, XOO0388, XOO1510, XOO2842, XOO1993, XOO1992, XOO1870, XOO1078, XOO1359, XOO1358, XOO0268, XOO1345, XOO2710, XOO2434, XOO3646, XOO0892, XOO1188, XOO0898, XOO4335, XOO1848, XOO0878, XOO0917, XOO4046, XOO0482, XOO0761, XOO0486, XOO2788, XOO3119, XOO1056, XOO1734, XOO4565, XOO0644, XOO1733, XOO2029, XOO1335, XOO2424, XOO3633, XOO0642, XOO0884, XOO0868, XOO0867, XOO1559, XOO2093, XOO0590, XOO0596, XOO02377, XOO4038, XOO0512, XOO1828, XOO3729, XOO4420, XOO2765, XOO0861, XOO2368, XOO1432, XOO2367, XOO4549, XOO0469, XOO2762, XOO0847, XOO1419, XOO0448, XOO0609, XOO0849, XOO1260, XOO1380, XOO0692, XOO0690, XOO0970, XOO0453, XOO0694, XOO3846, XOO0336, XOO2994, XOO2874, XOO0834, XOO0955, XOO2737, XOO1370, XOO2062, XOO2980, XOO1371, XOO4009, XOO0682, XOO4488, XOO1018, XOO0567, XOO0444, XOO0704, XOO0702, XOO4628, XOO2605, XOO0826, XOO2290, XOO2452, XOO0394, XOO1360, XOO3029, XOO2579, XOO2733, XOO1881, XOO2218, XOO2339, XOO2338, XOO4115, XOO0435, XOO1369, XOO0950
2	GO:0005215	transporter activity	Molecular Function	4.92	7.83	9	XOO0847, XOO0955, XOO2980, XOO0849, XOO2788, XOO2377, XOO3846, XOO0469, XOO2762
2	GO:0003824	catalytic activity	Molecular Function	25.35	56.52	65	XOO0937, XOO1828, XOO3729, XOO1071, XOO4420, XOO4065, XOO0388, XOO2368, XOO1993, XOO2367, XOO4549, XOO1078, XOO2762, XOO0690, XOO2710, XOO2434, XOO3646, XOO0453, XOO0694, XOO0892, XOO3846, XOO0898, XOO4335, XOO0336, XOO1848, XOO0834, XOO0878, XOO2737, XOO1370, XOO2062, XOO4046, XOO0482, XOO1371, XOO0486, XOO4009, XOO1056, XOO0682, XOO1734, XOO4565, XOO4488, XOO0567, XOO0644, XOO2424, XOO3633, XOO0444, XOO0884, XOO0642, XOO0868, XOO0702, XOO0867, XOO0826, XOO2290, XOO2093, XOO0596, XOO2733, XOO0595, XOO1881, XOO2218, XOO2339, XOO2338, XOO4115, XOO0435, XOO0831, XOO0435, XOO0512
5	GO:0004518	nuclease activity	Molecular Function	3	2.61	3	XOO0868, XOO0867, XOO2737
3	GO:0016874	ligase activity	Molecular Function	2	1.74	2	XOO4488, XOO0831
3	GO:0022857	transmembrane transporter activity	Molecular Function	7	6.09	7	XOO0955, XOO2980, XOO2788, XOO2377, XOO3846, XOO0469, XOO2762
4	GO:0003676	nucleic acid binding	Molecular Function	10.2	14.78	17	XOO0935, XOO0867, XOO0448, XOO1559, XOO0917, XOO0609, XOO1380, XOO0692, XOO2710, XOO1510, XOO1188, XOO1870, XOO0567, XOO1369, XOO2029, XOO0268, XOO2874
5	GO:0003677	DNA binding	Molecular Function	15	13.04	15	XOO0935, XOO0867, XOO0448, XOO1559, XOO0609, XOO1380, XOO0692, XOO1510, XOO1188, XOO1870, XOO0567, XOO1369, XOO2029, XOO0268, XOO2874
6	GO:0016462	pyrophosphatase activity	Molecular Function	2.16	4.35	5	XOO2062, XOO1071, XOO0388, XOO3846, XOO0567
3	GO:0016740	transferase activity	Molecular Function	8.88	17.39	20	XOO0935, XOO0867, XOO0448, XOO1559, XOO0609, XOO1380, XOO0692, XOO1510, XOO1188, XOO1870, XOO0567, XOO1369, XOO2029, XOO0268, XOO2874
4	GO:0016741	transferase activity, transferring one-carbon gr	Molecular Function	3.6	5.22	6	XOO0702, XOO0826, XOO2710, XOO4565, XOO0644, XOO4038
5	GO:0042578	phosphoric ester hydrolase activity	Molecular Function	0.6	0.87	1	XOO2434
2	GO:0001071	nucleic acid binding transcription factor activity	Molecular Function	6	5.22	6	XOO0935, XOO1380, XOO0448, XOO0692, XOO1369, XOO0268
3	GO:0016853	isomerase activity	Molecular Function	1	0.87	1	XOO0694
3	GO:0004871	signal transducer activity	Molecular Function	8	6.96	8	XOO1828, XOO2838, XOO2842, XOO4009, XOO0682, XOO0336, XOO0644, XOO0642
4	GO:0016788	hydrolase activity, acting on ester bonds	Molecular Function	2.16	3.48	4	XOO0868, XOO0867, XOO2737, XOO2434

3	GO:0043167	ion binding	Molecular Function	28	24.35	28	XOO0834, XOO2062, XOO1071, XOO0482, XOO0388, XOO0861, XOO1992, XOO0682, XOO4488, XOO0567, XOO1359, XOO1733, XOO2762, XOO1358, XOO2424, XOO0847, XOO1419, XOO0867, XOO0690, XOO1360, XOO2434, XOO3646, XOO0694, XOO3846, XOO0435, XOO0512, XOO0831, XOO2994
3	GO:0016829	lyase activity	Molecular Function	4	3.48	4	XOO0937, XOO0892, XOO1078, XOO0884
6	GO:0016791	phosphatase activity	Molecular Function	1	0.87	1	XOO2434
4	GO:0016798	hydrolase activity, acting on glycosyl bonds	Molecular Function	3	2.61	3	XOO4420, XOO1371, XOO0898
4	GO:0016810	hydrolase activity, acting on carbon-nitrogen (t	Molecular Function	6	5.22	6	XOO1370, XOO2368, XOO1993, XOO2367, XOO2733, XOO0435
4	GO:0016817	hydrolase activity, acting on acid anhydrides	Molecular Function	0.78	4.35	5	XOO2062, XOO1071, XOO0388, XOO3846, XOO0567
5	GO:0016818	hydrolase activity, acting on acid anhydrides, ii	Molecular Function	1.3	4.35	5	XOO2062, XOO1071, XOO0388, XOO3846, XOO0567
							XOO0935, XOO0867, XOO0448, XOO1559, XOO0917, XOO0609, XOO1380, XOO0692, XOO2710, XOO1510, XOO1188, XOO1870, XOO0567, XOO1369, XOO2029, XOO0268, XOO2874
7	GO:0017111	nucleoside-triphosphatase activity	Molecular Function	3.6	4.35	5	XOO2062, XOO1071, XOO0388, XOO3846, XOO0567
5	GO:0016301	kinase activity	Molecular Function	7	6.09	7	XOO1828, XOO4009, XOO4549, XOO0682, XOO0336, XOO0512, XOO0642
							XOO0868, XOO0834, XOO0867, XOO2737, XOO1370, XOO2062, XOO1071, XOO4420, XOO1371, XOO0388, XOO2434, XOO2368, XOO1993, XOO2367, XOO2733, XOO3846, XOO0898, XOO0567, XOO0435, XOO0444