Supplemental Material

Group B Streptococcus biofilm regulatory protein A contributes to bacterial physiology and innate immune resistance

Kathryn A. Patras[1,], Jaclyn Derieux[1], Mahmoud M. Al-Bassam[1], Nicole Adiletta[1], Alison Vrbanac[1], John D. Lapek[2], Karsten Zengler[1], David J. Gonzalez[2], Victor Nizet[1,2*]

[1]Division of Host-Microbe Systems & Therapeutics, Department of Pediatrics, UC San Diego, La Jolla, CA, USA.

[2] Department of Pharmacology, Skaggs School of Pharmacy and Pharmaceutical Sciences, UC San Diego, La Jolla, CA, USA.

Contents

Supplemental Methods

Construction of the GBS brpA Insertional Mutant

Targeted insertional mutagenesis was performed using vector pHY304 as described previously [1]. A ~300bp region of CNCTC 10/84 (GenBank: AIX04136.1, WP_000708159.1) was PCR-amplified using primers with NotI and XhoI restriction site overhangs: Forward **5’-TACTCGAGGCTGCCAATGAACCAGAGT-3’** and Reverse **5’-TAGCGGCCGCCTGCAAGTAGATGTTTCTTA-3’**. The amplicon was ligated into pHY304, and introduced by electroporation with recovery in THB + 0.25 M sucrose for 2 h before antibiotic selection on agar at 30°C. Single crossover insertions were selected by shifting to 37°C while maintaining Erm selection, and site-directed recombination was confirmed by PCR. For a revertant strain, selection for Δ*brpA* was relaxed by serial passage at 37 °C without antibiotics, and loss of insertion was identified as Erm sensitivity. Loss of insert and restoration of full-length *brpA* was confirmed by PCR using primers located external to *brpA*: Forward **5’-CTATGCTTCTGGTGGTGCGGAA-3’** and Reverse **5’-CCACTGTAACTTGGTGGTGCTTCTG-3’**.

RNA Isolation and Library Preparation

GBS strains were grown to late logarithmic phase (as cultures approached OD600nm = 0.8) in THB at 37°C. Per experimental replicate, four independent 10 mL cultures were pelleted at 3220 × g for 5 min and combined to form one experimental replicate. Two replicates were generated per strain. Cell pellets were immediately flash-frozen in liquid nitrogen, and cell lysates prepared by grinding the pellets in liquid nitrogen with 350-400 µL of RLT buffer (Qiagen). The resulting powder was mixed with 500 µL of Trizol reagent (Thermo Fisher Scientific). Next, 140 µL of chloroform was added, vortex-mixed, and centrifuged at 4ºC for 10 min. The aqueous fraction was isolated and total RNA extracted using the RNeasy mini kit (Qiagen) as per manufacturer's instruction with minor modifications. In brief, the volume was brought to 900 µL with RLT buffer and 600 µL of 95% ethanol was added. 80 µL of RNase-free DNase mix (10 µL DNase I [Roche] of 10 U/µl in 80 µL total volume) was added to the RNeasy columns. Agilent 4200 TapeStation System was used to determine the quality of total RNA, and only RNA with RIN ≥ 9 was used. Ribosomal RNA (rRNA) was depleted using the Ribo-Zero rRNA Removal kit for bacteria (Illumina) prior to RNA sequencing (RNA-seq). Strand-specific RNA-seq libraries were prepared using the Stranded mRNA-seq Kit (Kapa Biosystems) as per manufacturer's instruction. The libraries were sequenced with the Illumina HiSeqTM 4000 instrument with 150 nucleotide read lengths.

RNA-Sequencing and Bioinformatic Analysis

The adapter sequence was trimmed and low quality reads removed by Trim Galore [2]. Trimmed reads were aligned to the CNCTC 10/84 genome (accession CP006910.1) using bowtie2 with one mismatch allowed. Samtools was used for filtering out low quality alignments ($q < 10$) [3]. The number of reads per gene was obtained using Subread package-feature Counts (version 1.5.0-p1) [4]. Expression values were normalized to fragments per kilobase million (FPKM) and Pearson's correlations values for biological replicates were calculated using in-house python scripts. Relative expression ratios were obtained for WT versus Δ*brpA*. Differentially transcribed genes were identified using DESeq2 package in R [5], such that the adjusted p-values were <0.05 and at least are differentially expressed by 2-fold. The CNCTC 10/84 genome was annotated in the RAST database to systematically organize genes into categories, subcategories, and subsystems [6]. FPKM values for transcription were summed for genes per each RAST category. For each strain, subsystems were normalized as a percent ratio of the total transcription for subsystems annotated by RAST (i.e. genes that are not in RAST categories were not considered). To directly compare transcription across the two strains (row-wise), the normalized percent values (column-wise) described above, were summed for each strain and normalized to percent.

Transmission Electron Microscopy

Mid-logarithmic phase bacteria were pelleted, fixed with 3% formaldehyde, 1.5% glutaraldehyde, 0.1M sodium cacodylate trihydrate, 5 mM $CaCl_2$ and 2.5% sucrose at pH 7.4 buffer for 1 hour, and prepared for transmission EM as described previously [7]. Thin sections (70 nm) were viewed with a FEI Tecnai 12 transmission electron microscope and images acquired with Tietz 214 CCD camera at 4,800X and 30,000X magnification.

Hemolytic extracts and protease treatment

GBS hemolytic extracts were prepared as described previously [8]. Briefly, 500 mL of mid-logarithmic cultures were pelleted, washed 1X in PBS, and resuspended in 25 mL of PBS containing 1% glucose, 1% starch, and 3% Tween-80. Cells were incubated for 1 hour at 37 °C, bacteria pelleted, and supernatant containing hemolytic activity was sterile filtered using a 0.2 µm filter. Supernatant was mixed 1:1 with ice-cold methanol, and starch/hemolysin complex precipitated at -20 °C for at least 1 hour. Precipitates were pelleted at 3220 × *g* for 20 minutes at 4 °C, and supernatant discarded. Residual methanol was evaporated from the extract pellets, and pellets were resuspended in 1 mL of PBS for hemolysis assays. For protease treatment experiments, CNCTC 10/84 hemolytic extract was diluted 1:50 in 50 mM Tris-Base buffer with 3 mM DTT and 1 mM $CaCl_2$. Proteases proteinase K, trypsin, subtilisin A, papain, and chymotrypsin (Sigma Aldrich) were added to diluted extracts at 1mg/mL and incubated for 1 hour at 37 °C prior to hemolysis assays.

Hemolysis Assays

GBS hemolysis assays were conducted as described previously [8]. For whole bacteria hemolysis assays, mid-logarithmic GBS was washed once in PBS and resuspended at 5×10^6 CFU/mL in PBS. In a 96-well conical bottom plate, 100 µL (5×10^5 CFU) was added to each well. For extract hemolysis assays, 100 µL of 1:50 dilution of extract was added to each well. An equal volume of washed 1% human RBC's in PBS was added to each well and the plate incubated at 37 °C for 1 hour. PBS (negative) and 1% Triton-X (positive) were used as controls. To pellet un-lysed RBCs, plates were spun at 500 × *g* for 10 minutes and 100 µL of supernatant was transferred to a replicate plate. Hemoglobin release was quantified by measuring absorbance at 450nm. To assess the effect of protease treatment, data was expressed as a percentage of untreated WT extract.

Minimum inhibitory concentration assays

GBS strains were grown to mid-logarithmic phase, and diluted 1:100 in THB. Diluted bacteria (100 µL) was added to 96-well plates. Inhibitory agents (Sigma Aldrich) listed in **Supplemental Table 1** were diluted in THB and 100 µL added to bacteria plates. Plates were incubated at 37 °C for 18 hours and OD_{600nm} values were measured to determine MIC values. For MIC assays involving LL-37 (Bachem), both bacteria and LL-37 were diluted in RPMI 1640 supplemented with 10% THB [9]).

Statistical Analyses

All data were collected from at least three biological replicates performed in at least technical duplicate as part of at least two independent experiments. When biological replicates were not available (e.g. immortalized cell lines and bacteria only assays), experiments were performed independently at least 3 times. Mean value from technical replicates were used for statistical analyses, with independent experiment values or biological replicates represented in graphs with mean ± SEM or median with 95% confidence interval as indicated in figure legends. Exceptions were microscopy assays, which was performed twice independently, and RNA-seq, which was performed once on two biological replicates as described above. All data sets were subjected to D' Agostino & Pearson normality test to determine whether values displayed Gaussian distribution before selecting the appropriate parametric or non-parametric analyses. Data from growth curves, autolysis, and planktonic culture were assumed parametric. *Ex vivo* and *in vivo* experimental *n* were too small to determine normality so data was assumed non-parametric. The alpha level used for all tests was 0.05. GBS chain length and epithelial adherence were analyzed using two-tailed Mann-Whitney test. GBS growth, autolysis, viability (log10 transformed), and ROS assays were analyzed using two-way repeated measures ANOVA with Tukey's multiple comparisons test or Sidak's multiple comparisons test as indicated in figure legends. Biofilm assays were analyzed using one-way ANOVA with Holm-Sidak's multiple comparisons test. Whole blood and neutrophil killing assays were analyzed using Kruskal-Wallis with Dunn's multiple comparisons test. *In vivo* competition values were analyzed using two-tailed Wilcoxon matched-pairs signed rank test with Spearman's rank-order correlation to determine effective pairing. Statistical analyses were performed using GraphPad Prism, version 7.03 (GraphPad Software Inc., La Jolla, CA, USA). *P* values < 0.05 were considered statistically significant.

References

1. Pritzlaff CA, Chang JC, Kuo SP, Tamura GS, Rubens CE, Nizet V. Genetic basis for the beta-haemolytic/cytolytic activity of group B Streptococcus. Mol Microbiol **2001**; 39:236-47.

2. Krueger F. Trim_Galore!: DNA sequencing adaptor trimmer and quality control analyzer Available at: www.bioinformatics.babraham.ac.uk/projects/trim_galore/. Accessed 02/21/2018.

3. Li H, Handsaker B, Wysoker A, et al. The Sequence Alignment/Map format and SAMtools. Bioinformatics **2009**; 25:2078-9.

4. Liao Y, Smyth GK, Shi W. featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. Bioinformatics **2014**; 30:923-30.

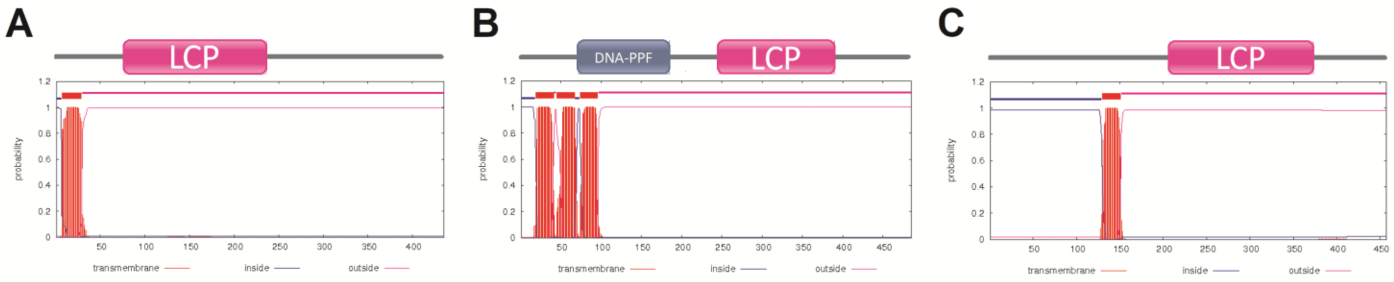
5. Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biol **2014**; 15:550.

6. Overbeek R, Olson R, Pusch GD, et al. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Res **2014**; 42:D206-14.

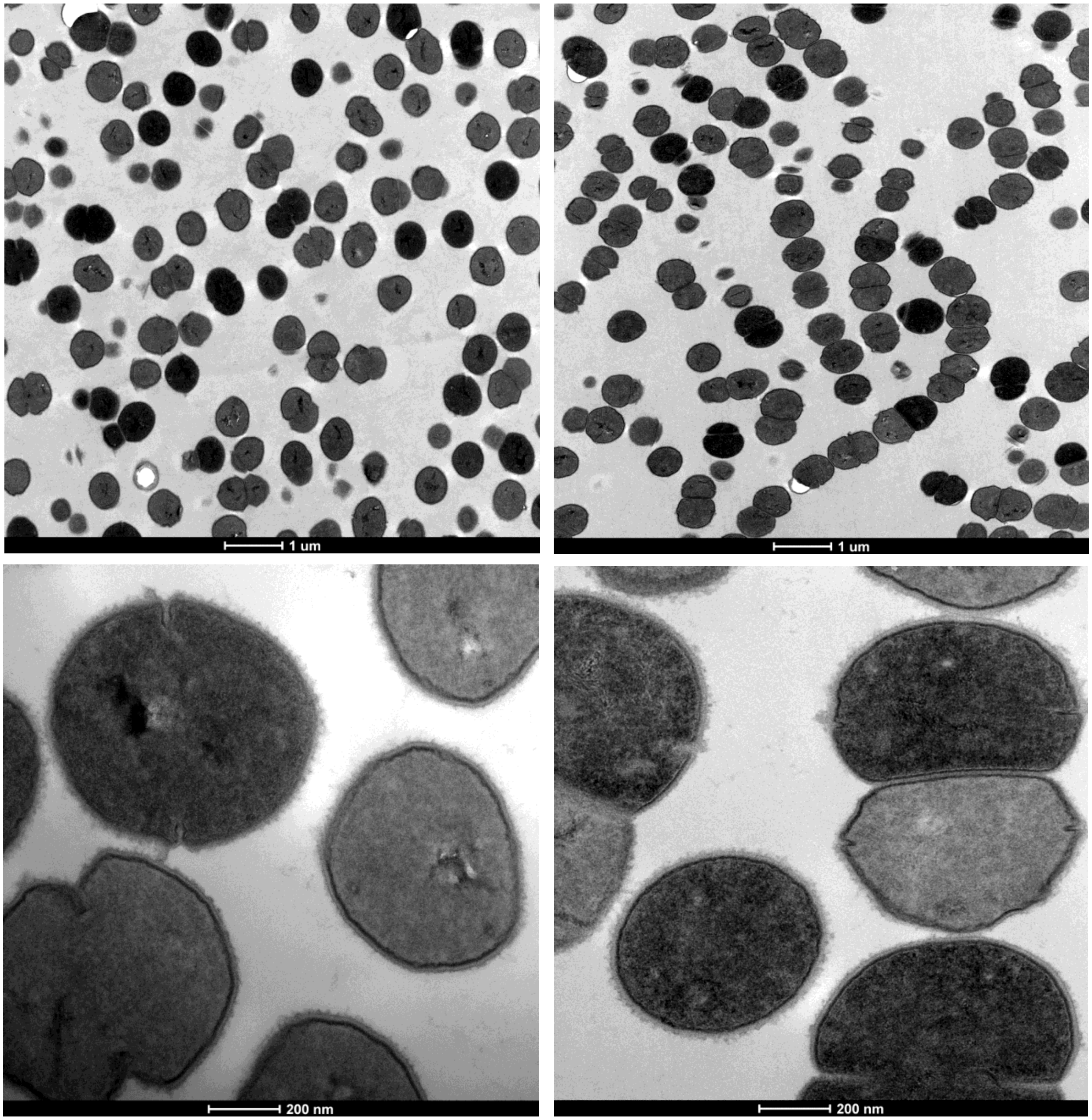
7. Uchiyama S, Dohrmann S, Timmer AM, et al. Streptolysin O Rapidly Impairs Neutrophil Oxidative Burst and Antibacterial Responses to Group A Streptococcus. Front Immunol **2015**; 6:581.

8. Nizet V, Gibson RL, Chi EY, Framson PE, Hulse M, Rubens CE. Group B streptococcal beta-hemolysin expression is associated with injury of lung epithelial cells. Infect Immun **1996**; 64:3818-26.

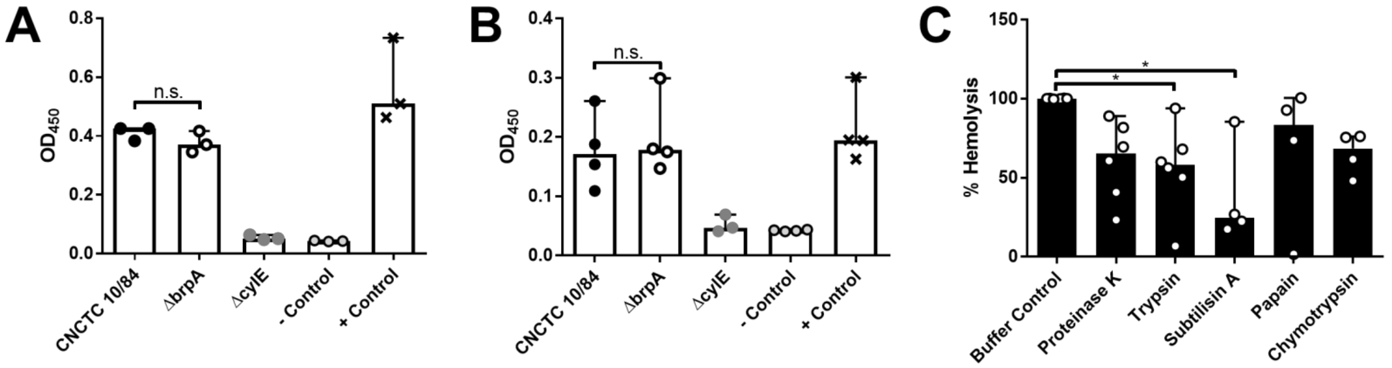
9. Munguia J, LaRock DL, Tsunemoto H, et al. The Mla pathway is critical for Pseudomonas aeruginosa resistance to outer membrane permeabilization and host innate immune clearance. J Mol Med (Berl) **2017**; 95:1127-36.



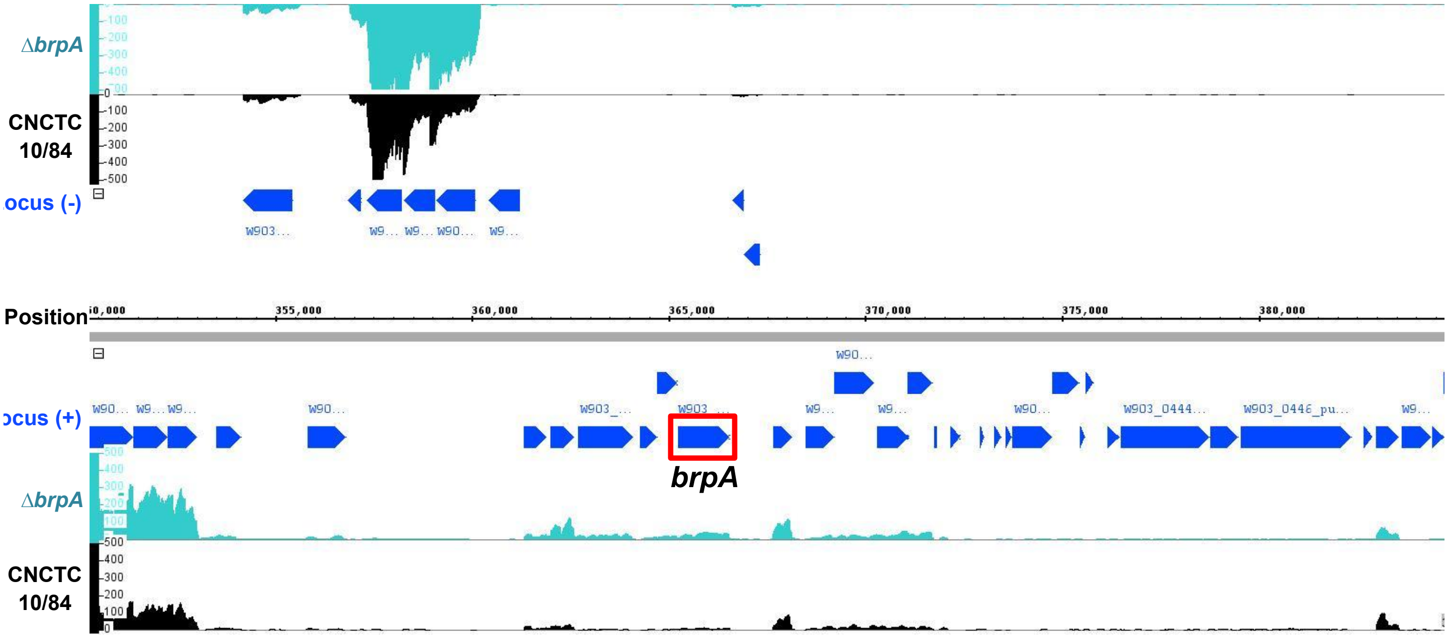
Supplemental Figure 1. Domains and transmembrane helix predictions of GBS LCP proteins. (**A**) *brpA* (W903_0426, accession: WP_000708159.1), (**B**) *cpsA* (W903_1258, accession: WP_000064987.1), and (**C**) putative *psr* (W903_0744, WP_000089333.1) conserved LCP domains were predicted using Pfam 31.0 (top images). Transmembrane helices were predicted using TMHMM Server v. 2.0 (bottom images).



Supplemental Figure 2. BrpA deficiency does not grossly alter cell shape, morphology, or division septa. Representative transmission electron microscopy images of mid-logarithmic WT (left column) and Δ*brpA* (right column) taken at 4,800X (top row) and 30,000X (bottom row) magnification.



Supplemental Figure 3. BrpA deficiency does not alter GBS hemolytic activity, however protease treatment reduces hemolysis of GBS WT extracts. Hemolysis assays with live bacteria (**A**) or hemolytic extracts (**B**) measured spectrophotometrically (OD_{450}) to determine hemoglobin release. A non-hemolytic mutant Δ*cylE* was used as a control as well as PBS (- Control) and PBS with 1% Triton-X (+ Control). (**C**) Hemolytic extracts treated with proteases (1 mg/mL) prior to hemolysis assays, and normalized to untreated extracts (Buffer Control). Independent experiments are shown (n = 3-6) and lines represent median ± 95% CI. Data was analyzed using Kruskal-Wallis with Dunn's multiple comparisons test. *$P<0.05$, or n.s. is not significant.



Supplemental Figure 4. Insertional mutagenesis of *brpA* does not alter expression of downstream genes. RNA-sequencing read alignment of late-logarithmic phase CNCTC 10/84 (black) and Δ*brpA* (teal). Raw number of reads is indicated on the y-axis, and individual loci on positive and negative strands are indicated in blue. The *brpA* gene (locus W903_0426) is boxed in red. Graphic was created using Integrated Genome Browser v. 9.0.0.

Supplemental Table 1. Minimum inhibitory concentrations for CNCTC 10/84 and ΔbrpA

Inhibitory Agent	**CNCTC 10/84**	**ΔbrpA**
LL-37	8 μM	8 μM
Lysozyme	1 mM	1 mM
H_2O_2	0.006%	0.006%
Penicillin	0.06 μg/mL	0.06 μg/mL
Ampicillin	0.5 μg/mL	0.5 μg/mL
Chloramphenicol	2 μg/mL	2 μg/mL

log2FoldChange	padj	gene_id	name	product
-1.0317	0.001706077	W903_0006		50S ribosome-binding GTPase family protein
-2.4288	0.001463064	W903_0007	pth	peptidyl-tRNA hydrolase
-1.8744	9.23562E-10	W903_0008	mfd	transcription-repair coupling factor
-1.5473	0.033578951	W903_0009		S4 domain protein
-1.8833	2.28904E-07	W903_0012		D-alanyl-D-alanine carboxypeptidase family protein
-1.5850	1.08062E-07	W903_0014	hpt	hypoxanthine phosphoribosyltransferase
-1.8180	7.02776E-17	W903_0015	hflB	ATP-dependent metallopeptidase HflB family protein
-2.4177	9.53314E-19	W903_0093	rpsJ	ribosomal protein S10
-2.6184	1.63675E-20	W903_0094	rplC	50S ribosomal protein L3
-2.3461	5.60321E-15	W903_0095	rplD	50S ribosomal protein L4
-2.3685	2.25893E-15	W903_0096	rplW	50S ribosomal protein L23
-2.3065	2.26025E-13	W903_0097	rplB	ribosomal protein L2
-1.8560	3.21296E-06	W903_0098	rpsS	ribosomal protein S19
-2.0356	5.44958E-09	W903_0099	rplV	ribosomal protein L22
-1.8741	4.40681E-06	W903_0100	rpsC	ribosomal protein S3
-1.7215	2.34437E-06	W903_0101	rplP	ribosomal protein L16
-1.5339	1.97073E-08	W903_0102	rpmC	ribosomal protein L29
-1.3990	0.000468404	W903_0103	rpsQ	30S ribosomal protein S17
-1.4853	4.15194E-05	W903_0104	rplN	ribosomal protein L14
-1.4706	3.02402E-05	W903_0105	rplX	ribosomal protein L24
-1.5625	5.76852E-05	W903_0106	rplE	50S ribosomal protein L5
-1.2868	0.010689547	W903_0107	rpsZ	30S ribosomal protein S14 type Z
-1.2983	0.004743184	W903_0108	rpsH	30S ribosomal protein S8
-1.2131	0.004856034	W903_0109	rplF	ribosomal protein L6
-1.2754	0.008514687	W903_0110	rplR	ribosomal protein L18
-1.0517	0.017394665	W903_0113	rplO	ribosomal protein L15
-1.8616	8.75418E-11	W903_0115	adk	adenylate kinase
-2.1689	7.96586E-10	W903_0116	infA	translation initiation factor IF-1
-2.0037	9.26829E-08	W903_0117	rpmJ	ribosomal protein L36
-1.9636	4.02469E-17	W903_0118	rpsM	30S ribosomal protein S13
-2.3981	2.06719E-20	W903_0119	rpsK	30S ribosomal protein S11
-2.2420	2.86761E-29	W903_0120	rpoA	DNA-directed RNA polymerase, alpha subunit
-2.1218	3.91606E-21	W903_0121	rplQ	ribosomal protein L17
-1.8482	6.57229E-10	W903_0163	tig	trigger factor
-1.2874	0.000122374	W903_0164		putative DNA-directed RNA polymerase subunit delta
-1.2106	1.19765E-05	W903_0165	pyrG	CTP synthase
-1.6739	0.00673142	W903_0170		carbonic anhydrase family protein
-1.1635	0.000115459	W903_0172	gltX	glutamate--tRNA ligase
-2.2330	2.66955E-08	W903_0187	rpmB	ribosomal protein L28
-2.0652	0.000273967	W903_0191		hypothetical protein
-1.8081	3.17203E-09	W903_0193		ABC transporter family protein
-1.6832	4.63454E-09	W903_0194		amino ABC transporter, permease, 3-TM region, His/Glu/Gln/Arg/opine family domain protein
-1.0144	0.003006663	W903_0197		negative regulator of genetic competence family protein
-1.0832	0.000237005	W903_0207		binding--dependent transport system inner membrane component family protein
-1.1711	0.014601568	W903_0208		N-terminal TM domain of oligopeptide transport permease C family protein
-1.4769	1.94069E-05	W903_0221	tyrS	tyrosine--tRNA ligase
-1.0663	4.23559E-08	W903_0223	rpoB	DNA-directed RNA polymerase, beta subunit
-1.1562	0.009016008	W903_0226		hypothetical protein
-1.1874	0.011780071	W903_0234		N-6 DNA Methylase family protein
-1.0975	5.87156E-06	W903_0235	ackA	acetate kinase
-1.2297	3.83893E-08	W903_0265	rpsO	ribosomal protein S15
-1.3248	1.47426E-05	W903_0266	pnp	polyribonucleotide nucleotidyltransferase
-1.3353	5.26308E-05	W903_0267		hypothetical protein
-1.6676	0.000103475	W903_0268	cysE	serine O-acetyltransferase
-1.2772	3.53802E-05	W903_0270	cysS	cysteine--tRNA ligase
-1.3372	0.001234669	W903_0271		ribonuclease III domain protein

-1.6389	6.47198E-06	W903_0278	rplM	ribosomal protein L13
-1.5121	4.5371E-09	W903_0279	rpsI	30S ribosomal protein S9
-1.1895	0.003434719	W903_0323		isoprenylcysteine carboxyl methyltransferase family protein
-3.5839	4.82581E-05	W903_0338		PTS system, glucose-like IIB component domain protein
-1.1303	0.003508755	W903_0341	rsmH	16S rRNA (cytosine(1402)-N(4))-methyltransferase
-1.1191	2.02599E-06	W903_0343		penicillin binding transpeptidase domain protein
-1.2714	0.000311011	W903_0344	mraY	phospho-N-acetylmuramoyl-pentapeptide- transferase
-1.7415	0.02702342	W903_0349		hypothetical protein
-1.8510	0.000251956	W903_0351		nicotinate phosphoribosyltransferase family protein
-1.2459	0.000456726	W903_0352	nadE	NAD+ synthetase
-1.3588	1.94242E-05	W903_0361	rny	ribonuclease Y
-1.1985	0.00053281	W903_0368	rpoZ	DNA-directed RNA polymerase, omega subunit
-1.5473	0.021343848	W903_0389		hypothetical protein
-1.8236	9.11452E-05	W903_0398		aspartate kinase domain protein
-2.0188	0.015771946	W903_0399		beta-phosphoglucomutase, putative
-1.8579	2.58821E-08	W903_0423		permease family protein
-1.6904	0.00304895	W903_0425		acetyltransferase family protein
-1.1245	0.000466382	W903_0490	tgt	queuine tRNA-ribosyltransferase
-1.9271	1.80925E-08	W903_0501	galU	UTP-glucose-1-phosphate uridylyltransferase
-1.7058	1.32695E-08	W903_0502	gpsA	glycerol-3-phosphate dehydrogenase
-1.1103	0.037490282	W903_0514		hypothetical protein
-1.5362	5.84356E-08	W903_0519	scpA	C5a peptidase
-1.0723	0.005172691	W903_0520		glycosyl transferase 2 family protein
-1.1990	0.041142099	W903_0593		hypothetical protein
-1.5767	1.60617E-11	W903_0596	typA	GTP-binding protein TypA/BipA
-1.9173	1.72901E-07	W903_0597		hypothetical protein
-1.3061	0.00055432	W903_0702		degT/DnrJ/EryC1/StrS aminotransferase family protein
-1.6233	1.4702E-07	W903_0703	asnS	asparagine--tRNA ligase
-1.5838	0.001320519	W903_0711		yodA lipocalin-like domain protein
-1.5279	1.65346E-13	W903_0712	rpmE	ribosomal protein L31
-2.2488	3.70518E-17	W903_0718	rplS	ribosomal protein L19
-1.5798	0.000183103	W903_0745		23S rRNA (uracil-5-)-methyltransferase RumA
-1.1119	0.001619551	W903_0749		beta-lactamase family protein
-2.5803	1.97343E-05	W903_0775		ABC transporter family protein
-1.8601	0.000485755	W903_0776		hypothetical protein
-1.0585	0.000206813	W903_0801		amino ABC transporter, permease, 3-TM region, His/Glu/Gln/Arg/opine family domain protein
-1.1758	0.000168861	W903_0802		amino ABC transporter, permease, 3-TM region, His/Glu/Gln/Arg/opine family domain protein
-1.6407	2.83742E-07	W903_0803		bacterial extracellular solute-binding s, 3 family protein
-1.4149	9.63974E-05	W903_0804		ABC transporter family protein
-1.1845	0.027332538	W903_0809	rnc	ribonuclease III
-1.4723	2.20757E-09	W903_0810	smc	chromosome segregation protein SMC
-1.1968	0.000627384	W903_0814		hypothetical protein
-1.0825	0.009135674	W903_0826		hypothetical protein
-1.7311	0.002811218	W903_0827		peptidase U32 family protein
-1.1085	0.0004026	W903_0828		peptidase U32 family protein
-1.9181	0.00072177	W903_0829		hypothetical protein
-1.5866	5.54196E-09	W903_0836	lysS	lysine--tRNA ligase
-2.8279	0.000101035	W903_0843		putative lipoprotein
-2.3422	1.38213E-13	W903_0856		penicillin binding transpeptidase domain protein
-2.1335	1.24752E-05	W903_0857	recR	recombination protein RecR
-1.5493	0.002542928	W903_0858	ddl	D-alanine--D-alanine ligase
-1.0956	0.000244579	W903_0859	murF	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase family protein
-2.1490	0.041142099	W903_0860		major Facilitator Superfamily protein
-1.4105	0.0001017	W903_0861		integral membrane family protein
-1.0185	9.1416E-05	W903_0864	prfC	peptide chain release factor 3
-1.5766	0.006468541	W903_0866		ABC transporter family protein
-1.4963	0.007610536	W903_0867		binding--dependent transport system inner membrane component family protein

-1.2458	0.010979512	W903_0868		NLPA lipofamily protein
-3.7112	2.09968E-27	W903_0869		helicase domain protein
-3.6681	0.001440001	W903_0877		alpha/beta hydrolase fold family protein
-1.5174	0.000636211	W903_0889	queA	tRNA ribosyltransferase-isomerase
-1.2357	0.009412631	W903_0890		VIT family protein
-2.2232	4.45566E-07	W903_0894		major Facilitator Superfamily protein
-1.1742	0.000419674	W903_0896		oligoendopeptidase F
-2.8031	0.000446261	W903_0897		HAD hydrolase, IA, variant 1 family protein
-1.8177	0.03379655	W903_0898		methyltransferase domain protein
-2.2934	1.24209E-22	W903_0899		PPIC-type PPIASE domain protein
-1.0578	0.000822428	W903_0900		tubby C 2 family protein
-1.2387	1.53498E-05	W903_0901	alaS	alanine--tRNA ligase
-1.4129	7.44649E-09	W903_0909		ribonucleotide reductase, small chain family protein
-1.6414	4.1582E-10	W903_0910		ribonucleoside-diphosphate reductase, alpha subunit
-1.6661	0.000989532	W903_0911	nrdH	glutaredoxin-like protein nrdH
-1.6338	7.37918E-13	W903_0914	gapN	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
-1.5067	0.003904969	W903_0918		GAF domain protein
-2.7454	1.44242E-06	W903_0923		coagulase family protein
-1.5488	0.022009055	W903_0924		hypothetical protein
-1.1454	0.000290125	W903_0933		UDP-N-acetylglucosamine 1-carboxyvinyltransferase
-2.6732	9.34801E-07	W903_0939	queT	queuosine transporter QueT
-1.0967	0.00033121	W903_0956		UDP-N-acetylglucosamine 1-carboxyvinyltransferase
-1.9415	0.01506343	W903_0957		DNA-directed RNA polymerase subunit beta family protein
-1.8402	2.79396E-06	W903_0959	pheS	phenylalanine--tRNA ligase, alpha subunit
-2.2530	1.69382E-17	W903_0961	pheT	phenylalanine--tRNA ligase, beta subunit
-1.7420	0.014019165	W903_0967		hypothetical protein
-2.0824	0.002792124	W903_0996		histidine triad domain protein
-1.3366	0.032511105	W903_0997		HD domain protein
-1.0036	5.18055E-07	W903_1008	pfkA	6-phosphofructokinase
-1.0649	4.58316E-07	W903_1009	pyk	pyruvate kinase
-1.9888	6.41862E-11	W903_1012	glmS	glutamine-fructose-6-phosphate transaminase
-2.9265	0.002079896	W903_1013		phnA family protein
-2.0433	0.001802746	W903_1014		amino ABC transporter, permease, 3-TM region, His/Glu/Gln/Arg/opine family domain protein
-2.1066	8.07322E-05	W903_1015		ABC transporter family protein
-2.7646	2.95233E-09	W903_1016		polar amino acid ABC uptake transporter substrate binding protein
-1.5470	9.88962E-06	W903_1017	rpsT	ribosomal protein S20
-1.2019	0.049328988	W903_1018	coaA	pantothenate kinase
-1.4960	0.016269866	W903_1019		mycolic acid cyclopropane synthetase family protein
-2.1897	8.6468E-17	W903_1025		putative NADH oxidase
-1.9625	2.13928E-14	W903_1039	guaA	GMP synthase domain protein
-1.3902	0.026116548	W903_1042		acetyltransferase family protein
-1.4546	0.000550707	W903_1054	ffh	signal recognition particle protein
-1.7863	5.13193E-11	W903_1058		peptidase M1 family protein
-1.1217	0.001549313	W903_1059		phosphate transport system regulatory protein PhoU
-1.0403	0.005262227	W903_1060		phosphate ABC transporter, ATP-binding protein
-1.5681	0.001081779	W903_1061		phosphate ABC transporter, ATP-binding protein
-1.4313	5.17858E-05	W903_1062		phosphate ABC transporter, permease protein PstA
-1.4290	0.000183248	W903_1063		phosphate ABC transporter, permease protein PstC
-1.5604	0.000192837	W903_1064	pstS	phosphate binding family protein
-1.3163	5.91621E-05	W903_1066		inositol monophosphatase family protein
-1.5929	0.0005196	W903_1068	spxA	regulatory protein spx
-2.2805	4.3936E-07	W903_1069	ribF	riboflavin biosynthesis protein RibF
-1.3146	0.007416594	W903_1070	truB	tRNA pseudouridine(55) synthase
-2.6982	1.58811E-12	W903_1077	topA	DNA topoisomerase I
-1.2613	0.001019384	W903_1079		hypothetical protein
-1.1367	0.002427193	W903_1081		fecCD transport family protein
-1.2737	0.013234831	W903_1083		bacterial transferase hexapeptide family protein

E171

-1.0783	0.007084229	W903_1126	esaA	type VII secretion protein EsaA
-1.5962	0.000115832	W903_1140	asd	aspartate-semialdehyde dehydrogenase
-1.0557	0.010905051	W903_1144		lipoyltransferase and lipoate-ligase family protein
-1.0235	0.021466323	W903_1145		hypothetical protein
-1.0282	0.018646592	W903_1146		macro domain protein
-1.9652	4.52485E-07	W903_1148		luciferase oxidoreductase, group 1 family protein
-1.4978	4.62467E-05	W903_1149		flavin oxidoreductase / NADH oxidase family protein
-1.9177	2.9405E-06	W903_1150		biotin/lipoate A/B ligase family protein
-3.5261	0.002456906	W903_1151	coaB	phosphopantothenate--cysteine ligase
-1.0168	0.042619323	W903_1153	panT	pantothenic acid transporter PanT
-1.0612	0.015848716	W903_1162	prfA	peptide chain release factor 1
-1.3358	0.020295222	W903_1163		thymidine kinase family protein
-4.5811	2.10149E-05	W903_1164		tautomerase enzyme family protein
-2.0968	1.77096E-05	W903_1169	pbuX	xanthine permease family protein
-2.0405	0.007198183	W903_1171	guaC	guanosine monophosphate reductase
-1.6974	0.01043461	W903_1172		major Facilitator Superfamily protein
-3.9360	0.000483987	W903_1173		hypothetical protein
-2.4649	2.32827E-15	W903_1174		potassium uptake protein
-1.1688	7.98419E-05	W903_1176	pta	phosphate acetyltransferase
-2.4526	0.000151467	W903_1192		bacterial extracellular solute-binding family protein
-1.6057	0.000295016	W903_1193		binding--dependent transport system inner membrane component family protein
-1.8815	2.49156E-06	W903_1194		binding--dependent transport system inner membrane component family protein
-2.0521	1.05235E-07	W903_1195		polyamine ABC transporter, ATP-binding family protein
-1.6478	0.004043221	W903_1196	murB	UDP-N-acetylenolpyruvoylglucosamine reductase
-1.3800	0.036406504	W903_1198	folB	dihydroneopterin aldolase
-1.4789	0.000889665	W903_1199	folP	dihydropteroate synthase
-2.0317	0.0041529	W903_1200	folE	GTP cyclohydrolase I
-1.2470	0.000629581	W903_1201	folC	bifunctional FolC family protein
-1.9432	4.82581E-05	W903_1202		eamA-like transporter family protein
-1.0453	0.020295222	W903_1203	thrB	homoserine kinase
-1.2084	0.00662178	W903_1204		homoserine dehydrogenase family protein
-1.8495	5.05511E-06	W903_1222	pcrA	ATP-dependent DNA helicase PcrA
-1.5816	0.02366	W903_1225	agcS	amino acid carrier family protein
-3.1213	5.45448E-33	W903_1231		S1 RNA binding domain protein
-1.0263	0.000852915	W903_1235	ilvE	branched-chain amino acid aminotransferase
-2.1710	1.8512E-16	W903_1236	parC	DNA topoisomerase IV, A subunit
-2.0967	3.92999E-08	W903_1237	parE	DNA topoisomerase IV, B subunit
-1.5673	0.000393855	W903_1241		GDSL-like Lipase/Acylhydrolase family protein
-1.4151	0.001925953	W903_1242		sugar O-acyltransferase, sialic acid O-acetyltransferase NeuD family protein
-1.5888	2.7951E-05	W903_1243	neuC	UDP-N-acetyl-D-glucosamine 2-epimerase, UDP-hydrolysing
-1.2842	0.003373789	W903_1244	neuB	N-acetylneuraminate synthase
-1.8680	5.45821E-06	W903_1246		glycosyltransferase 52 family protein
-2.3444	2.56688E-07	W903_1248		glycosyl transferase 2 family protein
-1.7915	3.90299E-05	W903_1249		glycosyl transferase 2 family protein
-2.0075	5.18678E-05	W903_1250		tcdA/TcdB catalytic glycosyltransferase domain protein
-1.7653	0.013686154	W903_1251		putative membrane protein
-2.0800	0.007065437	W903_1252		glycosyltransferase family 28 C-terminal domain protein
-1.7878	0.016657289	W903_1253		oligosaccharide biosynthesis Alg14 like family protein
-1.9020	1.04913E-07	W903_1254		exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase family protein
-1.5871	1.25067E-06	W903_1255	cpsD	tyrosine-protein kinase CpsD
-1.2729	0.000129158	W903_1256		chain length determinant family protein
-1.8443	1.95454E-06	W903_1257	cpsB	tyrosine-protein phosphatase CpsB
-1.3852	6.51839E-06	W903_1258		cell envelope-related function transcriptional attenuator common domain protein
-1.7923	0.003086565	W903_1273		fibronectin-binding A family protein
-1.3982	0.025945212	W903_1287		hypothetical protein
-1.5290	0.002691904	W903_1288		hypothetical protein
-1.9469	5.20496E-07	W903_1289	apt	adenine phosphoribosyltransferase
-1.0740	0.000768255	W903_1310		3-demethylubiquinone-9 3-methyltransferase family protein

-1.1334	0.001043878	W903_1311		hypothetical protein
-1.5821	0.028583095	W903_1319	mmuM	homocysteine S-methyltransferase
-1.2490	0.028158652	W903_1320		amino acid permease family protein
-2.5158	0.045462062	W903_1321		hypothetical protein
-1.1443	5.88842E-05	W903_1325	clpX	ATP-dependent Clp protease, ATP-binding subunit ClpX
-2.2170	0.00325327	W903_1326		putative membrane protein
-1.2308	0.001196702	W903_1327	dhfR	dihydrofolate reductase
-1.2100	0.007257452	W903_1328		thymidylate synthase family protein
-1.0083	0.006348185	W903_1329		hydroxymethylglutaryl-CoA synthase
-1.5140	2.22282E-05	W903_1336	fni	isopentenyl-diphosphate delta-isomerase, type 2
-1.7338	0.000465963	W903_1337		phosphomevalonate kinase
-1.5540	0.001364829	W903_1338	mvaD	diphosphomevalonate decarboxylase
-1.5244	0.004737833	W903_1339	mvk	mevalonate kinase
-2.0847	1.4789E-07	W903_1345		marR family protein
-1.0616	0.00029839	W903_1354		ABC transporter family protein
-1.8901	2.1893E-09	W903_1365		2-dehydropantoate 2-reductase family protein
-1.0534	0.001857938	W903_1366		phosphotransferase system, EIIC family protein
-2.1758	2.61159E-13	W903_1373		KH domain protein
-2.0404	1.32619E-08	W903_1374	rpsP	ribosomal protein S16
-1.2859	1.4001E-05	W903_1377		efflux transporter, RND family, MFP subunit
-1.5500	3.06225E-08	W903_1384	rpmA	ribosomal protein L27
-1.4529	7.26518E-10	W903_1385		hypothetical protein
-1.2925	4.41031E-07	W903_1386	rplU	ribosomal protein L21
-1.9071	1.1592E-07	W903_1388	thiI	tRNA sulfurtransferase ThiI
-1.3136	0.000526745	W903_1389		aminotransferase class-V family protein
-1.3852	0.023963568	W903_1390		hypothetical protein
-1.3556	0.003823331	W903_1395	aroD	3-dehydroquinate dehydratase
-1.7824	3.01784E-07	W903_1396		methyltransferase domain protein
-2.0850	4.79362E-14	W903_1397		sulfatase family protein
-1.4646	9.90091E-05	W903_1398	rplT	ribosomal protein L20
-1.3691	3.13013E-06	W903_1399	rpmI	ribosomal protein L35
-1.7772	4.70764E-13	W903_1400	infC	translation initiation factor IF-3
-1.0904	0.000114706	W903_1407	murE	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L- lysine ligase
-1.9254	0.029374108	W903_1408		ABC transporter family protein
-1.8433	7.81402E-05	W903_1409		periplasmic binding family protein
-1.6238	0.037360067	W903_1410		fecCD transport family protein
-2.4375	0.003039602	W903_1411		fecCD transport family protein
-1.6222	0.007303354	W903_1412		hypothetical protein
-1.0652	9.13639E-05	W903_1415		transporter associated domain protein
-2.0824	0.024141662	W903_1425		M trans-acting positive regulator (MGA) PRD domain protein
-1.1185	0.001050989	W903_1430		glycosyl transferase 2 family protein
-1.0850	0.008631855	W903_1431		glycosyl transferase 2 family protein
-1.2731	5.91621E-05	W903_1433		hypothetical protein
-1.0198	0.004770428	W903_1434		licD family protein
-1.4253	8.10496E-08	W903_1435		putative lipoprotein
-2.4994	0.000637659	W903_1436		hypothetical protein
-1.7018	1.24213E-05	W903_1437		glycosyl transferase 2 family protein
-1.7288	1.47526E-05	W903_1438		glycosyl transferase 2 family protein
-1.7626	2.35101E-05	W903_1439		glycosyl transferases group 1 family protein
-1.2265	1.47438E-05	W903_1445	rpsU	ribosomal protein S21
-1.7000	1.952E-07	W903_1450		rhodanese-like domain protein
-1.5017	1.27088E-06	W903_1475		serine-rich repeat adhesion glycoprotein
-1.7345	0.000418261	W903_1478		CAAX protease self-immunity family protein
-2.5093	2.362E-26	W903_1479		lysine-arginine-ornithine-binding periplasmic family protein
-1.9475	1.30898E-10	W903_1480		ABC transporter family protein
-1.5635	0.000468404	W903_1496	secG	preprotein translocase, SecG subunit
-1.2408	0.04292068	W903_1513		hypothetical protein

-2.6514	3.95378E-25	W903_1526	rplA	ribosomal protein L1
-2.5536	1.58883E-22	W903_1527	rplK	ribosomal protein L11
-3.2851	6.09005E-08	W903_1528	norB	quinolone resistance protein norB
-2.6094	1.6464E-05	W903_1529		amidohydrolase family protein
-2.1804	0.01043461	W903_1530		bacterial regulatory helix-turn-helix, lysR family protein
-1.2752	0.032589974	W903_1534		cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD family protein
-1.0841	0.004955738	W903_1552		glycosyl transferase 2 family protein
-1.4492	1.91381E-05	W903_1553		hypothetical protein
-1.2016	0.000265359	W903_1554		cotH family protein
-1.3360	0.009182514	W903_1555		hypothetical protein
-1.2841	0.000486899	W903_1566		ACT domain protein
-2.9728	0.000105131	W903_1567		acetyltransferase, GNAT family
-2.4003	3.28228E-05	W903_1568	serC	phosphoserine transaminase
-1.1085	0.030580351	W903_1571		hypothetical protein
-3.0349	0.012397949	W903_1580		hypothetical protein
-2.0563	9.62654E-08	W903_1585		amino acid permease family protein
-1.3240	3.9823E-05	W903_1586		NAD-dependent glycerol-3-phosphate dehydrogenase family protein
-1.5838	1.07136E-07	W903_1587		cation transport family protein
-1.0002	0.007146995	W903_1606		putative ABC transporter extracellular-binding protein yckB
-2.8460	4.84176E-09	W903_1608	greA	transcription elongation factor GreA domain protein
-1.6433	5.37642E-12	W903_1609		yceG-like family protein
-1.0461	0.001716695	W903_1610		acetyltransferase family protein
-1.1111	0.001079569	W903_1624		cation transport family protein
-1.3297	0.002693187	W903_1625		oxidoreductase, NAD-binding Rossmann fold family protein
-1.0020	0.03729348	W903_1628		ECF-type riboflavin transporter, S component family protein
-1.9556	3.02402E-05	W903_1629		dicarboxylate symporter family protein
-1.0334	0.004801631	W903_1634		peptidase M20/M25/M40 family protein
-1.0195	0.000159092	W903_1637		glutamine amidotransferase class-I family protein
-1.0739	0.041142099	W903_1649		ubiE/COQ5 methyltransferase family protein
-1.2464	0.001153735	W903_1652		HD domain protein
-1.7368	5.31797E-07	W903_1653	nadD	nicotinate (nicotinamide) nucleotide adenylyltransferase
-1.3220	0.002079896	W903_1654		CRS1 / YhbY domain protein
-1.6555	8.94746E-06	W903_1655	yqeH	ribosome biogenesis GTPase YqeH
-1.4853	0.001066577	W903_1657		eamA-like transporter family protein
-1.3914	0.029198564	W903_1665		isochorismatase family protein
-1.5616	4.93065E-05	W903_1666	codY	GTP-sensing transcriptional pleiotropic repressor CodY
-1.7117	2.45782E-07	W903_1667		aminotransferase class-V family protein
-1.6336	0.000619108	W903_1669		cof-like hydrolase family protein
-1.1109	0.047956913	W903_1670		asparaginase family protein
-1.4889	1.10997E-13	W903_1674		mannosyl-glycoendo-beta-N-acetylglucosaminidase family protein
-1.0114	0.000697373	W903_1696		H+ antiporter-2 family protein
-1.3346	0.000692598	W903_1699		hypothetical protein
-1.3580	0.000285506	W903_1700		corA-like Mg2+ transporter family protein
-1.6813	2.75644E-14	W903_1701	rpsR	ribosomal protein S18
-1.4967	2.54936E-14	W903_1702		single-stranded DNA-binding family protein
-1.4478	1.7186E-09	W903_1703	rpsF	ribosomal protein S6
-1.6113	7.4264E-05	W903_1712		signal peptidase I
-1.9904	1.37427E-06	W903_1713		viral (Super1) RNA helicase family protein
-1.1886	0.000707074	W903_1718		beta-lactamase family protein
-1.1070	0.003075502	W903_1719	cppA	C3-degrading proteinase
-1.8966	1.47438E-05	W903_1721	gla	glycerol facilitator-aquaporin gla
-1.3236	7.08734E-05	W903_1725	pepX	xaa-Pro dipeptidyl-peptidase
-1.8646	8.87409E-05	W903_1736		DNA-binding protein, YbaB/EbfC family
-1.1184	0.022271734	W903_1745	rpsN2	alternate 30S ribosomal protein S14
-1.9035	0.0017476	W903_1746		aminotransferase class-V family protein
-2.2072	1.57362E-19	W903_1760	rpsG	ribosomal protein S7
-1.6864	4.79362E-14	W903_1761	rpsL	ribosomal protein S12

-1.2994	0.002642471	W903_1768		methyltransferase domain protein	
-1.0040	0.009512159	W903_1769	ksgA	dimethyladenosine transferase	
-1.4813	0.008666748	W903_1770		glycerophosphoryl diester phosphodiesterase family protein	
-1.3655	0.006458624	W903_1772		hydrolase, TatD family protein	
-1.8555	3.22716E-08	W903_1784	rpmH	ribosomal protein L34	
-2.0497	2.60906E-06	W903_1785		nucleoside recognition family protein	
-1.4468	1.53126E-09	W903_1808	purA	adenylosuccinate synthase	
-1.3516	9.41512E-07	W903_1811	gshAB	glutamate--cysteine ligase/gamma-glutamylcysteine synthetase	
-1.5040	0.001059046	W903_1814		hsp33 family protein	
-2.2999	7.43023E-07	W903_1815		TIM-barrel, nifR3 family protein	
-1.1285	0.023658872	W903_1816		deoxyguanosine kinase	
-2.2112	0.000676143	W903_1817		acetyltransferase family protein	
-1.3119	2.89656E-09	W903_1821	tsf	translation elongation factor Ts	
-1.4728	2.75644E-14	W903_1822	rpsB	ribosomal protein S2	
-1.7705	0.000136181	W903_1831		major Facilitator Superfamily protein	
-1.4613	0.041374127	W903_1848		mannosyl-glycoendo-beta-N-acetylglucosaminidase family protein	
-1.3951	6.66493E-05	W903_1853	yajC	preprotein translocase, YajC subunit	
-1.3813	0.039834901	W903_1854		thioredoxin family protein	
-2.9321	0.016334902	W903_1935		histidine phosphatase super family protein	
-2.4081	0.001794147	W903_1943		PAP2 superfamily protein	
-1.0095	0.049609635	W903_1946		CAAX protease self-immunity family protein	
-1.4269	1.73709E-05	W903_1953		hypothetical protein	
-1.0178	1.39695E-05	W903_1963	leuS	leucine--tRNA ligase	
-1.0037	0.003614448	W903_1966	nusG	transcription termination/antitermination factor NusG	
-2.1477	0.0039701	W903_1970		pseudouridine synthase, RluA family protein	
-3.5616	5.17608E-34	W903_2003		'Cold-shock' DNA-binding domain protein	
-1.4480	1.04673E-06	W903_2004	mutS	DNA mismatch repair protein MutS	
-1.0424	0.004662329	W903_2008		hypothetical protein	
-1.3096	2.52479E-06	W903_2009		hypothetical protein	
-1.1796	1.62415E-06	W903_2010	aspS	aspartate--tRNA ligase	
-1.8479	6.20182E-05	W903_2012	rpmF	ribosomal protein L32	
-1.6689	5.00046E-11	W903_2013	rpmG	ribosomal protein L33	
-3.0690	0.010979512	W903_2015		bacterial regulatory, arsR family protein	
-1.7007	0.017018331	W903_2037		yhgE/Pip N-terminal domain protein	
-2.7831	1.22382E-21	W903_2040	rpsD	ribosomal protein S4	
-1.5100	0.010970714	W903_2052	ecfT	energy-coupling factor transporter transmembrane protein EcfT	
-1.2720	0.00301513	W903_2073		hypothetical protein	
-1.6918	9.99304E-11	W903_2074		ABC transporter family protein	
-1.2452	0.001383438	W903_2075		bacterial membrane YfhO family protein	
-1.2761	4.90943E-10	W903_2080		trypsin family protein	

log2FoldChange	padj	gene_id	name	product
2.759438555	0.000385063	W903_0063	purN	phosphoribosylglycinamide formyltransferase
3.931870993	1.17352E-30	W903_0068		putative N-acetylmannosamine-6-phosphate 2-epimerase
4.93730386	8.8977E-114	W903_0069		bacterial extracellular solute-binding family protein
5.542474849	7.5017E-70	W903_0070		binding--dependent transport system inner membrane component family protein
5.689098222	4.96605E-63	W903_0071		binding--dependent transport system inner membrane component family protein
5.25963945	3.08353E-48	W903_0072		hypothetical protein
5.369475699	1.21189E-54	W903_0073		hypothetical protein
5.482337967	1.10091E-49	W903_0074		dihydrodipicolinate synthetase family protein
5.65498241	2.61369E-83	W903_0075		ROK family protein
5.244566903	1.67564E-33	W903_0076	axe1	xylan esterase 1
2.16436403	2.19875E-07	W903_0078	purD	phosphoribosylamine--glycine ligase
2.027932499	0.001070243	W903_0079	purE	phosphoribosylaminoimidazole carboxylase, catalytic subunit
2.131131682	2.15301E-05	W903_0080	purK	phosphoribosylaminoimidazole carboxylase, ATPase subunit
1.354445773	0.001111165	W903_0081		putative phosphoribosylaminoimidazole carboxylase ATPase subunit
3.204319546	6.93455E-71	W903_0089		aldehyde dehydrogenase family protein
3.741689467	1.81623E-96	W903_0090		zinc-binding dehydrogenase family protein
1.611904819	9.23639E-12	W903_0091	thrC	threonine synthase
1.052766838	1.85811E-05	W903_0092		MATE efflux family protein
1.134206133	5.0264E-07	W903_0147		hypothetical protein
1.504531052	4.01703E-05	W903_0152	hrcA	heat-inducible transcription repressor HrcA
1.608468611	8.09617E-08	W903_0153		grpE family protein
1.619732786	2.18727E-15	W903_0154	dnaK	chaperone protein DnaK
1.412512244	1.77015E-07	W903_0155		hypothetical protein
1.078934276	0.011676259	W903_0161		hypothetical protein
1.903226467	6.91699E-21	W903_0171		NAD-dependent glycerol-3-phosphate dehydrogenase family protein
2.600975055	5.58845E-18	W903_0173		sugar-binding protein
2.31804587	2.90856E-12	W903_0174		branched-chain amino acid transport system / permease component family protein
1.889853157	1.32695E-08	W903_0175		heme ABC exporter, ATP-binding protein CcmA
1.209686516	0.009182514	W903_0176	rbsD	D-ribose pyranase
1.797825719	0.006204462	W903_0183	argG	argininosuccinate synthase
1.388010347	2.22282E-05	W903_0186		L-2-hydroxyisocaproate dehydrogenase
1.17740199	0.001156656	W903_0195		hypothetical protein
1.066038903	0.001680448	W903_0247		HAD hydrolase, IA, variant 1 family protein
1.689694513	8.43823E-14	W903_0248		histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein
1.504455389	2.40738E-05	W903_0249		response regulator
3.663144472	1.17183E-44	W903_0250		lrgA family protein
4.447698363	1.17543E-94	W903_0251	lrgB	antiholin-like protein LrgB
2.165694591	8.6468E-17	W903_0257	treP	PTS system, trehalose-specific IIBC component
2.861309452	4.5682E-43	W903_0258	treC	alpha,alpha-phosphotrehalase
2.407230904	1.49493E-34	W903_0259		PRD domain protein
3.23255427	9.7954E-31	W903_0260		PTS system, Lactose/Cellobiose specific IIB subunit
3.363150788	3.12386E-40	W903_0261		PTS system sugar-specific permease component family protein
3.269872346	1.79205E-28	W903_0262		thiamine pyrophosphate enzyme, C-terminal TPP binding domain protein
3.306672849	4.73393E-25	W903_0263		transketolase, pyrimidine binding domain protein
1.640993562	4.90884E-08	W903_0280		virulence factor esxA
2.020474347	1.16898E-15	W903_0281		hypothetical protein
2.116030349	5.13855E-24	W903_0282		hypothetical protein
2.113562418	2.37075E-17	W903_0283		hypothetical protein
2.186261063	2.42432E-16	W903_0284		hypothetical protein
1.272922527	0.00072177	W903_0309		acetyltransferase domain protein
1.171667414	0.000675058	W903_0310		acetyltransferase family protein
1.259905893	3.88301E-05	W903_0311		acetyltransferase domain protein
1.142416828	0.027965228	W903_0313		RNA polymerase sigma factor, sigma-70 family protein
1.731315558	8.2482E-07	W903_0322	nagA	N-acetylglucosamine-6-phosphate deacetylase
2.584691658	1.09653E-31	W903_0329	glpK	glycerol kinase
3.384394824	4.02475E-60	W903_0330		FAD dependent oxidoreductase family protein

E41

3.173619681	4.29452E-39	W903_0331		MIP channel s family protein	
1.902655934	2.25893E-15	W903_0332		pyridine nucleotide-disulfide oxidoreductase family protein	
1.638912692	5.34845E-12	W903_0333		mga helix-turn-helix domain protein	
1.107365295	0.000876182	W903_0335		enterocin A Immunity family protein	
1.090816925	9.62141E-06	W903_0336		ABC transporter family protein	
1.106012885	8.5669E-07	W903_0337		putative membrane protein	
2.157946922	0.003582701	W903_0379		glycyl-radical enzyme activating family protein	
1.748472377	0.005262227	W903_0384		PTS system, lactose/cellobiose IIC component family protein	
2.836237921	2.13546E-22	W903_0385		glycyl radical enzyme, PFL2/glycerol dehydratase family protein	
2.657997695	1.38443E-09	W903_0386		transaldolase family protein	
2.772856522	3.31816E-11	W903_0387	gldA	glycerol dehydrogenase	
3.147499479	2.77117E-51	W903_0392	raiA	ribosomal subunit interface protein	
1.044535769	0.003075321	W903_0430		ABC transporter family protein	
1.198978966	2.9405E-06	W903_0431		bacterial ABC transporter EcsB family protein	
3.420745791	0.001312215	W903_0436		glycerophosphoryl diester phosphodiesterase family protein	
2.257430196	0.024176152	W903_0440		glycerophosphoryl diester phosphodiesterase family protein	
1.945999037	0.001260991	W903_0444		LPXTG cell wall anchor domain protein	
2.006702015	0.005189755	W903_0445		LPXTG cell wall anchor domain protein	
2.0491312	4.05978E-08	W903_0446		putative cross-wall-targeting lipoprotein signal	
1.36030164	1.1327E-05	W903_0448		hypothetical protein	
2.670517542	0.019216512	W903_0452		hypothetical protein	
1.571308931	0.024141662	W903_0453		AAA-like domain protein	
2.205858613	0.019324722	W903_0454		hypothetical protein	
2.042462772	0.026712989	W903_0456		peptidase M23 family protein	
1.788680748	0.020318962	W903_0463		hypothetical protein	
1.030604191	0.017617574	W903_0470		hypothetical protein	
1.433974327	3.05749E-05	W903_0478		copper transport repressor, CopY/TcrY family	
2.074589501	1.00874E-25	W903_0479		copper-translocating P-type ATPase	
2.282870075	9.47741E-16	W903_0480		heavy-metal-associated domain protein	
2.072102402	5.10074E-08	W903_0486		LPXTG cell wall anchor domain protein	
1.000870152	0.00545364	W903_0487		putative transcriptional activator CadC	
2.156710163	1.98347E-29	W903_0494		metallo-beta-lactamase superfamily protein	
2.350252767	1.6637E-25	W903_0495		cytidine and deoxycytidylate deaminase zinc-binding region family protein	
1.776843143	2.76267E-07	W903_0499		rhomboid family protein	
1.0518174	7.50035E-05	W903_0500		basic membrane family protein	
2.879340157	5.9612E-34	W903_0526		gyrI-like small molecule binding domain protein	
2.82726745	4.25263E-28	W903_0527		hypothetical protein	
2.56650954	3.16569E-24	W903_0528		carboxymuconolactone decarboxylase family protein	
2.648941558	1.24147E-22	W903_0529		cupin domain protein	
2.890584967	1.74912E-26	W903_0530	adhR	HTH-type transcriptional regulator AdhR	
2.392261838	2.50355E-30	W903_0531		zinc-binding dehydrogenase family protein	
2.487353626	4.73431E-20	W903_0532		aldo/keto reductase family protein	
2.234962711	1.57998E-09	W903_0533		cation diffusion facilitator transporter family protein	
2.282273104	1.115E-12	W903_0539		cupin domain protein	
2.583123732	3.10469E-18	W903_0540		cupin domain protein	
2.130605939	1.90645E-17	W903_0541		methyltransferase domain protein	
1.39979856	0.008659979	W903_0542		deoR-like helix-turn-helix domain protein	
1.773419739	4.77728E-05	W903_0543		phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 family protein	
2.689930173	4.04256E-11	W903_0544		PTS system, Lactose/Cellobiose specific IIB subunit	
3.11821918	9.7954E-31	W903_0545		PTS system sugar-specific permease component family protein	
3.052767086	1.85602E-27	W903_0546		class II Aldolase and Adducin N-terminal domain protein	
1.656365333	0.000149391	W903_0547		phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 family protein	
2.249132518	1.24411E-20	W903_0548		PTS system sugar-specific permease component family protein	
2.976671733	1.11099E-14	W903_0549		PTS system, Lactose/Cellobiose specific IIB subunit	
1.899848163	0.022554087	W903_0553		binding--dependent transport system inner membrane component family protein	
2.478234853	0.0039701	W903_0554		binding--dependent transport system inner membrane component family protein	
2.90733249	2.09318E-13	W903_0555		glycosyl hydrolases 31 family protein	

2.796457486	5.54196E-09	W903_0556	galK	galactokinase
3.045852931	2.12858E-10	W903_0557	galT	galactose-1-phosphate uridylyltransferase
2.104728343	4.01703E-05	W903_0558		UDP-glucose 4-epimerase GalE
2.643424997	1.97129E-07	W903_0559		aldose 1-epimerase family protein
1.597816515	0.000764	W903_0568		hypothetical protein
1.057723291	0.000132869	W903_0570		oxidoreductase, NAD-binding Rossmann fold family protein
1.05752532	0.004206156	W903_0579		5'-nucleotidase, C-terminal domain protein
1.615681861	4.79292E-13	W903_0608		hypothetical protein
2.523783939	8.2448E-27	W903_0610		istB-like ATP binding family protein
1.773105117	3.60477E-22	W903_0614		phosphoglucomutase/phosphomannomutase, C-terminal domain protein
1.150698535	9.46079E-08	W903_0617	xseA	exodeoxyribonuclease VII, large subunit
1.39496808	5.88959E-11	W903_0619		polyprenyl synthetase family protein
1.342922063	1.04604E-08	W903_0620		hemolysin TlyA family protein
1.399583795	8.4976E-06	W903_0621		arginine repressor, DNA binding domain protein
1.317289678	2.65277E-11	W903_0622	recN	DNA repair protein RecN
1.054323367	0.001788995	W903_0628		hypothetical protein
1.104535873	0.003814779	W903_0634		putative excisionase
2.40408743	0.000675058	W903_0635		hypothetical protein
1.164079858	0.000914007	W903_0638		AAA ATPase domain protein
1.026431192	0.006470314	W903_0639		AAA domain protein
1.196678067	0.00415907	W903_0640		putative phage protein
1.121716304	6.67899E-05	W903_0643		hypothetical protein
1.115467475	0.003072391	W903_0644		DEAD/DEAH box helicase family protein
1.256673101	0.009833728	W903_0646		glycerophosphoryl diester phosphodiesterase family protein
1.271004449	0.000810135	W903_0647		AAA domain protein
1.237251278	0.045072877	W903_0648		putative rNA polymerase sigma factor
1.295448285	0.000258191	W903_0649		endodeoxyribonuclease RusA family protein
1.10319063	0.042708675	W903_0651		hypothetical protein
1.240723834	0.016687681	W903_0652		phage transcriptional regulator, RinA family protein
1.1437769	0.00312847	W903_0654		terminase, small subunit
1.161354203	0.000828279	W903_0655		phage terminase, large subunit, PBSX family
1.385797499	2.8002E-05	W903_0656		phage portal protein, SPP1 family
1.585220649	5.53218E-06	W903_0657		phage head morphogenesis, SPP1 gp7 family domain protein
1.669033575	1.40827E-05	W903_0658		putative membrane protein
1.604626304	1.50081E-09	W903_0659		hypothetical protein
1.637508757	1.33849E-05	W903_0660		hypothetical protein
1.50090363	2.0719E-05	W903_0661		putative head protein
1.527083156	2.92161E-05	W903_0662		phage gp6-like head-tail connector family protein
1.764035718	1.22803E-09	W903_0663		hypothetical protein
1.361885054	0.000676143	W903_0664		hypothetical protein
1.474805899	3.0549E-05	W903_0665		putative phage protein
1.62238482	2.122E-06	W903_0666		phage major tail protein, TP901-1 family
1.635632356	1.02456E-06	W903_0667		phage family protein
1.646101338	9.60138E-09	W903_0668		hypothetical protein
1.607821516	6.3779E-07	W903_0669		tape measure domain protein
1.654726594	6.69682E-09	W903_0670		phage tail family protein
1.735978153	3.33326E-09	W903_0671		prophage endopeptidase tail family protein
1.777014676	6.84061E-09	W903_0672		gp58-like family protein
1.658824435	9.42928E-09	W903_0673		glycerophosphoryl diester phosphodiesterase family protein
1.572046967	2.39451E-07	W903_0674		hypothetical protein
1.484338907	2.4642E-06	W903_0675		hypothetical protein
1.84914023	2.67855E-07	W903_0676		putative phage protein
1.722158	1.08564E-08	W903_0677		holin, phage phi LC3 family
1.711079212	1.69435E-07	W903_0678		mannosyl-glycoendo-beta-N-acetylglucosaminidase family protein
1.115000545	0.000820279	W903_0679		hypothetical protein
1.33503149	0.001644695	W903_0680		csbD-like family protein
1.501526512	0.00410635	W903_0681		putative nicotinate phosphoribosyltransferase

1.169807235	1.38051E-05	W903_0688		putative hydrolase
1.505837529	3.3173E-11	W903_0689		HD domain protein
1.445244959	3.5672E-07	W903_0693	fbp	fructose-1,6-bisphosphatase class 3
1.396426637	4.02998E-09	W903_0694	queG	epoxyqueuosine reductase
3.542720506	1.28449E-87	W903_0700		acetoin reductases family protein
1.027390038	0.000475263	W903_0708		hypothetical protein
1.099342504	8.94544E-07	W903_0710	pepD	dipeptidase
1.148482432	2.95478E-05	W903_0713		DHHA1 domain protein
1.701215504	0.000105131	W903_0738		NUDIX domain protein
2.767718925	1.66517E-49	W903_0741		DNA/RNA non-specific endonuclease family protein
2.222674291	1.58811E-12	W903_0754		glycerophosphoryl diester phosphodiesterase family protein
2.538427512	2.65972E-37	W903_0755		glycerophosphoryl diester phosphodiesterase family protein
2.808110743	3.61242E-55	W903_0756		short chain dehydrogenase family protein
2.571371979	8.38501E-32	W903_0757		phosphopantetheine attachment site family protein
2.539538809	4.67113E-34	W903_0758		fabA-like domain protein
2.475844854	1.66235E-46	W903_0759		ABC transporter family protein
2.105358625	2.35506E-26	W903_0760		ABC-2 type transporter family protein
2.086994057	2.46855E-33	W903_0761		putative cylE
2.02766284	1.50966E-32	W903_0762		aminomethyltransferase folate-binding domain protein
1.952417307	1.54986E-31	W903_0763		beta-ketoacyl synthase, C-terminal domain protein
1.923984184	1.30597E-25	W903_0764		UDP-glucoronosyl and UDP-glucosyl transferase family protein
1.662377875	5.73343E-20	W903_0765		hypothetical protein
3.118439982	5.35176E-14	W903_0773		DNA/RNA non-specific endonuclease family protein
1.519182631	0.00011354	W903_0781	ldhD	D-lactate dehydrogenase
1.927706033	0.00021076	W903_0786		2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase family protein
2.437307851	1.17805E-14	W903_0787		glucuronate isomerase family protein
2.867243215	8.87395E-20	W903_0788	uxuA	mannonate dehydratase
2.562966773	2.42649E-11	W903_0789		hypothetical protein
2.043371518	1.84828E-06	W903_0790		HAD hydrolase, IA, variant 1 family protein
2.540493048	3.41638E-18	W903_0791		glycosyl hydrolase family 3 N terminal domain protein
1.011830079	5.77852E-08	W903_0792		metallopeptidase M24 family protein
2.94335458	4.002E-21	W903_0800		peptidase propeptide and YPEB domain protein
1.251101023	3.87276E-05	W903_0806		sensory box protein
1.270544884	0.002315455	W903_0820		pspC domain protein
1.403644579	7.37918E-13	W903_0822	hprK	HPr(Ser) kinase/phosphatase
1.621707555	4.41623E-18	W903_0823	lgt	prolipoprotein diacylglyceryl transferase
2.336944473	2.63461E-27	W903_0824		hypothetical protein
2.427513794	1.48816E-29	W903_0825		hypothetical protein
1.000954968	0.010139204	W903_0830		putative membrane protein
2.426521209	7.37339E-30	W903_0838		histidine phosphatase super family protein
1.171445886	0.002539989	W903_0839		bacteriocin-type signal sequence domain protein
1.569482439	0.000154372	W903_0878		methyltransferase domain protein
1.683405648	0.026782391	W903_0938		gtrA-like family protein
1.17520161	9.59329E-08	W903_0940	ligA	DNA ligase, NAD-dependent
1.447527198	3.82407E-09	W903_0941		lipid kinase, YegS/Rv2252/BmrU family protein
1.331449867	3.25453E-10	W903_0942	pulA	pullulanase, type I
3.397736489	1.66962E-88	W903_0943	glgB	1,4-alpha-glucan branching enzyme
3.899520314	3.97386E-95	W903_0944	glgC	glucose-1-phosphate adenylyltransferase
3.869588732	1.5009E-110	W903_0945	glgD	glucose-1-phosphate adenylyltransferase, GlgD subunit
3.717325366	1.4112E-106	W903_0946	glgA	glycogen/starch synthase, ADP-glucose type family protein
1.17337821	5.0423E-10	W903_0971		e3 binding domain protein
1.098306698	0.000229138	W903_0973		lipoyltransferase and lipoate-ligase family protein
1.701565839	1.70343E-17	W903_0985		HNH endonuclease family protein
1.736439589	3.72653E-16	W903_0986	cas1	CRISPR-associated endonuclease Cas1
1.892877784	2.01622E-07	W903_0987	cas2	CRISPR-associated endoribonuclease Cas2
2.047965393	9.45115E-23	W903_0988		CRISPR-associated family protein
1.992279479	2.26025E-13	W903_0989		hypothetical protein
2.503130559	9.95355E-14	W903_0990		glycerophosphoryl diester phosphodiesterase family protein

2.045429432	8.75013E-17	W903_1000		HAD ATPase, P-type, IC family protein
2.511163604	3.44898E-35	W903_1001		hypothetical protein
1.114593637	8.92121E-06	W903_1010		signal peptidase I
2.119759875	0.028548269	W903_1045		peptidase S41 family protein
1.389647569	1.74635E-05	W903_1049		histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein
1.074092813	4.46389E-05	W903_1072		hypothetical protein
1.734538523	6.03814E-10	W903_1075		ftsX-like permease family protein
1.150540585	0.005200057	W903_1076		ABC transporter family protein
1.482109114	0.017482957	W903_1096		hypothetical protein
1.945237302	1.41996E-12	W903_1102		carbon starvation CstA family protein
1.154367227	0.008834602	W903_1131	carB	carbamoyl-phosphate synthase, large subunit
1.350687028	1.6464E-05	W903_1139		ATP cone domain protein
2.565039966	2.2449E-29	W903_1207	ssdh	NAD-dependent aldehyde dehydrogenase
1.487770618	2.32658E-07	W903_1210		putative streptokinase-like protein
1.086386693	0.000953717	W903_1213		DNA alkylation repair enzyme family protein
1.805138687	6.15131E-15	W903_1214		HAD hydrolase, IIB family protein
2.620332922	4.37883E-45	W903_1215		deoR-like helix-turn-helix domain protein
3.274699965	1.4272E-88	W903_1216		asp23 family protein
3.385597593	3.68077E-87	W903_1217		csbD-like family protein
3.264101558	2.24951E-73	W903_1218		asp23 family protein
3.193479308	6.48096E-48	W903_1219		hypothetical protein
2.947877948	1.30182E-35	W903_1220		hypothetical protein
2.396245703	3.98665E-27	W903_1221		transglycosylase associated family protein
1.200985345	6.42014E-09	W903_1260		CRISPR-associated family protein
1.051408546	6.38412E-05	W903_1261	deoD	purine nucleoside phosphorylase
1.119341611	0.000571419	W903_1262		voltage gated chloride channel family protein
1.167151322	3.27001E-06	W903_1263		purine nucleoside phosphorylase I, inosine and guanosine-specific
1.209413727	4.64523E-06	W903_1295	hflX	GTP-binding protein HflX
1.211451143	0.000333572	W903_1296	miaA	tRNA dimethylallyltransferase
1.260417086	0.002948399	W903_1299		pullulanase, extracellular
1.831523106	4.68005E-06	W903_1318		putative ATP-dependent Clp protease ATP-binding subunit
1.141010895	0.006569918	W903_1334		glutathione S-transferase, C-terminal domain protein
1.263647584	0.018646592	W903_1343		hypothetical protein
2.279477475	1.50766E-39	W903_1344		LPXTG cell wall anchor domain protein
1.748365108	3.25453E-10	W903_1360	fruA	PTS system, fructose subfamily, IIA component domain protein
1.239514692	1.08068E-07	W903_1361	pfkB	1-phosphofructokinase
1.970985021	3.10051E-11	W903_1364		gram-positive signal peptide, YSIRK family domain protein
1.478373848	1.1592E-07	W903_1372		M trans-acting positive regulator (MGA) PRD domain protein
1.327874612	6.57229E-10	W903_1378		carbamoyl-phosphate synthase L chain, ATP binding domain protein
1.111851915	2.18101E-06	W903_1379		carbamoyl-phosphate synthase, small subunit
1.226482959	0.003099902	W903_1380	pyrR	bifunctional protein pyrR
1.445692204	1.4E-08	W903_1387		bacterial capsule synthesis PGA_cap family protein
1.399770785	1.18145E-09	W903_1402		hypothetical protein
1.334767817	3.24444E-05	W903_1404		putative pore forming protein
1.036506283	2.55131E-05	W903_1405	pepT	peptidase T
1.693959301	1.88698E-10	W903_1453	glgP	glycogen/starch/alpha-glucan phosphorylases family protein
1.184788596	0.00010931	W903_1454	malQ	4-alpha-glucanotransferase
2.020277092	2.40773E-23	W903_1456		bacterial extracellular solute-binding family protein
2.169469315	2.0077E-20	W903_1457		binding--dependent transport system inner membrane component family protein
2.512557272	4.51659E-34	W903_1458		binding--dependent transport system inner membrane component family protein
1.193877515	3.32497E-05	W903_1485		thermophilic metalloprotease family protein
1.834322677	7.21937E-10	W903_1489		aldo/keto reductase family protein
1.857849421	1.28448E-14	W903_1490		putative NAD(P)H nitroreductase yfkO
1.536916222	2.45782E-07	W903_1491	gloA	lactoylglutathione lyase
1.28271871	0.000159025	W903_1492		glycosyl transferase 2 family protein
1.147076148	0.019437677	W903_1501	mutM	formamidopyrimidine-DNA glycosylase
1.552685226	4.17739E-13	W903_1515		myosin-cross-reactive antigen family protein

1.276928882	0.033954635	W903_1521		ABC transporter family protein
1.300415227	0.043315726	W903_1523		binding--dependent transport system inner membrane component family protein
1.514926196	0.022060579	W903_1524		binding--dependent transport system inner membrane component family protein
1.362639627	8.71329E-08	W903_1538	scaR	metalloregulator ScaR
1.448946643	0.001232459	W903_1546		ASCH domain protein
1.821826446	0.000175109	W903_1547		hypothetical protein
1.113431497	0.006359424	W903_1548		short chain dehydrogenase family protein
1.601247549	0.001215832	W903_1549		hypothetical protein
1.054234556	0.035433479	W903_1550		putative ybaK/prolyl-tRNA synthetase associated domain-containing protein
1.149018597	2.76638E-09	W903_1600		inhibitor of apoptosis-promoting Bax1 family protein
1.046011634	4.39188E-06	W903_1601		hypothetical protein
1.22418596	0.005108609	W903_1603		acylphosphatase family protein
2.062342169	4.83352E-25	W903_1613		helicase domain protein
1.033130059	0.018632007	W903_1617	nrdR	transcriptional regulator NrdR
3.029513177	2.61885E-31	W903_1631		zinc-binding dehydrogenase family protein
2.875335522	2.89235E-13	W903_1641	dhaK	dihydroxyacetone kinase, DhaK subunit
3.005914027	2.37838E-14	W903_1642	dhaL	dihydroxyacetone kinase, L subunit
2.900882642	2.31796E-16	W903_1643	dhaM	PTS-dependent dihydroxyacetone kinase, phosphotransferase subunit dhaM
2.779795292	7.47861E-16	W903_1644		MIP channel s family protein
1.170015238	6.24085E-06	W903_1645		cupin domain protein
2.34356666	2.95233E-09	W903_1661	ppdK	pyruvate, phosphate dikinase
1.668577384	1.51928E-05	W903_1664		NAD-dependent glycerol-3-phosphate dehydrogenase family protein
3.126806836	4.42806E-41	W903_1668		universal stress family protein
2.936272251	1.64882E-16	W903_1680		ROK family protein
3.23808446	1.30893E-59	W903_1681		PTS system, sucrose-specific IIBC component
1.518789904	4.21705E-08	W903_1682		sucrose-6-phosphate hydrolase family protein
2.023989375	1.75632E-11	W903_1683		helix-turn-helix family protein
1.255501562	0.021454179	W903_1687		glycerophosphoryl diester phosphodiesterase family protein
1.007666806	0.033118663	W903_1688		hypothetical protein
1.605996435	9.56335E-07	W903_1715		impB/mucB/samB family protein
2.620645601	3.22886E-37	W903_1716	pflB	formate acetyltransferase
2.21894548	3.77035E-23	W903_1717		FMN-binding protein
2.287563401	0.000685019	W903_1734		hypothetical protein
1.150443047	0.000159568	W903_1737		methyltransferase domain protein
1.317132503	5.75145E-14	W903_1756		phosphoglycerate kinase family protein
2.375920367	4.2032E-25	W903_1757		5'-nucleotidase, lipoprotein e(P4) family
2.338660352	3.15673E-15	W903_1789	xpkA	xylulose-5-phosphate phosphoketolase
2.247470126	4.1817E-17	W903_1790		beta-lactamase superfamily domain protein
2.525588059	0.012872409	W903_1793		badF/BadG/BcrA/BcrD ATPase family protein
2.580317094	0.000154372	W903_1794		amidohydrolase family protein
3.13110154	1.59862E-07	W903_1795		PTS system sugar-specific permease component family protein
3.111767342	2.86665E-09	W903_1796	gyaR	glyoxylate reductase
2.185872943	0.000120878	W903_1797		hypothetical protein
2.259792743	4.98015E-06	W903_1799	fsa	fructose-6-phosphate aldolase
2.306673548	9.62428E-08	W903_1800		class II Aldolase and Adducin N-terminal domain protein
2.126406086	2.31781E-05	W903_1801		xylose isomerase-like TIM barrel family protein
1.977014031	5.22662E-07	W903_1802		orotidine 5'-phosphate decarboxylase / HUMPS family protein
1.413430505	0.005331261	W903_1803	ulaC	ascorbate-specific phosphotransferase enzyme IIA component
1.696224167	0.000177525	W903_1804	ulaB	ascorbate-specific phosphotransferase enzyme IIB component
2.510950633	5.85824E-30	W903_1823	ahpC	peroxiredoxin
2.800301225	8.73482E-34	W903_1824	ahpF	alkyl hydroperoxide reductase subunit F
1.727890075	0.011391168	W903_1835		heparinase II/III-like family protein
3.013938023	1.34042E-10	W903_1836		PTS system mannose/fructose/sorbose IID component family protein
3.137258128	8.99655E-11	W903_1837		PTS system sorbose-specific iic component family protein
2.818716761	0.000201219	W903_1838		PTS system sorbose subIIB component family protein
2.636048234	1.91087E-06	W903_1839		unsaturated glucuronyl hydrolase
2.052197175	0.020532942	W903_1841		short chain dehydrogenase family protein

2.654343851	0.001505243	W903_1843		pfkB carbohydrate kinase family protein
3.80380928	0.000105414	W903_1844		2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase family protein
3.351179911	4.00422E-19	W903_1855		malic enzyme, NAD binding domain protein
2.686851855	9.94901E-15	W903_1856		citrate carrier, CCS family protein
1.369438945	9.51904E-06	W903_1857		putative sensor kinase dpiB
2.084056612	3.01693E-07	W903_1858		response regulator
1.573191722	1.56451E-08	W903_1860	dexB	glucan 1,6-alpha-glucosidase
4.16854036	6.85679E-38	W903_1863		aldose 1-epimerase family protein
4.359487079	2.24586E-72	W903_1864	lacD	tagatose 1,6-diphosphate aldolase
4.205088433	6.44939E-95	W903_1865	lacC	tagatose-6-phosphate kinase
3.70336727	6.639E-68	W903_1866	lacB	galactose-6-phosphate isomerase, LacB subunit
3.305501068	1.58333E-66	W903_1867	lacA	galactose-6-phosphate isomerase, LacA subunit
1.495733384	5.0423E-10	W903_1868		BNR repeat-like domain protein
3.998170503	1.10984E-85	W903_1869		PTS system sugar-specific permease component family protein
3.806537282	5.37225E-54	W903_1870		PTS system, Lactose/Cellobiose specific IIB subunit
3.515499202	1.48078E-74	W903_1871		phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 family protein
2.648691665	3.57593E-28	W903_1872		deoR C terminal sensor domain protein
2.895051713	1.52384E-19	W903_1877	yfkN	trifunctional nucleotide phosphoesterase protein YfkN
1.878372722	2.48791E-09	W903_1882		bacterial extracellular solute-binding family protein
2.1177586	1.40412E-08	W903_1883		response regulator
2.320078124	4.02418E-13	W903_1884		histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein
3.748199832	2.34314E-24	W903_1885		PTS system mannose/fructose/sorbose IID component family protein
3.393337919	1.45002E-19	W903_1886		PTS system sorbose-specific iic component family protein
3.330184609	4.56713E-12	W903_1887		putative phosphotransferase enzyme IIB component
2.175597455	1.11478E-08	W903_1888		PTS system fructose IIA component family protein
2.474209208	1.1355E-13	W903_1895		endonuclease/Exonuclease/phosphatase family protein
2.397804262	2.54813E-30	W903_1896	ptbA	PTS system, glucose subfamily, IIA component domain protein
1.272820559	0.011392721	W903_1898		putative transcriptional activator CadC
1.295221716	2.55732E-05	W903_1906		RNA methyltransferase, RsmE family protein
1.261578549	0.000167466	W903_1907	prmA	ribosomal protein L11 methyltransferase
2.791828176	4.74769E-26	W903_1910		hypothetical protein
2.457406725	2.02327E-13	W903_1911		helix-turn-helix family protein
1.100944644	0.000879733	W903_1917		lipase family protein
1.239247145	0.001451659	W903_1918		hypothetical protein
2.33035926	4.75739E-06	W903_1919		hypothetical protein
2.255961428	7.66743E-07	W903_1926		putative membrane protein
1.418698617	0.000475263	W903_1932		streptomycin adenylyltransferase family protein
1.08594743	0.04106164	W903_1937		acetyltransferase family protein
1.673461893	0.000427968	W903_1938		ABC-2 transporter family protein
1.068889851	0.044277538	W903_1939		ABC transporter family protein
1.522782853	0.000745867	W903_1941		helix-turn-helix family protein
1.461877937	0.008759376	W903_1945		putative lysine decarboxylase family protein
1.935031589	2.83717E-11	W903_1947		rhodanese-like domain protein
1.471807872	3.34625E-06	W903_1948		protein B
1.185202367	0.036359144	W903_1960		response regulator
1.38447661	0.001334609	W903_1961		his Kinase A domain protein
1.445885621	0.000879733	W903_1962		putative exported protein
1.291023205	0.000121378	W903_1965		patatin-like phospholipase family protein
2.045549719	2.07071E-23	W903_1967		LPXTG cell wall anchor domain protein
2.091270171	1.356E-11	W903_1974	deoC	deoxyribose-phosphate aldolase
2.007753456	3.00766E-21	W903_1975		na+ dependent nucleoside transporter family protein
2.010366969	2.85637E-14	W903_1976	udp	uridine phosphorylase
1.753505172	7.69561E-11	W903_1983		HAD hydrolase, IIB family protein
3.047708859	0.006390605	W903_2019		ftsK/SpoIIIE family protein
1.365967308	0.006281996	W903_2030		histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein
1.788808695	0.001078314	W903_2031		response regulator
1.365089437	5.81588E-10	W903_2034		hypothetical protein
1.017073142	1.85201E-05	W903_2035		alpha/beta hydrolase fold family protein

1.017073142	1.85201E-05	W903_2035		alpha/beta hydrolase fold family protein	
1.375774789	3.03417E-07	W903_2048	sdaAB	L-serine dehydratase, iron-sulfur-dependent, beta subunit	
1.859129922	1.97864E-25	W903_2049	sdaAA	L-serine dehydratase, iron-sulfur-dependent, alpha subunit	
1.768147655	8.67151E-10	W903_2063		arginine regulator	
1.235518737	0.000175109	W903_2064		cyclic nucleotide-binding domain protein	
3.48905717	8.03258E-72	W903_2066	arcA	arginine deiminase	
3.8591757	3.34856E-55	W903_2067		acetyltransferase family protein	
3.856857227	4.18167E-60	W903_2068		ornithine carbamoyltransferase	
3.991534722	3.11702E-72	W903_2069	arcD	arginine-ornithine antiporter	
3.821921525	3.9178E-71	W903_2070		carbamate kinase	