Additional file 5: Clusters of differential expressed genes in *C. beijerinckii* DSM6423 glucose fermentation

Clusters	**genes**	
name	**nb**	**%**
6up++	18	44%
6up+	58	21%
6up	431	1%
6down	203	21%
6down-	14	6%
8up+	8	2%
8up	206	0%
8down	6	1%
11up	23	1%
Unclassified	20	2%
TOTAL	987	

Genes	**Cluster**	**log2(FC vs T3h)**				**functional annotation**	
ID	name	T6/T3	T8/T3	T11/T3	T24/T3	gene name	function
CIBE_0313	6up++	5.3	6.2	7.2	5.8	-	conserved protein of unknown function
CIBE_0312	6up++	5.0	6.3	7.4	5.6	-	conserved protein of unknown function
CIBE_0311	6up++	5.0	6.4	7.0	5.3	-	conserved protein of unknown function
CIBE_0314	6up++	4.1	5.9	7.0	5.8	-	conserved protein of unknown function
CIBE_0315	6up++	5.1	5.9	6.1	5.0	-	Radical SAM-family protein
CIBE_0310	6up++	4.7	6.3	5.9	4.6	-	putative ABC transporter ATP-binding protein
CIBE_3477	6up++	5.5	5.6	5.4	4.4	-	Accessory gene regulator B
CIBE_3478	6up++	5.3	5.8	5.0	4.3	-	conserved membrane protein of unknown function
CIBE_0316	6up++	4.5	5.5	5.6	4.2	-	conserved protein of unknown function
CIBE_4430	6up++	4.4	6.4	5.4	3.6	-	putative permease
CIBE_4429	6up++	3.7	5.7	4.8	3.5	-	putative permease
CIBE_0280	6up++	4.5	4.9	4.3	3.9	-	conserved exported protein of unknown function
CIBE_3828	6up++	4.4	5.6	4.4	3.2	-	Glycosyl transferase
CIBE_4431	6up++	2.7	5.4	5.5	3.6	-	conserved exported protein of unknown function
CIBE_4419	6up++	3.7	5.5	4.4	3.1	-	conserved exported protein of unknown function
CIBE_4428	6up++	3.1	5.4	4.7	3.2	glr	Transporter
CIBE_4418	6up++	3.4	5.4	4.4	2.4	-	conserved exported protein of unknown function
CIBE_3476	6up+	4.4	4.6	4.3	3.6	-	conserved protein of unknown function
CIBE_3751	6up+	3.8	5.2	3.8	3.1	-	conserved protein of unknown function
CIBE_3750	6up+	3.9	4.6	3.7	3.4	-	conserved protein of unknown function
CIBE_4789	6up+	3.7	4.3	3.9	3.5	cfg	putative AgrB-like protein
CIBE_0824	6up+	4.8	3.9	3.8	2.7	-	Type 11 methyltransferase
CIBE_3749	6up+	4.1	4.4	3.5	2.8	-	Peptide synthetase
CIBE_5303	6up+	4.6	4.0	3.1	2.7	-	conserved protein of unknown function
CIBE_2622	6up+	2.8	3.7	3.9	4.0	adh	NADPH-dependent butanol dehydrogenase
CIBE_4040	6up+	3.0	3.3	4.1	3.7	-	Aliphatic sulfonates family ABC transporter, periplsmic ligand-binding protein
CIBE_3079	6up+	4.3	3.5	3.3	2.8	panD	aspartate 1-decarboxylase
CIBE_4039	6up+	2.9	3.2	3.9	4.1	tauB	taurine transporter subunit ; ATP-binding component of ABC superfamily
CIBE_3082	6up+	4.2	3.4	3.0	2.9	-	conserved protein of unknown function
CIBE_4610	6up+	2.1	4.1	4.1	3.3	-	Peptidase C1A, papain
CIBE_4417	6up+	3.1	4.7	3.5	2.2	-	conserved membrane protein of unknown function
CIBE_3475	6up+	3.5	3.7	3.4	2.8	-	Histidine kinase
CIBE_4036	6up+	2.7	3.0	3.9	3.7	-	Thioredoxin reductase
CIBE_3355	6up+	3.8	3.0	3.1	3.3	-	RNA polymerase sigma factor SigI
CIBE_3081	6up+	4.1	3.4	2.9	2.8	panB	ketopantoate hydroxymethyltransferase
CIBE_4038	6up+	2.8	2.8	3.8	3.7	-	Type I phosphodiesterase/nucleotide pyrophosphatase
CIBE_2623	6up+	2.6	3.3	3.8	3.3	-	conserved protein of unknown function
CIBE_5304	6up+	4.3	3.6	2.7	2.4	-	conserved protein of unknown function
CIBE_3537	6up+	2.9	4.5	2.5	3.1	-	putative transcriptional regulator
CIBE_5707	6up+	3.0	3.4	3.6	2.9	-	conserved protein of unknown function
CIBE_0782	6up+	2.2	2.8	3.7	4.1	-	Nitrogenase
CIBE_4041	6up+	2.3	3.1	3.8	3.6	tauC	taurine transporter subunit ; membrane component of ABC superfamily
CIBE_2624	6up+	2.2	3.3	3.8	3.5	sudA	Sulfide dehydrogenase subunit alpha
CIBE_3080	6up+	4.0	3.3	3.1	2.3	panC	pantothenate synthetase
CIBE_3353	6up+	3.5	2.7	2.7	3.4	-	Beta-glucanase (fragment)
CIBE_4861	6up+	1.9	3.8	3.2	3.4	-	conserved protein of unknown function
CIBE_3700	6up+	1.2	3.3	3.9	3.9	-	YIEGIA protein
CIBE_3753	6up+	3.1	3.6	2.4	3.1	-	protein of unknown function
CIBE_3354	6up+	3.8	2.9	2.6	2.8	bglA	Beta-glucanase
CIBE_3748	6up+	3.7	3.7	2.7	2.0	-	putative cyclic peptide transporter
CIBE_4416	6up+	3.2	4.3	3.2	1.2	-	conserved membrane protein of unknown function
CIBE_1176	6up+	4.3	3.3	2.6	1.7	rplY	50S ribosomal protein L25
CIBE_4788	6up+	3.2	3.5	2.6	2.4	-	CHAP domain containing protein
CIBE_3357	6up+	4.2	2.8	2.3	2.5	-	Carbohydrate-binding family V/XII
CIBE_2891	6up+	3.7	3.1	2.3	2.6	-	Electron transport complex, RnfABCDGE type, D subunit
CIBE_6013	6up+	4.4	3.5	1.9	1.7	-	conserved protein of unknown function
CIBE_0281	6up+	3.7	3.9	3.3	0.7	-	conserved membrane protein of unknown function
CIBE_4862	6up+	1.8	3.3	3.1	3.3	-	2-hydroxyglutaryl-CoA dehydratase
CIBE_5605	6up+	2.2	2.8	3.5	3.0	-	conserved protein of unknown function
CIBE_2892	6up+	3.8	3.0	2.2	2.3	-	Electron transport complex, RnfABCDGE type, G subunit
CIBE_5208	6up+	3.0	2.9	3.1	2.4	-	Nucleotidyl transferase
CIBE_0725	6up+	2.5	2.9	3.1	2.5	cstA	carbon starvation-induced membrane protein
CIBE_3837	6up+	3.0	3.7	2.1	2.2	yqaJ	putative nuclease; skin element
CIBE_4414	6up+	2.7	3.7	2.8	1.7	-	Cell wall-associated hydrolase-like protein
CIBE_4037	6up+	2.2	2.3	3.5	2.8	-	Thioredoxin domain
CIBE_5606	6up+	2.2	2.7	3.2	2.8	-	Membrane spanning protein
CIBE_3761	6up+	3.7	2.9	2.4	1.4	-	Multidrug transporter MatE
CIBE_3441	6up+	1.6	3.4	3.1	2.4	-	ABC transporter substrate-binding protein
CIBE_2221	6up+	1.1	3.7	3.5	2.0	ytfJ	Uncharacterized spore protein YtfJ
CIBE_2951	6up+	1.4	3.5	2.8	2.3	-	conserved protein of unknown function
CIBE_2222	6up+	1.4	3.5	3.0	1.6	-	conserved membrane protein of unknown function
CIBE_3534	6up+	1.4	3.3	2.3	2.0	-	putative DnaD-like protein, phage replisome organizer

CIBE_4415	6up+	2.4	3.5	2.6	0.5	-	conserved protein of unknown function
CIBE_0309	6up+	1.4	3.2	2.4	1.1	-	protein of unknown function
CIBE_3352	6up	3.7	3.0	2.1	3.2	-	conserved protein of unknown function
CIBE_3401	6up	3.1	2.8	2.2	3.8	-	conserved protein of unknown function
CIBE_3752	6up	2.9	3.4	2.3	3.1	-	protein of unknown function
CIBE_2321	6up	3.6	2.6	2.5	2.7	-	Membrane-like protein
CIBE_2893	6up	3.6	2.9	2.3	2.5	-	Electron transport complex subunit E
CIBE_0460	6up	1.9	1.7	0.0	-0.2	-	conserved protein of unknown function
CIBE_4600	6up	2.6	1.9	1.1	1.5	-	conserved protein of unknown function
CIBE_3469	6up	2.9	2.8	2.6	2.5	-	conserved protein of unknown function
CIBE_2894	6up	3.4	3.0	2.1	2.1	rsxA	putative inner membrane subunit of an electron transport system
CIBE_4602	6up	2.8	1.3	0.9	0.0	-	ThiJ/PfpI domain protein
CIBE_2895	6up	3.5	2.8	2.1	2.2	-	Protein RnfB
CIBE_3350	6up	3.9	2.3	2.0	2.4	-	Beta and gamma crystallin
CIBE_3770	6up	3.2	2.8	2.7	1.8	-	Multi-sensor signal transduction histidine kinase
CIBE_3468	6up	2.6	2.6	2.5	2.7	sudA	Sulfide dehydrogenase subunit alpha
CIBE_3356	6up	3.6	2.2	1.4	3.3	-	Glycoside hydrolase, family 18 (modular protein)
CIBE_2889	6up	3.2	2.7	2.2	2.2	-	Positive regulator of sigma E, RseC/MucC
CIBE_6055	6up	2.7	2.0	1.6	4.0	pdxS	glutamine amidotransferase for pyridoxal phosphate synthesis
CIBE_3769	6up	2.8	2.6	3.0	1.9	-	conserved protein of unknown function
CIBE_4538	6up	2.4	2.2	2.7	2.9	-	RNA polymerase, sigma-24 subunit, ECF subfamily
CIBE_5205	6up	2.9	2.5	2.8	1.9	phnW	2-aminoethylphosphonate--pyruvate transaminase
CIBE_0282	6up	3.0	3.3	2.4	1.5	-	conserved membrane protein of unknown function
CIBE_6021	6up	3.5	2.6	2.1	1.9	-	conserved exported protein of unknown function
CIBE_p0005	6up	3.8	2.5	1.8	2.0	-	putative Peptidase M10A and M12B matrixin and adamalysin
CIBE_3470	6up	2.6	2.4	2.5	2.4	adh	NADP-dependent isopropanol dehydrogenase
CIBE_3827	6up	3.1	3.2	1.7	2.0	-	protein of unknown function
CIBE_5206	6up	2.8	2.5	2.6	2.0	-	Phosphoenolpyruvate decarboxylase
CIBE_3176	6up	2.8	2.5	2.0	2.7	-	Coagulation factor 5/8 type domain protein
CIBE_3835	6up	2.7	3.2	1.8	2.2	-	putative Phage replisome organizer
CIBE_6054	6up	2.5	1.8	1.5	4.0	pdxT	glutamine amidotransferase for pyridoxal phosphate synthesis
CIBE_3351	6up	3.4	2.5	2.0	1.9	-	Chitinase
CIBE_3419	6up	3.5	2.5	2.0	1.7	-	conserved protein of unknown function
CIBE_4603	6up	2.8	1.5	0.8	0.1	-	protein of unknown function
CIBE_5207	6up	2.7	2.4	2.5	1.9	-	Cytidyltransferase-related domain
CIBE_0579	6up	1.7	2.9	2.7	2.3	spoIIID	transcriptional regulator
CIBE_2890	6up	3.1	2.3	2.0	2.1	rnfC	Electron transport complex subunit RnfC
CIBE_0283	6up	2.6	3.1	2.5	1.3	yybJ	putative ATP-binding cassette protein
CIBE_3110	6up	3.2	2.6	0.9	2.9	-	protein of unknown function
CIBE_3194	6up	3.4	2.0	2.0	2.1	-	GCN5-related N-acetyltransferase
CIBE_3909	6up	3.2	2.2	1.9	2.2	-	protein of unknown function
CIBE_5701	6up	2.7	2.3	1.9	2.5	-	Glutamine transport ATP-binding protein GlnQ (fragment)
CIBE_1173	6up	2.5	1.8	2.0	3.0	-	Membrane protein
CIBE_6000	6up	2.6	2.3	2.5	1.9	-	GntR family transcriptional regulator
CIBE_5300	6up	3.2	2.3	1.8	2.0	-	FHA domain containing protein
CIBE_5290	6up	3.9	2.4	1.8	1.1	-	conserved protein of unknown function
CIBE_2455	6up	2.2	3.4	1.7	1.9	-	conserved protein of unknown function
CIBE_2050	6up	3.5	2.5	1.6	1.6	adh	NADPH-dependent butanol dehydrogenase
CIBE_3200	6up	3.5	2.3	1.8	1.5	-	Cytidine deaminase
CIBE_0834	6up	2.7	2.5	1.9	2.0	amyA	Alpha-amylase
CIBE_1313	6up	3.3	2.5	2.1	1.3	-	conserved exported protein of unknown function
CIBE_5299	6up	3.2	2.3	2.0	1.5	-	Protein phosphatase
CIBE_misc_RNA_38	6up	2.8	2.5	1.9	1.8	-	TPP
CIBE_3423	6up	3.0	1.9	1.8	2.3	-	Amino acid adenylation domain protein
CIBE_misc_RNA_6	6up	2.0	2.7	2.2	2.1	-	ydaO-yuaA
CIBE_3421	6up	2.8	1.9	1.9	2.3	-	Long-chain-fatty-acid--(Acyl-carrier-protein) ligase., 6-deoxyerythronolide-B synthase
CIBE_p0006	6up	3.2	2.5	1.7	1.5	-	exported protein of unknown function
CIBE_3169	6up	3.1	2.6	1.6	1.4	ycbN	putative ABC efflux transporter (ATP-binding protein)
CIBE_1314	6up	3.5	2.4	1.3	1.5	-	protein of unknown function
CIBE_6115	6up	1.6	3.2	1.8	2.0	yyaC	conserved hypothetical protein
CIBE_6012	6up	3.5	2.3	1.4	1.3	-	conserved protein of unknown function
CIBE_3109	6up	2.9	2.0	0.9	2.9	-	conserved protein of unknown function
CIBE_5297	6up	3.0	2.0	2.0	1.6	-	Normocyte binding protein 2b
CIBE_3434	6up	2.9	2.1	1.5	2.1	lctP	L-lactate permease
CIBE_5706	6up	2.4	2.5	2.2	1.4	lagD	Lactococcin-G-processing and transport ATP-binding protein LagD
CIBE_5291	6up	3.4	2.0	1.9	1.2	-	conserved protein of unknown function
CIBE_5288	6up	3.4	2.2	1.8	1.2	-	conserved protein of unknown function
CIBE_4321	6up	1.9	2.2	2.3	2.1	-	RNA polymerase subunit sigma-24
CIBE_6020	6up	3.3	2.6	1.7	0.9	-	conserved protein of unknown function
CIBE_3420	6up	3.1	2.1	1.8	1.5	-	FMN-binding protein
CIBE_0019	6up	1.9	3.1	1.8	1.6	-	conserved protein of unknown function
CIBE_4317	6up	2.8	2.1	1.5	2.0	-	conserved protein of unknown function
CIBE_5296	6up	3.2	2.2	1.9	1.2	-	conserved protein of unknown function
CIBE_5286	6up	3.3	2.0	1.6	1.5	-	YD repeat protein (fragment)
CIBE_1337	6up	1.0	2.8	2.4	2.2	-	conserved membrane protein of unknown function
CIBE_4539	6up	2.1	1.6	2.2	2.5	-	conserved protein of unknown function
CIBE_5302	6up	3.2	2.2	1.6	1.4	-	Heat shock protein DnaJ domain protein
CIBE_1004	6up	1.5	3.3	1.2	2.4	-	conserved exported protein of unknown function
CIBE_5294	6up	3.6	2.2	1.8	0.8	-	conserved protein of unknown function
CIBE_6065	6up	3.0	2.3	1.3	1.7	-	protein of unknown function
CIBE_5999	6up	2.5	1.7	2.3	1.8	-	SAM-dependent methyltransferase
CIBE_1287	6up	1.6	1.9	2.0	2.7	-	Glycosyl transferase
CIBE_1294	6up	1.7	2.0	2.1	2.6	-	membrane protein of unknown function
CIBE_3203	6up	3.3	2.0	1.4	1.5	-	Valyl-tRNA synthetase (fragment)
CIBE_3247	6up	2.9	1.8	1.8	1.8	-	Acetolactate synthase
CIBE_6011	6up	3.2	2.3	1.3	1.5	-	conserved protein of unknown function
CIBE_4689	6up	1.7	1.7	1.9	3.0	-	Alcohol dehydrogenase GroES domain protein
CIBE_5301	6up	2.9	2.2	1.6	1.5	-	conserved protein of unknown function
CIBE_1847	6up	2.6	3.3	1.6	0.5	-	putative pilus biogenesis protein
CIBE_2425	6up	2.7	2.2	1.5	1.7	-	putative molybdenum-pterin-binding protein
CIBE_5287	6up	3.1	1.9	1.7	1.4	-	conserved protein of unknown function

CIBE_5705	6up	2.2	2.4	2.2	1.3	-	conserved protein of unknown function
CIBE_3762	6up	3.0	2.0	1.4	1.7	-	Helix-turn-helix-domain containing protein, AraC type
CIBE_3641	6up	2.2	2.3	1.7	1.9	-	conserved protein of unknown function
CIBE_5295	6up	3.3	1.9	1.6	1.1	-	Molecular chaperone
CIBE_3766	6up	2.3	2.1	2.2	1.3	-	conserved protein of unknown function
CIBE_5804	6up	2.0	2.6	1.6	1.8	-	protein of unknown function
CIBE_4320	6up	1.8	2.0	2.1	1.9	-	conserved protein of unknown function
CIBE_4537	6up	2.0	1.6	2.2	2.1	-	conserved membrane protein of unknown function
CIBE_2940	6up	3.1	2.0	1.3	1.4	-	Lactate racemization operon protein LarA
CIBE_0284	6up	2.3	3.0	2.4	0.2	-	conserved protein of unknown function
CIBE_6001	6up	2.4	1.9	2.1	1.5	-	conserved protein of unknown function
CIBE_5042	6up	2.1	1.5	2.1	2.0	-	Sulfate adenylyltransferase
CIBE_4315	6up	2.9	1.8	1.4	1.7	-	conserved protein of unknown function
CIBE_3435	6up	2.9	2.1	1.4	1.4	-	Electron transfer flavoprotein, alpha subunit-like protein
CIBE_4919	6up	3.1	2.5	1.5	0.6	-	SAM-dependent methyltransferase
CIBE_3422	6up	2.6	1.9	1.8	1.5	-	Major facilitator superfamily MFS_1
CIBE_3167	6up	2.7	1.8	1.1	2.1	-	protein of unknown function
CIBE_2391	6up	0.9	2.4	2.5	1.8	xerD	Tyrosine recombinase XerD
CIBE_1297	6up	1.6	2.2	1.9	1.8	-	Polysaccharide biosynthesis protein
CIBE_4604	6up	3.6	2.4	0.9	0.7	-	conserved membrane protein of unknown function
CIBE_0792	6up	1.0	1.1	2.7	2.8	mccB	cystathionine gamma-lyase and homocysteine gamma-lyase for reverse transsulfuration pathway
CIBE_4729	6up	3.0	1.9	1.5	1.1	-	conserved exported protein of unknown function
CIBE_3637	6up	2.8	2.5	0.8	1.3	-	protein of unknown function
CIBE_6002	6up	2.4	1.7	1.8	1.6	-	Membrane protein
CIBE_4690	6up	1.8	1.4	1.7	2.5	-	Aminotransferase class-III
CIBE_5044	6up	2.0	1.4	2.1	2.0	-	Adenylylsulfate reductase subunit beta
CIBE_4730	6up	2.9	1.9	1.6	1.0	-	Transcriptional regulator, MerR family
CIBE_5050	6up	1.8	1.4	2.1	2.1	sbp	sulfate transporter subunit ; periplasmic-binding component of ABC superfamily
CIBE_0829	6up	2.4	2.2	1.6	1.1	-	conserved protein of unknown function
CIBE_1292	6up	1.5	1.5	1.9	2.4	-	Glycosyl transferase family 2
CIBE_4168	6up	2.2	1.8	1.7	1.6	-	4Fe-4S ferredoxin
CIBE_0046	6up	0.6	2.4	2.2	2.1	-	conserved membrane protein of unknown function
CIBE_3248	6up	2.7	1.4	1.8	1.4	-	NADH:flavin oxidoreductase/NADH oxidase
CIBE_4195	6up	2.3	1.9	1.5	1.6	-	conserved protein of unknown function
CIBE_3197	6up	2.6	1.7	1.8	1.2	-	conserved exported protein of unknown function
CIBE_3432	6up	2.8	1.8	1.3	1.3	acdA	acyl-CoA dehydrogenase
CIBE_5043	6up	2.0	1.3	2.0	2.0	cysD	sulfate adenylyltransferase, subunit 2
CIBE_1115	6up	2.7	2.2	1.2	1.1	-	Fucose 4-O-acetylase
CIBE_3343	6up	2.9	1.5	1.2	1.5	-	protein of unknown function
CIBE_0103	6up	0.7	2.5	2.2	1.8	-	YabP family protein
CIBE_3086	6up	2.7	2.0	1.5	0.8	fabG	3-oxoacyl-[acyl-carrier-protein] reductase FabG
CIBE_2160	6up	0.8	2.4	2.5	1.4	-	Cobalamin synthesis protein, P47K
CIBE_3344	6up	2.8	1.9	1.4	1.1	-	protein of unknown function
CIBE_2454	6up	1.9	2.9	1.1	1.3	-	protein of unknown function
CIBE_2805	6up	2.5	1.9	1.7	1.0	-	GCN5-related N-acetyltransferase
CIBE_3747	6up	1.6	2.3	1.9	1.3	grsB	Gramicidin S synthase 2
CIBE_5298	6up	2.5	1.8	1.6	1.2	-	Serine/threonine protein phosphatase
CIBE_3251	6up	3.5	2.1	1.1	0.4	-	conserved exported protein of unknown function
CIBE_4606	6up	3.2	2.7	2.6	2.5	eutE	Ethanolamine utilization protein EutE
CIBE_2390	6up	0.8	2.4	2.3	1.6	-	Sporulation stage II, protein M
CIBE_3198	6up	3.2	2.2	0.1	1.6	-	conserved exported protein of unknown function
CIBE_3433	6up	2.7	1.8	1.3	1.3	-	2-hydroxy-acid oxidase
CIBE_5289	6up	3.3	1.7	1.2	0.8	-	conserved protein of unknown function
CIBE_2942	6up	2.3	2.0	1.4	1.3	-	Transcriptional regulator
CIBE_1296	6up	1.6	1.7	1.7	2.0	-	Glycosyltransferase
CIBE_5292	6up	3.1	1.8	1.5	0.6	-	conserved protein of unknown function
CIBE_1367	6up	1.5	1.8	1.9	1.7	phoU	Phosphate-specific transport system accessory protein PhoU homolog
CIBE_4731	6up	2.8	2.0	1.6	0.5	-	Acetyltransferase
CIBE_3786	6up	2.0	1.9	1.4	1.7	-	Ser/Thr phosphatase family protein
CIBE_1357	6up	1.8	2.2	1.5	1.4	sigG	RNA polymerase sporulation-specific sigma factor (sigma-G)
CIBE_2403	6up	1.6	1.8	2.0	1.6	hyuA	D-stereospecific phenylhydantoinase
CIBE_4820	6up	2.4	2.0	1.6	0.9	pepO	Neutral endopeptidase PepO
CIBE_2751	6up	1.7	1.3	1.7	2.1	yxjH	putative methyl-tetrahydrofolate methyltransferase
CIBE_2420	6up	2.7	1.8	1.3	1.0	-	Molybdopterin binding domain
CIBE_0299	6up	1.8	1.7	1.9	1.4	-	conserved protein of unknown function
CIBE_3910	6up	2.9	1.7	1.2	0.9	-	protein of unknown function
CIBE_1633	6up	0.7	2.2	2.3	1.6	-	Pyruvate kinase
CIBE_3202	6up	2.9	1.5	1.1	1.3	-	Valyl-tRNA synthetase (fragment)
CIBE_p0012	6up	2.8	2.0	0.9	1.0	-	conserved protein of unknown function
CIBE_4173	6up	2.7	1.9	1.1	1.1	-	Abortive infection protein
CIBE_4540	6up	1.8	1.7	2.0	1.3	-	Membrane protein
CIBE_4251	6up	3.0	1.5	0.9	1.3	-	conserved protein of unknown function
CIBE_0481	6up	2.2	2.5	0.9	1.1	-	protein of unknown function
CIBE_3195	6up	2.8	1.5	0.9	1.4	-	Homocysteine S-methyltransferase
CIBE_3788	6up	2.9	1.8	1.1	0.7	-	protein of unknown function
CIBE_3246	6up	2.4	1.5	1.2	1.5	-	Carboxymuconolactone decarboxylase
CIBE_0218	6up	0.4	2.4	2.0	1.8	-	Cell wall hydrolase, SleB
CIBE_2419	6up	2.3	1.7	1.3	1.3	-	LysR family transcriptional regulator
CIBE_4322	6up	2.0	1.6	1.6	1.4	-	conserved exported protein of unknown function
CIBE_1363	6up	1.6	1.6	1.7	1.6	pstS	phosphate ABC transporter (binding lipoprotein)
CIBE_misc_RNA_2	6up	1.5	1.7	1.1	2.2	-	6S
CIBE_misc_RNA_44	6up	1.8	1.9	1.7	1.2	-	Purine
CIBE_4170	6up	2.0	1.5	1.4	1.6	-	conserved protein of unknown function
CIBE_2964	6up	1.7	2.1	1.5	1.2	-	Aldehyde dehydrogenase
CIBE_misc_RNA_11	6up	1.5	1.5	1.2	2.3	-	Glycine
CIBE_2418	6up	1.8	1.7	1.9	1.1	-	Molybdopterin dehydrogenase, FAD-binding
CIBE_0799	6up	0.7	2.3	2.1	1.4	-	2', 3'-cyclic nucleotide 2'-phosphodiesterase
CIBE_0476	6up	2.4	2.5	0.8	0.7	-	protein of unknown function
CIBE_3446	6up	1.8	1.9	1.7	1.1	-	conserved protein of unknown function
CIBE_2132	6up	1.6	1.6	1.9	1.3	-	Single-stranded DNA-binding protein
CIBE_0482	6up	2.4	2.5	0.8	0.6	-	protein of unknown function

CIBE_4468	6up	1.9	1.6	1.5	1.4	lacA	Galactoside O-acetyltransferase
CIBE_p0013	6up	2.7	1.5	1.2	0.9	-	conserved protein of unknown function
CIBE_5803	6up	1.7	1.4	1.4	1.8	-	conserved protein of unknown function
CIBE_5305	6up	2.4	1.5	1.4	1.0	-	conserved protein of unknown function
CIBE_4198	6up	2.4	1.7	1.2	0.9	-	Acetyltransferase, GNAT family
CIBE_4323	6up	2.1	1.5	1.4	1.2	-	conserved exported protein of unknown function
CIBE_4174	6up	2.7	1.8	1.1	0.6	-	Methyltransferase type 12
CIBE_4733	6up	3.1	1.9	1.1	0.0	-	Phosphinothricin N-acetyltransferase
CIBE_0471	6up	2.3	2.4	0.7	0.8	-	conserved protein of unknown function
CIBE_0444	6up	2.6	2.1	0.7	0.7	-	conserved protein of unknown function
CIBE_2826	6up	1.8	2.3	1.1	0.8	glnH	glutamine transporter subunit ; periplasmic binding component of ABC superfamily
CIBE_0250	6up	0.4	1.8	2.0	1.9	-	Extracellular solute-binding protein, family 1
CIBE_2017	6up	0.8	2.7	1.4	1.2	-	conserved protein of unknown function
CIBE_3870	6up	2.7	1.7	1.1	0.6	-	Histidine triad (HIT) protein
CIBE_3168	6up	2.8	2.3	0.8	0.2	-	conserved membrane protein of unknown function
CIBE_2878	6up	1.7	1.3	1.5	1.6	-	Phospho-2-dehydro-3-deoxyheptonate aldolase
CIBE_3782	6up	2.7	1.4	1.0	1.0	-	Acetyltransferase, GNAT family (fragment)
CIBE_4171	6up	2.3	1.6	1.1	1.1	-	exported protein of unknown function
CIBE_3324	6up	2.1	1.7	1.1	1.2	-	conserved protein of unknown function
CIBE_3193	6up	2.6	1.2	1.3	0.9	-	conserved protein of unknown function
CIBE_3287	6up	2.5	1.7	1.5	0.3	-	putative cell wall binding repeat-containing protein
CIBE_4466	6up	2.3	1.6	1.4	0.7	-	conserved protein of unknown function
CIBE_0470	6up	2.2	2.5	0.6	0.6	-	conserved protein of unknown function
CIBE_0537	6up	0.6	2.2	1.8	1.4	-	conserved protein of unknown function
CIBE_3640	6up	1.8	1.8	1.1	1.3	-	conserved protein of unknown function
CIBE_2404	6up	1.6	1.6	1.8	0.8	-	YheO domain protein
CIBE_3436	6up	2.5	1.6	0.9	0.9	-	Electron transfer flavoprotein, alpha/beta-subunit-like protein
CIBE_4413	6up	0.6	2.5	1.7	1.2	-	conserved protein of unknown function
CIBE_5285	6up	2.7	1.8	1.1	0.4	-	conserved protein of unknown function
CIBE_1820	6up	2.0	2.1	1.4	0.5	-	conserved protein of unknown function
CIBE_4252	6up	2.7	1.4	0.9	0.9	-	Radical SAM domain protein
CIBE_3471	6up	2.3	1.4	1.3	0.7	stc	Signal-transduction and transcriptional-control protein
CIBE_3899	6up	2.2	1.7	1.1	0.8	-	Glyoxalase/bleomycin resistance protein/dioxygenase
CIBE_3787	6up	2.3	0.8	0.8	1.9	-	protein of unknown function
CIBE_0473	6up	2.6	2.4	0.6	0.2	-	conserved protein of unknown function
CIBE_2417	6up	1.7	1.5	1.6	1.1	ndhS	Nicotinate dehydrogenase small FeS subunit
CIBE_0486	6up	2.4	2.8	0.7	-0.1	-	conserved protein of unknown function
CIBE_3340	6up	2.3	1.3	1.1	1.1	-	Elongation factor G, domain IV
CIBE_3410	6up	2.2	1.3	1.4	0.9	opuCA	glycine betaine/carnitine/choline/choline sulfate ABC transporter (ATP-binding protein)
CIBE_4467	6up	1.9	1.4	1.5	0.9	-	conserved protein of unknown function
CIBE_2655	6up	2.4	1.7	1.4	0.2	-	Flavodoxin
CIBE_0828	6up	2.2	1.9	0.9	0.7	-	putative AgrB-like protein 1
CIBE_3868	6up	2.4	1.4	1.0	1.0	-	conserved protein of unknown function
CIBE_3249	6up	2.2	1.1	1.5	1.0	-	Histidine kinase
CIBE_4250	6up	2.7	1.6	0.9	0.6	-	conserved protein of unknown function
CIBE_6019	6up	2.5	1.6	1.4	0.2	-	Transcriptional regulator, RpiR family
CIBE_4139	6up	2.8	1.8	0.9	0.3	-	Acetyltransferase
CIBE_3347	6up	2.1	1.5	1.0	1.2	-	ATPase AAA (fragment)
CIBE_0943	6up	2.0	0.8	0.8	2.0	-	O-acetylhomoserine aminocarboxypropyltransferase
CIBE_2343	6up	2.3	1.2	1.0	1.2	fldZ	2-enoate reductase FldZ
CIBE_3199	6up	2.7	1.5	0.9	0.6	-	Nicotinamidase-like amidase
CIBE_3773	6up	1.7	1.5	1.6	0.9	-	Accessory gene regulator B
CIBE_1022	6up	0.5	2.0	1.9	1.2	-	conserved protein of unknown function
CIBE_3397	6up	2.3	1.7	0.9	0.6	-	conserved protein of unknown function
CIBE_2171	6up	2.5	2.1	0.4	0.6	-	RNA polymerase, sigma 28 subunit, FliA/WhiG family
CIBE_3034	6up	0.4	2.0	2.0	1.2	-	conserved protein of unknown function
CIBE_1036	6up	0.5	2.1	1.8	1.2	-	Spore coat protein CotS
CIBE_1458	6up	1.2	2.8	0.9	0.8	-	conserved protein of unknown function
CIBE_4773	6up	2.0	1.1	1.4	1.1	-	conserved protein of unknown function
CIBE_5284	6up	2.3	1.4	0.9	0.9	-	Wall-associated protein WapA (fragment)
CIBE_4253	6up	2.4	1.5	0.9	0.8	-	2-dehydropantoate 2-reductase
CIBE_misc_RNA_61	6up	2.3	1.9	0.6	0.8	-	Intron_gpI
CIBE_4444	6up	2.0	1.2	1.2	1.2	-	MarR family transcriptional regulator
CIBE_2825	6up	2.3	2.6	0.6	0.0	-	GntR family transcriptional regulator
CIBE_4197	6up	2.3	1.5	1.0	0.7	-	cAMP-binding protein
CIBE_3789	6up	2.3	1.4	1.1	0.7	-	conserved protein of unknown function
CIBE_3962	6up	2.3	1.5	1.0	0.7	bglF	fused beta-glucoside-specific PTS enzymes: IIA component ; IIB component ; IIC component
CIBE_4196	6up	1.8	1.5	1.0	1.1	-	Short-chain dehydrogenase
CIBE_2591	6up	2.5	2.1	0.5	0.4	-	conserved protein of unknown function
CIBE_0897	6up	2.0	1.5	0.8	1.1	-	Carbohydrate ABC transporter membrane protein 1, CUT1 family
CIBE_0104	6up	0.4	2.2	1.6	1.2	-	Spore cortex biosynthesis protein YabQ
CIBE_4137	6up	2.7	1.6	1.0	0.1	-	conserved protein of unknown function
CIBE_3826	6up	2.9	2.0	0.4	0.0	-	HAD hydrolase, family IA, variant 3
CIBE_4090	6up	1.6	1.5	1.6	0.7	-	Cell wall-binding protein
CIBE_1638	6up	1.7	1.7	1.4	0.5	-	Appr-1-p processing domain protein
CIBE_0464	6up	2.6	2.6	0.4	-0.2	-	conserved protein of unknown function
CIBE_0477	6up	2.2	2.3	0.6	0.3	-	protein of unknown function
CIBE_3902	6up	2.2	1.1	0.6	1.3	-	protein of unknown function
CIBE_3338	6up	1.8	1.3	1.1	1.2	-	Transcription activator, effector binding
CIBE_5293	6up	3.1	1.3	1.2	-0.2	-	conserved membrane protein of unknown function
CIBE_2782	6up	2.2	1.3	1.0	0.7	-	protein of unknown function
CIBE_4735	6up	2.6	1.5	1.2	0.0	-	putative lipoprotein
CIBE_b0020	6up	2.0	1.9	1.0	0.3	-	protein of unknown function
CIBE_4607	6up	2.8	2.2	2.3	2.4	yodS	putative aminoacyloate CoA-transferase
CIBE_3901	6up	2.0	1.6	1.1	0.5	-	putative cell wall binding repeat-containing protein
CIBE_4712	6up	2.0	1.4	0.9	0.9	-	conserved protein of unknown function
CIBE_3911	6up	2.7	1.4	1.0	0.1	-	Putative cell wall binding repeat protein (fragment)
CIBE_5268	6up	2.0	1.2	0.9	1.1	-	conserved protein of unknown function
CIBE_4140	6up	2.7	1.7	0.4	0.4	-	conserved membrane protein of unknown function
CIBE_3871	6up	2.6	1.4	1.2	0.0	-	conserved protein of unknown function
CIBE_4136	6up	2.6	1.4	0.7	0.4	-	Transcriptional regulator, HxlR family

CIBE_0450	6up	2.3	2.0	0.4	0.5	-	conserved protein of unknown function
CIBE_2172	6up	2.2	1.5	0.8	0.6	-	conserved protein of unknown function
CIBE_4143	6up	3.0	2.1	0.7	-0.7	-	ABC transporter related (fragment)
CIBE_3368	6up	1.8	1.4	1.2	0.6	-	putative membrane protein
CIBE_0472	6up	2.1	2.1	0.6	0.3	-	Minor capsid
CIBE_1572	6up	1.7	1.2	0.9	1.2	hisB	imidazoleglycerol-phosphate dehydratase
CIBE_3903	6up	2.4	1.4	0.7	0.5	-	conserved protein of unknown function
CIBE_3639	6up	2.0	1.6	1.3	0.1	-	GCN5-related N-acetyltransferase
CIBE_2421	6up	2.5	1.4	0.7	0.3	moaA	Cyclic pyranopterin monophosphate synthase
CIBE_4316	6up	2.1	0.9	0.8	1.2	-	conserved exported protein of unknown function
CIBE_4608	6up	3.1	2.5	2.4	2.8	yodR	putative acyloate-acetoacetate CoA-transferase
CIBE_0075	6up	1.8	1.1	1.1	1.0	leuA	2-isopropylmalate synthase 2
CIBE_2021	6up	1.6	2.4	0.8	0.2	-	Stage III sporulation protein AB
CIBE_4445	6up	1.7	1.3	1.1	0.9	-	Beta-lactamase
CIBE_5457	6up	2.3	1.2	0.2	1.3	yrbE	putative oxidoreductase
CIBE_3980	6up	2.1	1.9	0.8	0.1	-	conserved protein of unknown function
CIBE_1281	6up	1.9	1.0	0.4	1.6	-	ABC transporter
CIBE_1570	6up	1.5	0.9	1.3	1.2	hisD	histidinol dehydrogenase
CIBE_6076	6up	2.1	1.1	1.3	0.4	-	Acyl-CoA dehydrogenase
CIBE_3245	6up	2.1	1.3	0.1	1.4	-	PAS/PAC sensor signal transduction histidine kinase
CIBE_0438	6up	2.2	2.0	0.4	0.3	-	protein of unknown function
CIBE_0994	6up	2.5	1.5	0.5	0.3	sigF	RNA polymerase sporulation-specific sigma factor (sigma-F)
CIBE_3000	6up	2.0	1.1	0.9	0.7	-	Intermediate filament protein:ATP/GTP-binding site motif A
CIBE_1450	6up	0.2	1.7	1.6	1.3	tepA	protein export-enhancing protease
CIBE_1240	6up	1.7	1.0	1.1	0.9	ilvE	Branched-chain-amino-acid aminotransferase
CIBE_0055	6up	0.4	1.9	1.5	0.9	-	Spore maturation protein
CIBE_4472	6up	2.5	1.5	0.6	0.1	dkgB	2,5-diketo-D-gluconic acid reductase B
CIBE_1794	6up	2.1	2.0	0.4	0.2	-	conserved protein of unknown function
CIBE_3780	6up	2.0	1.3	0.9	0.5	-	membrane protein of unknown function
CIBE_2201	6up	1.7	1.1	0.9	0.9	-	DegV domain-containing protein CA_C1624
CIBE_5267	6up	1.9	1.1	0.7	1.0	-	YD repeat protein
CIBE_0475	6up	2.3	2.3	0.2	-0.1	-	Bacteriophage Gp15 protein
CIBE_0551	6up	1.3	2.3	0.8	0.3	-	conserved protein of unknown function
CIBE_3869	6up	2.2	0.9	0.6	0.9	-	Metal-dependent phosphohydrolase HD sub domain containing protein
CIBE_5423	6up	1.6	1.4	1.1	0.5	argC	N-acetylglutamate gamma-semialdehyde dehydrogenase
CIBE_5270	6up	1.9	1.1	0.8	0.8	-	Pentapeptide repeat protein
CIBE_4183	6up	1.9	1.4	0.7	0.5	-	Ketopantoate reductase ApbA/PanE, N-terminal domain protein
CIBE_3908	6up	2.4	1.6	0.6	-0.2	-	Cyanophycinase
CIBE_0918	6up	2.5	1.8	0.1	0.1	-	ErfK/YbiS/YcfS/YnhG family protein
CIBE_1608	6up	0.2	1.8	1.4	1.1	-	Membrane protein
CIBE_3790	6up	1.9	1.4	1.1	0.0	-	conserved protein of unknown function
CIBE_3396	6up	2.0	1.3	0.8	0.3	-	conserved protein of unknown function
CIBE_0076	6up	2.2	0.9	0.8	0.5	-	Aconitate hydratase
CIBE_3877	6up	2.2	1.1	0.9	0.2	-	conserved protein of unknown function
CIBE_5882	6up	2.1	1.6	0.4	0.3	-	conserved protein of unknown function
CIBE_2932	6up	2.0	1.3	0.5	0.6	-	protein of unknown function
CIBE_3201	6up	2.4	1.0	0.7	0.4	-	conserved protein of unknown function
CIBE_3367	6up	1.8	1.1	1.0	0.5	-	putative cell wall binding protein
CIBE_0479	6up	1.9	2.0	0.4	0.0	-	Phage minor structural protein (modular protein)
CIBE_5271	6up	1.7	1.0	0.9	0.7	-	conserved protein of unknown function
CIBE_p0004	6up	1.7	1.5	0.8	0.3	-	Putative cell wall binding protein (fragment)
CIBE_1609	6up	2.3	1.4	0.4	0.2	-	conserved protein of unknown function
CIBE_0992	6up	2.4	1.3	0.6	0.0	spoIIAA	Anti-sigma F factor antagonist
CIBE_1686	6up	1.9	1.3	0.5	0.6	kdpB	potassium translocating ATPase, subunit B
CIBE_3185	6up	1.6	1.1	1.0	0.6	-	conserved protein of unknown function
CIBE_6075	6up	2.1	1.0	1.0	0.1	-	Beta-lactamase domain protein
CIBE_4279	6up	2.4	0.8	0.5	0.5	-	conserved protein of unknown function
CIBE_4736	6up	2.3	1.6	0.7	-0.3	-	conserved protein of unknown function
CIBE_3236	6up	1.8	1.3	0.6	0.5	-	Alpha/beta hydrolase fold protein
CIBE_3395	6up	2.1	0.9	1.0	0.1	-	N-acetylmuramoyl-L-alanine amidase family 2
CIBE_5280	6up	1.6	0.9	1.2	0.5	ymdB	conserved hypothetical protein
CIBE_4182	6up	2.0	1.3	0.7	0.2	-	DNA mismatch repair protein MutS domain protein
CIBE_0487	6up	2.1	2.1	0.4	-0.4	-	conserved protein of unknown function
CIBE_1611	6up	2.0	1.3	0.4	0.6	-	conserved exported protein of unknown function
CIBE_0457	6up	1.7	1.7	0.4	0.3	-	conserved protein of unknown function
CIBE_5283	6up	2.0	1.4	0.5	0.2	-	putative transcriptional regulatory protein, AsnC family
CIBE_4142	6up	2.5	1.2	0.3	0.0	-	ABC transporter (fragment)
CIBE_1573	6up	1.6	0.9	0.9	0.7	hisH	amidotransferase (glutaminase)
CIBE_5881	6up	1.8	1.3	0.5	0.5	acpS	holo-acyl carrier protein synthase
CIBE_0478	6up	1.9	2.2	0.6	-0.6	-	putative Phage tail component
CIBE_1335	6up	1.6	1.5	0.9	0.0	-	conserved protein of unknown function
CIBE_4135	6up	2.4	1.1	0.5	0.1	-	Phosphatidylethanolamine-binding protein
CIBE_0467	6up	2.1	2.0	0.2	-0.3	-	protein of unknown function
CIBE_4734	6up	2.1	1.2	0.7	0.1	-	conserved membrane protein of unknown function
CIBE_3290	6up	1.7	1.2	0.7	0.4	-	conserved exported protein of unknown function
CIBE_4138	6up	2.3	1.4	0.6	-0.3	-	conserved membrane protein of unknown function
CIBE_1487	6up	2.2	1.0	0.0	0.7	-	conserved protein of unknown function
CIBE_2304	6up	2.0	0.9	0.6	0.5	-	conserved protein of unknown function
CIBE_0289	6up	1.5	1.0	1.0	0.5	rbr	Rubrerythrin
CIBE_2931	6up	2.0	1.5	0.5	0.0	-	conserved protein of unknown function
CIBE_0461	6up	2.0	1.9	0.2	-0.2	-	conserved protein of unknown function
CIBE_4009	6up	1.9	1.7	0.3	0.0	-	Membrane protein
CIBE_5425	6up	1.5	1.3	0.9	0.2	argB	Acetylglutamate kinase
CIBE_3409	6up	1.7	0.9	0.9	0.4	-	ABC transporter permease
CIBE_0468	6up	2.2	2.1	0.0	-0.4	-	Phage coat protein
CIBE_4134	6up	2.2	1.3	0.3	0.1	-	GCN5 family acetyltransferase
CIBE_5458	6up	1.7	1.0	0.5	0.6	iolD	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase
CIBE_0445	6up	2.1	1.6	-0.1	0.2	-	Gp49 homologous (fragment)
CIBE_1162	6up	2.2	0.4	0.9	0.4	-	Polysaccharide biosynthesis protein
CIBE_3905	6up	1.8	0.9	0.6	0.6	-	Alpha/beta hydrolase fold
CIBE_1398	6up	0.4	2.1	0.9	0.4	-	Sporulation integral membrane protein YlbJ

CIBE_4367	6up	1.9	1.4	0.6	-0.1	-	DNA mismatch repair protein MutS (fragment)
CIBE_2568	6up	2.1	1.7	0.2	-0.3	-	putative cell wall binding repeat-containing protein
CIBE_0896	6up	2.0	1.4	0.7	-0.4	-	ABC transporter substrate-binding protein
CIBE_3784	6up	2.1	0.9	0.5	0.0	-	protein of unknown function
CIBE_3281	6up	1.9	1.3	0.2	0.1	gldA	glycerol dehydrogenase, NAD
CIBE_3342	6up	1.9	0.7	0.5	0.3	-	conserved protein of unknown function
CIBE_0469	6up	2.0	2.1	-0.1	-0.4	-	conserved protein of unknown function
CIBE_3893	6up	2.0	0.9	0.6	0.0	pspB	putative phosphoserine phosphatase 2
CIBE_4609	6up	3.2	2.4	2.3	2.7	adc	Acetoacetate decarboxylase
CIBE_0993	6up	2.3	1.1	0.3	-0.2	spoIIAB	anti-sigma factor (antagonist of sigma(F)) and serine kinase
CIBE_2043	6up	1.7	1.2	0.5	0.1	-	conserved protein of unknown function
CIBE_0474	6up	2.0	1.8	-0.1	-0.3	-	conserved protein of unknown function
CIBE_3894	6up	2.1	1.2	0.5	-0.4	-	ADP-ribose pyrophosphatase
CIBE_0594	6up	1.6	1.9	0.0	-0.1	-	conserved membrane protein of unknown function
CIBE_0867	6up	1.7	0.7	0.4	0.5	-	Histidine kinase
CIBE_3172	6up	2.2	1.5	0.5	-1.0	-	conserved protein of unknown function
CIBE_0751	6up	1.7	1.0	0.4	0.2	nth	Endonuclease III
CIBE_4366	6up	1.7	1.1	0.2	0.2	-	DNA mismatch repair protein MutS (fragment)
CIBE_3233	6up	1.9	1.1	0.6	-0.4	-	conserved protein of unknown function
CIBE_3811	6up	1.9	0.8	0.4	0.0	-	Fumarylacetoacetate (FAA) hydrolase
CIBE_1605	6up	0.4	2.0	0.7	0.0	-	Sporulation protein SpoVB
CIBE_0462	6up	1.6	1.6	0.2	-0.2	-	putative SPP1 gp7 family phage head morphogenesis protein
CIBE_2040	6up	3.0	0.9	-0.3	-0.6	-	protein of unknown function
CIBE_0416	6up	1.9	1.0	0.2	-0.1	-	Two component regulator three Y domain protein
CIBE_2305	6up	1.8	0.5	0.3	0.3	-	Methyl-accepting chemotaxis protein
CIBE_3892	6up	2.2	0.6	0.2	-0.2	-	conserved protein of unknown function
CIBE_4975	6up	1.8	0.9	0.1	0.1	hsp	18 kDa heat shock protein
CIBE_0277	6up	1.9	0.8	0.8	-0.5	-	Cyclase
CIBE_0357	6up	2.0	0.8	0.0	0.0	-	protein of unknown function
CIBE_4848	6up	2.1	1.1	0.1	-0.5	-	Methyl-accepting chemotaxis sensory transducer
CIBE_2629	6up	1.5	1.2	0.3	-0.2	-	conserved protein of unknown function
CIBE_5615	6up	1.8	0.9	-0.1	0.2	-	Cell wall hydrolase
CIBE_2933	6up	1.8	0.7	0.2	0.1	-	conserved protein of unknown function
CIBE_5880	6up	2.1	1.1	-0.1	-0.3	-	Carbohydrate kinase
CIBE_0488	6up	1.7	1.9	-0.3	-0.7	-	Glycoside hydrolase, family 25
CIBE_3984	6up	1.6	0.7	0.1	0.2	-	conserved protein of unknown function
CIBE_4984	6up	1.6	0.7	0.4	0.0	-	Alpha amylase, catalytic region
CIBE_3783	6up	1.8	0.7	0.3	-0.2	-	conserved protein of unknown function
CIBE_2783	6up	1.7	0.5	0.6	-0.2	-	conserved protein of unknown function
CIBE_1355	6up	1.5	1.6	0.0	-0.5	-	Peptidase U4
CIBE_2168	6up	1.6	0.7	0.3	0.0	-	ATP-dependent DNA helicase RecQ
CIBE_0435	6up	1.6	1.3	0.2	-0.6	-	conserved protein of unknown function
CIBE_0974	6up	1.9	1.0	0.1	-0.6	-	Universal stress protein
CIBE_0466	6up	1.8	1.8	-0.4	-1.0	-	conserved protein of unknown function
CIBE_4280	6up	1.9	0.8	0.3	-0.6	-	Metallo-beta-lactamase superfamily protein
CIBE_4435	6up	1.8	0.9	0.6	-1.0	-	conserved protein of unknown function
CIBE_5924	6up	1.8	0.8	0.0	-0.4	glgC	glucose-1-phosphate adenylyltransferase (ADP-glucose pyrophosphorylase) subunit alpha
CIBE_2041	6up	2.0	0.6	-0.1	-0.3	spo0A	response regulator
CIBE_0456	6up	0.9	1.6	-0.5	0.3	-	conserved protein of unknown function
CIBE_4732	6up	2.1	1.2	0.1	-1.2	lepB	Signal peptidase I
CIBE_0831	6up	1.5	0.6	0.1	0.0	sudA	Sulfide dehydrogenase subunit alpha
CIBE_5056	6up	2.0	0.5	0.2	-0.6	-	Isocitrate dehydrogenase [NADP]
CIBE_4859	6up	1.8	0.7	-0.2	-0.3	-	Cell wall hydrolase/autolysin
CIBE_0088	6up	1.5	0.7	0.1	-0.4	-	protein of unknown function
CIBE_0307	6up	1.8	0.4	0.1	-0.3	-	Two component transcriptional regulator, LytTR family
CIBE_2617	6up	1.9	1.0	0.1	-1.0	-	conserved protein of unknown function
CIBE_3978	6up	1.8	1.1	-0.4	-0.7	-	conserved protein of unknown function
CIBE_5925	6up	1.6	0.5	-0.2	-0.2	-	Alpha-amylase
CIBE_3846	6up	1.6	0.4	0.1	-0.5	thrZ	threonyl-tRNA synthetase
CIBE_5923	6up	1.9	0.7	-0.3	-0.8	-	Glucose-1-phosphate adenylyltransferase
CIBE_0279	6up	2.2	0.3	0.6	-1.8	-	Methyl-accepting chemotaxis sensory transducer
CIBE_0628	6up	1.7	0.4	-0.3	-0.6	-	protein of unknown function
CIBE_0436	6up	1.5	1.1	-0.7	-0.8	-	Excisionase family
CIBE_3001	6up	1.6	0.1	-0.2	-0.4	ftnA	Ferritin
CIBE_0465	6up	1.8	1.5	-0.6	-1.6	-	protein of unknown function
CIBE_2317	6up	1.2	1.2	-0.5	-1.0	-	conserved protein of unknown function
CIBE_3891	6up	2.0	0.3	-0.4	-1.0	-	conserved membrane protein of unknown function
CIBE_0278	6up	1.9	0.0	0.3	-2.5	-	Transcriptional regulator
CIBE_tRNA57	6down	-1.7	-1.4	-0.1	0.4	-	Ala tRNA
CIBE_4931	6down	-1.7	-1.2	-0.4	-0.3	ydaO	Uncharacterized amino acid permease YdaO
CIBE_1058	6down	-1.6	-0.5	-0.9	-0.9	amtB	ammonium transporter
CIBE_misc_RNA_81	6down	-1.6	-1.5	-0.9	-0.4	-	T-box
CIBE_5854	6down	-1.6	-1.2	-0.9	-0.8	-	putative enzyme
CIBE_3636	6down	-2.1	-1.4	-0.4	-0.7	-	putative galactoside ABC transporter
CIBE_tRNA46	6down	-2.2	-1.5	-0.9	0.0	-	Ile tRNA
CIBE_1055	6down	-1.6	-1.3	-0.9	-1.3	-	DNA topoisomerase
CIBE_0267	6down	-1.6	-1.5	-1.2	-0.9	glmS	Glutamine--fructose-6-phosphate aminotransferase [isomerizing]
CIBE_1412	6down	-1.6	-1.2	-1.1	-1.4	ffh	signal recognition particle-like (SRP) GTPase
CIBE_4870	6down	-1.9	-2.7	-0.1	-0.5	-	conserved protein of unknown function
CIBE_5529	6down	-1.7	-1.3	-1.0	-1.4	-	Glycosyl transferase
CIBE_5213	6down	-1.6	-1.6	-1.0	-1.2	-	Sodium:dicarboxylate symporter
CIBE_5723	6down	-1.9	-1.7	-0.9	-0.8	-	conserved exported protein of unknown function
CIBE_5772	6down	-1.8	-1.3	-0.9	-1.4	-	Methyl-accepting chemotaxis sensory transducer
CIBE_2630	6down	-1.7	-1.5	-1.3	-1.2	-	conserved exported protein of unknown function
CIBE_0191	6down	-1.6	-1.4	-1.3	-1.4	mapA	methionine aminopeptidase
CIBE_0637	6down	-1.8	-1.6	-1.1	-1.4	-	2-nitropropane dioxygenase, NPD
CIBE_5709	6down	-1.8	-1.5	-1.0	-1.6	artQ	high affinity arginine ABC transporter (permease)
CIBE_1369	6down	-1.7	-1.7	-1.3	-1.3	-	Fe-S oxidoreductase
CIBE_0805	6down	-2.0	-1.6	-1.2	-1.1	-	conserved protein of unknown function
CIBE_0418	6down	-2.0	-1.3	-1.0	-1.7	ytzG	putative 16S pseudouridylate synthase
CIBE_1014	6down	-1.7	-1.7	-1.3	-1.3	trmB	tRNA (guanine-N(7)-)-methyltransferase

CIBE_1411	6down	-2.0	-1.2	-1.3	-1.6	ylxM	conserved hypothetical protein
CIBE_5007	6down	-1.7	-1.2	-1.0	-2.3	-	conserved protein of unknown function
CIBE_5698	6down	-2.2	-1.4	-1.3	-1.2	-	Cation diffusion facilitator family transporter
CIBE_5863	6down	-1.9	-1.8	-1.1	-1.5	murB	UDP-N-acetylenolpyruvoylglucosamine reductase
CIBE_4421	6down	-2.3	-1.7	-1.7	-0.7	-	transposase (fragment)
CIBE_1001	6down	-1.8	-1.0	-1.3	-2.2	rpsT	ribosomal protein S20 (BS20)
CIBE_0198	6down	-1.5	-1.3	-1.5	-2.1	rpoA	RNA polymerase (alpha subunit)
CIBE_0566	6down	-1.6	-1.8	-1.3	-1.7	-	conserved membrane protein of unknown function
CIBE_1624	6down	-1.7	-1.5	-1.5	-1.8	-	conserved protein of unknown function
CIBE_4992	6down	-1.5	-1.6	-1.6	-1.8	nupQ	permease of ABC guanosine transporter
CIBE_2872	6down	-1.5	-1.6	-1.3	-2.2	-	Ribose-phosphate pyrophosphokinase
CIBE_5607	6down	-1.8	-1.3	-1.5	-2.1	-	Polysaccharide biosynthesis protein
CIBE_0050	6down	-1.7	-1.4	-1.6	-2.0	regA	HTH-type transcriptional regulator RegA
CIBE_1414	6down	-1.6	-1.5	-1.6	-2.0	ylqC	putative RNA binding protein
CIBE_5948	6down	-1.8	-1.9	-1.4	-1.6	-	putative transcriptional regulator, TetR family
CIBE_2478	6down	-1.7	-2.1	-1.6	-1.3	-	conserved protein of unknown function
CIBE_4210	6down	-1.1	-0.3	-2.4	-3.0	-	Extracellular solute-binding protein, family 1
CIBE_5783	6down	-2.0	-1.6	-1.3	-1.8	-	Dehydrogenase
CIBE_2956	6down	-1.8	-1.5	-1.6	-1.8	-	Polar amino acid ABC transporter, inner membrane subunit
CIBE_4864	6down	-2.5	-1.7	-1.3	-1.3	steT	Serine/threonine exchanger SteT
CIBE_1190	6down	-1.9	-1.8	-1.7	-1.3	-	Tetratricopeptide TPR_2 repeat protein
CIBE_6107	6down	-1.5	-1.6	-1.7	-2.1	rpsR	ribosomal protein S18
CIBE_6116	6down	-2.3	-1.5	-1.4	-1.7	-	transposase (fragment)
CIBE_4945	6down	-2.7	-1.9	-1.1	-1.1	ycaM	putative transporter
CIBE_4830	6down	-1.8	-1.5	-1.6	-1.9	-	Signal peptidase I
CIBE_3454	6down	-2.3	-1.8	-1.7	-1.2	-	protein of unknown function
CIBE_1330	6down	-1.7	-1.6	-1.6	-2.0	rarA	DNA-dependent ATPase
CIBE_1490	6down	-1.8	-1.9	-1.3	-1.9	kup	putative potassium transport system protein kup
CIBE_5914	6down	-1.8	-1.3	-2.0	-1.9	-	Peptidase A8
CIBE_5729	6down	-1.7	-1.7	-1.5	-2.1	-	conserved protein of unknown function
CIBE_5126	6down	-1.5	-2.1	-1.6	-1.7	-	Flagellar hook capping protein (fragment)
CIBE_0735	6down	-1.8	-1.6	-1.4	-2.2	-	conserved protein of unknown function
CIBE_1565	6down	-1.9	-1.9	-1.4	-1.9	iscS	Cysteine desulfurase
CIBE_1427	6down	-1.7	-1.4	-1.5	-2.4	tsf	elongation factor Ts
CIBE_6030	6down	-1.5	-1.6	-1.6	-2.3	-	DEAD/DEAH box helicase domain protein
CIBE_3635	6down	-1.8	-1.2	-1.2	-2.9	-	Rubrerythrin
CIBE_misc_RNA_46	6down	-3.1	-2.4	-0.9	-0.7	-	Purine
CIBE_0162	6down	-1.6	-1.8	-1.6	-2.2	rpsL	ribosomal protein S12 (BS12)
CIBE_2562	6down	-1.6	-1.9	-1.8	-2.0	aspS	Aspartate--tRNA ligase
CIBE_0197	6down	-1.8	-1.6	-1.7	-2.2	rpsD	30S ribosomal subunit protein S4
CIBE_0679	6down	-1.8	-1.6	-1.8	-2.2	rplU	ribosomal protein L21 (BL20)
CIBE_5784	6down	-2.2	-1.5	-1.8	-1.8	-	Xylose isomerase domain protein TIM barrel
CIBE_4906	6down	-3.5	-1.9	-0.9	-1.0	-	conserved membrane protein of unknown function
CIBE_1623	6down	-1.9	-1.7	-1.8	-2.0	-	conserved protein of unknown function
CIBE_2076	6down	-1.8	-1.8	-1.6	-2.2	-	Rrf2 family transcriptional regulator
CIBE_misc_RNA_45	6down	-3.2	-3.2	-0.7	-0.4	-	Purine
CIBE_5855	6down	-1.7	-2.0	-1.5	-2.3	pyk	pyruvate kinase
CIBE_0903	6down	-2.1	-2.4	-1.3	-1.7	-	FMN reductase
CIBE_4960	6down	-1.8	-2.1	-1.7	-1.9	ydeP	Uncharacterized HTH-type transcriptional regulator YdeP
CIBE_1566	6down	-1.7	-2.0	-1.4	-2.4	trmI	persulfide ATP pyrophosphatase involved in tRNA modification
CIBE_5118	6down	-1.6	-2.0	-2.0	-2.0	-	Flagellar biosynthetic protein FlhB
CIBE_4098	6down	-1.6	-1.8	-2.5	-1.7	-	conserved protein of unknown function
CIBE_5130	6down	-1.8	-2.2	-1.4	-2.2	-	Flagellar biosynthesis/type III secretory pathway-like protein
CIBE_0024	6down	-2.1	-1.7	-1.5	-2.3	-	Haloacid dehalogenase
CIBE_0680	6down	-1.6	-1.5	-1.9	-2.6	-	conserved protein of unknown function
CIBE_0025	6down	-2.0	-2.0	-1.6	-2.2	ykpA	ABC efflux transporter (ATP-binding protein)
CIBE_6056	6down	-2.5	-1.8	-1.7	-1.8	-	RNA methyltransferase
CIBE_1403	6down	-1.6	-1.9	-1.9	-2.5	rpmF	ribosomal protein L32
CIBE_5945	6down	-1.7	-2.2	-1.6	-2.4	-	Adenosylhomocysteine nucleosidase
CIBE_1265	6down	-1.8	-2.0	-2.0	-2.2	-	conserved exported protein of unknown function
CIBE_5131	6down	-2.0	-2.3	-1.7	-2.0	fliG	flagellar motor switching and energizing component
CIBE_misc_RNA_43	6down	-3.5	-2.6	-1.1	-0.7	-	Purine
CIBE_2029	6down	-1.8	-1.7	-1.8	-2.7	nusB	N utilization substance protein B homolog
CIBE_4120	6down	-2.3	-2.5	-1.5	-1.7	ydeD	putative permease
CIBE_5135	6down	-1.9	-2.2	-1.6	-2.3	-	Flagellar basal body rod protein FlgB
CIBE_tRNA89	6down	-2.9	-1.8	-2.3	-1.2	-	Asp tRNA
CIBE_1068	6down	-2.7	-2.0	-3.0	-0.4	-	conserved protein of unknown function
CIBE_0298	6down	-2.2	-2.0	-2.1	-1.9	-	conserved protein of unknown function
CIBE_1418	6down	-1.9	-2.0	-1.9	-2.4	rbgA	ribosome biogenesis GTPase A
CIBE_0682	6down	-1.8	-1.9	-1.7	-2.9	obgE	ppGpp-binding GTPase involved in cell portioning, DNA repair and ribosome assembly
CIBE_0158	6down	-1.9	-1.8	-1.9	-2.6	rplJ	ribosomal protein L10 (BL5)
CIBE_1419	6down	-2.2	-1.7	-1.9	-2.5	rnhB	ribonuclease HII
CIBE_5117	6down	-1.6	-2.3	-2.0	-2.4	flhA	component of the flagellar export machinery
CIBE_5334	6down	-3.0	-2.6	-2.1	-0.7	rbsA	ribose ABC transporter (ATP-binding protein)
CIBE_5122	6down	-1.6	-2.1	-1.8	-2.9	-	Flagellar basal body-associated protein FliL
CIBE_5132	6down	-2.1	-2.4	-1.9	-2.0	-	Flagellar M-ring protein
CIBE_2477	6down	-2.1	-2.1	-1.9	-2.4	-	Zinc chelation protein SecC
CIBE_4853	6down	-2.0	-2.1	-2.1	-2.3	-	Methyl-accepting chemotaxis protein
CIBE_5144	6down	-1.6	-2.1	-1.8	-3.1	rmlC	dTDP-4-deoxyrhamnose-3,5-epimerase
CIBE_5944	6down	-1.8	-2.2	-2.1	-2.5	tcdA	tRNA threonylcarbamoyladenosine dehydratase
CIBE_2073	6down	-2.1	-2.8	-1.5	-2.3	-	conserved membrane protein of unknown function
CIBE_0074	6down	-1.8	-2.1	-2.0	-2.7	-	Anaerobic ribonucleoside-triphosphate reductase
CIBE_2295	6down	-3.3	-2.5	-1.2	-1.6	yjeM	putative transporter
CIBE_2930	6down	-2.4	-2.1	-1.9	-2.3	-	Zinc chelation protein SecC
CIBE_4105	6down	-1.9	-2.1	-3.0	-1.7	-	Phage-like element pbsx protein XkdK
CIBE_4283	6down	-2.9	-3.0	-2.6	-0.2	-	conserved protein of unknown function
CIBE_1059	6down	-1.8	-2.4	-1.8	-2.8	-	Methyl-accepting chemotaxis protein
CIBE_3993	6down	-1.9	-2.3	-2.1	-2.6	-	Chemotaxis protein
CIBE_4060	6down	-2.4	-2.3	-2.0	-2.1	-	Sigma54 specific transcriptional regulator, Fis family
CIBE_2075	6down	-3.0	-2.4	-1.5	-2.0	-	RNA helicase
CIBE_4104	6down	-1.8	-2.1	-3.1	-1.9	-	Phage-like element pbsx protein XkdM

CIBE_5324	6down	-2.0	-2.2	-2.7	-2.0	-	Radical SAM domain protein
CIBE_0642	6down	-1.8	-2.1	-2.4	-2.6	-	Metallophosphoesterase
CIBE_1639	6down	-2.5	-1.7	-1.9	-2.9	-	conserved protein of unknown function
CIBE_5123	6down	-1.6	-2.1	-2.0	-3.2	ylzI	putative flagellar protein
CIBE_0159	6down	-1.8	-2.0	-2.1	-3.1	rplL	ribosomal protein L12 (BL9)
CIBE_2115	6down	-3.0	-2.5	-2.5	-0.9	-	protein of unknown function
CIBE_misc_RNA_56	6down	-2.3	-2.1	-1.8	-2.8	-	L10_leader
CIBE_0893	6down	-0.4	-2.2	-2.7	-3.9	dhaS	3-hydroxypropionaldehyde dehydrogenase
CIBE_1621	6down	-2.3	-2.3	-1.7	-2.7	-	Metal-dependent hydrolase of the beta-lactamase superfamily
CIBE_5032	6down	-2.2	-2.5	-2.0	-2.4	-	conserved membrane protein of unknown function
CIBE_4234	6down	-2.2	-2.2	-2.8	-1.9	-	FMN-binding protein
CIBE_1172	6down	-2.6	-2.1	-1.9	-2.5	-	Major facilitator superfamily MFS_1
CIBE_5143	6down	-2.2	-2.5	-2.1	-2.4	-	Glycosyltransferase, group 2 family protein
CIBE_tRNA88	6down	-3.3	-2.2	-2.5	-1.2	-	Phe tRNA
CIBE_2192	6down	-0.6	-2.4	-2.9	-3.3	sufB	FeS cluster formation protein
CIBE_0365	6down	-2.2	-2.3	-2.1	-2.6	-	protein of unknown function
CIBE_5154	6down	-2.0	-2.3	-2.0	-2.9	-	Group 2 glycosyl transferase
CIBE_tRNA47	6down	-1.9	-1.9	-1.8	-3.6	-	Asn tRNA
CIBE_1417	6down	-2.1	-2.1	-2.2	-2.9	rplS	ribosomal protein L19
CIBE_3861	6down	-1.7	-1.8	-2.2	-3.6	gltT	proton/sodium-glutamate symport protein
CIBE_5137	6down	-1.9	-2.4	-1.5	-3.5	-	MotA/TolQ/ExbB proton channel
CIBE_0955	6down	-1.5	-2.4	-2.3	-3.2	-	Thioredoxin reductase
CIBE_4548	6down	-2.7	-2.4	-2.2	-2.1	yiaI	putative hydrogenase, 4Fe-4S ferredoxin-type component
CIBE_1212	6down	-1.8	-2.7	-1.9	-3.0	-	conserved protein of unknown function
CIBE_0681	6down	-2.1	-2.0	-2.3	-3.0	rpmA	ribosomal protein L27 (BL24)
CIBE_1127	6down	-2.3	-2.5	-2.5	-2.1	-	Membrane protein
CIBE_0552	6down	-2.4	-2.2	-2.1	-2.8	pyrG	CTP synthetase
CIBE_2480	6down	-2.6	-2.2	-2.3	-2.4	amtB	ammonium transporter
CIBE_5895	6down	-2.1	-2.1	-2.3	-3.0	-	HAD family hydrolase
CIBE_0522	6down	-1.9	-2.3	-2.5	-2.9	-	Sulfatase
CIBE_0832	6down	-2.8	-2.6	-1.9	-2.3	-	Membrane protein
CIBE_0954	6down	-2.0	-2.3	-2.5	-2.9	bsaA	putative bacillithiol peroxidase
CIBE_1130	6down	-2.0	-2.3	-2.1	-3.2	-	Flavin reductase domain protein, FMN-binding
CIBE_4027	6down	-2.3	-2.7	-2.3	-2.4	-	conserved exported protein of unknown function
CIBE_2191	6down	-0.7	-2.6	-3.1	-3.4	sufC	sulfur mobilizing ABC protein, ATPase
CIBE_1211	6down	-2.3	-2.9	-2.2	-2.6	-	conserved exported protein of unknown function
CIBE_3033	6down	-2.1	-1.9	-2.2	-3.7	-	Cof-like hydrolase
CIBE_3372	6down	-2.1	-3.1	-2.7	-2.1	-	SCP-like extracellular protein
CIBE_5104	6down	-2.3	-2.5	-2.0	-3.3	-	Haloacid dehalogenase
CIBE_0081	6down	-2.9	-2.9	-2.1	-2.3	-	HD family phosphohydrolase
CIBE_1090	6down	-1.9	-2.7	-2.7	-2.9	-	Ig-like domain-containing protein,putative cell wall binding protein (fragment)
CIBE_5342	6down	-1.7	-2.6	-2.5	-3.4	-	conserved protein of unknown function
CIBE_5325	6down	-1.9	-2.3	-3.3	-2.7	-	conserved protein of unknown function
CIBE_5134	6down	-2.3	-2.8	-2.0	-3.1	flgC	flagellar component of cell-proximal portion of basal-body rod
CIBE_0141	6down	-2.0	-2.1	-2.9	-3.3	-	Uncharacterized glutaredoxin-like 8.6 kDa protein in rubredoxin operon
CIBE_1803	6down	-2.6	-2.7	-2.3	-2.8	yfmM	putative ATP-binding protein
CIBE_0288	6down	-2.4	-2.6	-2.3	-3.1	-	Methyl-accepting chemotaxis sensory transducer
CIBE_4949	6down	-2.3	-2.6	-2.5	-2.9	-	Secretion protein HlyD family protein
CIBE_0541	6down	-1.8	-2.2	-3.4	-3.0	-	protein of unknown function
CIBE_5155	6down	-2.3	-2.8	-1.9	-3.4	-	conserved protein of unknown function
CIBE_5138	6down	-2.1	-2.7	-2.2	-3.5	-	Flagellin
CIBE_4324	6down	-2.3	-2.0	-2.7	-3.7	-	Methyl-accepting chemotaxis protein
CIBE_tRNA19	6down	-3.1	-2.7	-2.2	-2.7	-	Asn tRNA
CIBE_5156	6down	-2.3	-2.5	-2.2	-3.8	-	Glycosyltransferase
CIBE_5136	6down	-2.8	-2.6	-1.4	-3.9	-	OmpA/MotB domain protein
CIBE_5091	6down	-2.9	-2.6	-2.0	-3.3	hpt	Hypoxanthine phosphoribosyltransferase
CIBE_5694	6down	-2.5	-2.6	-3.7	-2.0	-	exported protein of unknown function
CIBE_5133	6down	-2.2	-2.4	-2.0	-4.0	fliE	Flagellar hook-basal body complex protein FliE
CIBE_5946	6down	-2.2	-2.8	-2.5	-3.4	-	Methyl-accepting chemotaxis sensory transducer
CIBE_5061	6down	-2.4	-2.3	-2.9	-3.2	-	putative Methyl-accepting chemotaxis protein
CIBE_0351	6down	-3.2	-3.6	-2.0	-2.2	guaA	GMP synthetase
CIBE_0539	6down	-1.6	-2.5	-3.1	-3.8	gpo	Glutathione peroxidase
CIBE_5693	6down	-2.3	-2.8	-2.8	-3.1	-	S-layer domain-containing protein (fragment)
CIBE_4777	6down	-2.4	-2.8	-2.6	-3.2	-	Methyl-accepting chemotaxis protein
CIBE_4855	6down	-2.3	-2.3	-3.2	-3.3	-	Chemotaxis protein CheA
CIBE_3862	6down	-1.7	-2.4	-3.5	-3.6	ansB	L-aspartase (aspartate ammonia lyase)
CIBE_1125	6down	-2.2	-3.1	-2.5	-3.5	-	Murein hydrolase transporter LrgA
CIBE_4550	6down	-2.8	-3.1	-2.9	-2.5	-	Molybdopterin-guanine dinucleotide biosynthesis protein B
CIBE_5335	6down	-2.6	-2.2	-3.6	-2.8	mglB	methyl-galactoside transporter subunit ; periplasmic-binding component of ABC superfamily
CIBE_4284	6down	-2.4	-3.1	-3.8	-2.0	-	ApbE family lipoprotein
CIBE_1062	6down	-2.8	-2.8	-2.4	-3.5	-	Methyl-accepting chemotaxis protein
CIBE_2186	6down	-3.2	-3.3	-2.4	-2.7	fruK	fructose-1-phosphate kinase
CIBE_3458	6down	-3.4	-2.7	-3.0	-2.5	-	Methyl-accepting chemotaxis protein
CIBE_4553	6down	-3.0	-3.2	-3.0	-2.5	-	conserved protein of unknown function
CIBE_1126	6down	-2.2	-3.7	-2.6	-3.3	-	protein of unknown function
CIBE_2185	6down	-2.8	-3.3	-2.5	-3.3	fruR	transcriptional regulator (DeoR family)
CIBE_4551	6down	-3.3	-3.4	-2.6	-2.6	-	Molybdenum cofactor biosynthesis protein
CIBE_2187	6down	-3.0	-3.5	-2.6	-2.9	fruA	phosphotransferase system (PTS) fructose-specific enzyme IIABC component
CIBE_3631	6down	-1.6	-2.6	-3.1	-4.6	-	Cation transporter
CIBE_5785	6down	-2.0	-3.0	-3.2	-3.8	-	Oxidoreductase
CIBE_4844	6down	-3.2	-3.0	-2.7	-3.3	maeB	NADP-dependent malic enzyme (conversion of malate into pyruvate)
CIBE_4856	6down	-2.8	-3.1	-3.4	-3.4	cheY	regulator of chemotaxis and motility
CIBE_0214	6down	-2.6	-2.6	-3.0	-4.6	nrdB	Ribonucleoside-diphosphate reductase subunit beta
CIBE_4282	6down	-2.0	-3.7	-3.4	-4.0	-	FMN-binding domain protein
CIBE_0213	6down	-2.5	-3.3	-3.0	-4.5	-	protein of unknown function
CIBE_3630	6down	-2.7	-3.4	-3.5	-3.9	csoR	repressor of copper utilisation proteins - Cu(I)
CIBE_1061	6down	-3.0	-3.4	-2.6	-4.5	-	Transferase
CIBE_0212	6down	-3.0	-3.2	-3.5	-4.6	nrdA	Ribonucleoside-diphosphate reductase subunit alpha
CIBE_2867	6down-	-3.8	-4.0	-1.9	-2.2	-	conserved membrane protein of unknown function
CIBE_4061	6down-	-4.1	-3.5	-2.9	-2.1	-	Glycoside hydrolase, family 18
CIBE_4547	6down-	-2.3	-4.2	-3.2	-3.4	hndD	NADP-reducing hydrogenase subunit HndC

CIBE_4549	6down-	-2.8	-4.5	-3.0	-2.8	fdhD	Protein FdhD homolog
CIBE_2868	6down-	-4.1	-4.5	-2.0	-2.7	xpt	xanthine phosphoribosyltransferase
CIBE_4976	6down-	-2.4	-4.4	-3.3	-5.1	-	Methyl-accepting chemotaxis sensory transducer
CIBE_4552	6down-	-3.5	-3.6	-3.9	-4.5	fdhF	Formate dehydrogenase H
CIBE_4062	6down-	-3.1	-3.6	-4.3	-4.8	ytbE	promiscuous aldo/keto reductase
CIBE_0397	6down-	-3.4	-4.1	-3.9	-4.5	-	Bacterial surface protein
CIBE_1759	6down-	-3.5	-3.5	-4.5	-5.0	gltT	proton/sodium-glutamate symport protein
CIBE_1119	6down-	-3.8	-3.6	-4.2	-5.0	-	conserved membrane protein of unknown function
CIBE_4063	6down-	-3.1	-4.0	-4.6	-5.4	-	FMN reductase
CIBE_1120	6down-	-4.8	-3.8	-4.5	-6.4	-	conserved membrane protein of unknown function
CIBE_3701	8up+	1.1	3.7	4.0	3.9	-	conserved protein of unknown function
CIBE_5020	8up+	0.3	5.1	3.9	3.1	bceA	bacitracin ABC efflux transporter (ATP-binding protein)
CIBE_1732	8up+	0.4	2.8	4.6	3.9	yraG	putative spore coat protein
CIBE_4645	8up+	0.5	4.7	3.2	3.1	-	Erythromycin esterase
CIBE_3257	8up+	-0.3	2.8	4.6	3.8	-	PTS beta-glucoside transporter subunit IIBC
CIBE_4643	8up+	0.3	3.9	2.6	2.8	yxdL	ABC transporter (ATP-binding protein); efflux of cationic peptides
CIBE_5019	8up+	-0.2	4.4	2.8	2.6	-	conserved membrane protein of unknown function
CIBE_0318	8up	0.5	3.1	4.1	4.5	-	ABC transporter, ATP-binding protein
CIBE_2546	8up	0.3	2.4	2.8	6.4	-	protein of unknown function
CIBE_0317	8up	0.4	3.1	3.9	4.5	-	ABC transporter, permease protein
CIBE_5103	8up	0.6	3.1	3.8	4.2	-	Membrane protein
CIBE_3697	8up	0.1	2.4	2.1	6.9	-	conserved protein of unknown function
CIBE_5102	8up	0.8	2.8	3.6	4.0	-	Diguanylate cyclase
CIBE_1783	8up	-0.1	1.5	4.6	5.1	-	conserved protein of unknown function
CIBE_2954	8up	0.5	2.4	3.7	3.9	-	conserved protein of unknown function
CIBE_4796	8up	-0.4	2.9	4.4	3.6	-	conserved protein of unknown function
CIBE_3575	8up	-0.3	2.8	4.4	3.5	cooS	Carbon monoxide dehydrogenase
CIBE_4568	8up	0.7	2.9	3.5	3.3	yvcR	putative ABC transporter (ATP-binding protein)
CIBE_0820	8up	0.1	2.2	4.2	3.6	-	Polysaccharide deacetylase
CIBE_5655	8up	0.3	2.8	3.6	3.5	-	Tyrosine protein kinase
CIBE_2308	8up	0.2	2.5	3.9	3.4	-	LemA family protein
CIBE_1684	8up	-0.5	2.1	4.2	3.8	nifJ	Pyruvate-flavodoxin oxidoreductase
CIBE_3300	8up	0.6	2.8	3.6	2.5	cspC	cold-shock protein
CIBE_1784	8up	-0.5	1.2	4.0	4.7	rpsD	30S ribosomal protein S4 B
CIBE_3596	8up	0.2	2.4	3.9	2.9	-	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen
CIBE_1336	8up	1.2	3.0	2.8	2.3	-	PRC-barrel domain protein
CIBE_1733	8up	0.0	2.2	3.8	3.2	yraF	putative spore coat protein
CIBE_5645	8up	0.3	2.9	3.1	3.0	-	Glycosyl transferase, group 1
CIBE_3725	8up	0.2	2.4	3.4	3.3	-	D-galactose-binding periplasmic protein
CIBE_5519	8up	-0.3	2.4	4.2	2.9	-	conserved protein of unknown function
CIBE_3507	8up	0.7	2.2	3.4	2.9	-	conserved protein of unknown function
CIBE_3163	8up	0.4	2.0	3.4	3.4	celB	Cellobiose permease IIC component
CIBE_0545	8up	0.4	2.6	3.2	3.0	-	Cyanophycinase
CIBE_2771	8up	1.3	2.8	2.9	2.1	-	conserved protein of unknown function
CIBE_2045	8up	-0.1	2.9	3.4	2.7	-	conserved protein of unknown function
CIBE_3260	8up	-1.2	2.3	4.1	3.6	-	Transaldolase
CIBE_5520	8up	-0.5	2.1	4.3	3.0	-	Coat F domain protein
CIBE_1086	8up	-0.3	3.0	3.2	2.8	-	conserved exported protein of unknown function
CIBE_5517	8up	-0.6	2.5	4.2	2.6	-	conserved protein of unknown function
CIBE_5328	8up	0.0	2.0	3.0	3.6	-	putative galactoside ABC transporter
CIBE_3572	8up	0.0	2.1	3.5	3.0	norV	flavorubredoxin oxidoreductase
CIBE_0127	8up	0.9	2.6	2.8	2.2	-	Amidohydrolase
CIBE_0098	8up	-0.2	2.9	3.5	2.4	spoVT	transcriptional regulator
CIBE_2663	8up	-0.8	2.6	3.6	3.1	-	Amidohydrolase
CIBE_0544	8up	0.1	2.8	2.8	2.5	-	conserved protein of unknown function
CIBE_3528	8up	0.1	2.5	3.5	2.2	-	Coat F domain protein
CIBE_3577	8up	-0.2	1.4	3.6	3.5	-	Cupin 2 conserved barrel protein
CIBE_0546	8up	0.2	2.2	3.1	2.9	-	Cyanophycin synthetase
CIBE_5454	8up	0.6	2.1	3.2	2.3	yngF	putative Methylglutaconyl-CoA hydratase
CIBE_2057	8up	0.0	1.9	3.0	3.3	-	Glycosyl transferase
CIBE_3642	8up	0.6	2.5	2.4	2.7	-	D-galactose-binding periplasmic protein
CIBE_3958	8up	0.6	2.5	3.1	2.0	-	conserved protein of unknown function
CIBE_5420	8up	-1.2	2.2	3.6	3.6	-	conserved protein of unknown function
CIBE_4858	8up	0.3	2.1	3.1	2.7	bglB	Thermostable beta-glucosidase B
CIBE_2362	8up	-0.3	2.0	3.3	3.1	yhcV	CBS domain-containing protein YhcV
CIBE_1750	8up	0.4	1.5	3.3	2.8	-	conserved protein of unknown function
CIBE_2002	8up	0.6	2.2	2.9	2.2	-	conserved protein of unknown function
CIBE_4218	8up	0.8	2.4	2.7	2.1	acdA	acyl-CoA dehydrogenase
CIBE_4985	8up	-0.2	2.8	3.2	2.2	-	conserved exported protein of unknown function
CIBE_4745	8up	-0.6	2.0	3.2	3.4	-	putative galactoside ABC transporter
CIBE_1188	8up	-0.7	1.2	3.8	3.7	-	Delta-lactam-biosynthetic de-N-acetylase
CIBE_5101	8up	-0.3	2.3	3.2	2.7	-	conserved protein of unknown function
CIBE_4567	8up	0.4	2.1	2.5	2.8	-	conserved membrane protein of unknown function
CIBE_0757	8up	0.6	2.2	3.0	2.1	-	conserved protein of unknown function
CIBE_1745	8up	-0.9	1.5	4.1	3.1	-	conserved protein of unknown function
CIBE_1226	8up	0.4	2.1	2.8	2.4	-	conserved protein of unknown function
CIBE_0065	8up	0.4	2.3	2.7	2.3	-	conserved exported protein of unknown function
CIBE_1734	8up	-0.3	1.5	3.4	2.9	adhB	putative oxidoreductase
CIBE_3627	8up	-0.2	1.9	3.2	2.7	-	FAD-dependent oxidoreductase
CIBE_1669	8up	-0.3	2.1	3.1	2.6	amyC	putative starch degradation products transport system permease protein AmyC
CIBE_5518	8up	-0.6	1.9	3.7	2.5	-	Coat F domain protein
CIBE_3927	8up	-0.1	2.6	2.2	2.8	-	conserved protein of unknown function
CIBE_0306	8up	-0.7	1.9	3.6	2.6	adhE	fused acetaldehyde-CoA dehydrogenase ; iron-dependent alcohol dehydrogenase ; pyruvate-formate lyase deactivase
CIBE_1229	8up	-0.8	2.3	3.1	2.8	-	Stage V sporulation protein AF
CIBE_4835	8up	0.2	1.7	3.0	2.5	-	Ferredoxin hydrogenase
CIBE_2743	8up	-0.4	2.3	3.2	2.2	-	conserved protein of unknown function
CIBE_1494	8up	-0.2	1.3	3.2	2.9	-	Protein CA_C1420
CIBE_5646	8up	0.3	2.3	2.7	1.9	-	conserved membrane protein of unknown function
CIBE_2218	8up	-0.9	1.6	3.6	3.0	dacF	D-alanyl-D-alanine carboxypeptidase DacF
CIBE_2307	8up	-0.5	1.5	3.1	3.1	-	conserved exported protein of unknown function
CIBE_5419	8up	-1.0	1.7	2.9	3.6	-	conserved protein of unknown function

CIBE_2131	8up	0.4	2.0	2.6	2.2	-	Deacetylase
CIBE_2056	8up	-0.2	1.9	3.2	2.2	-	conserved protein of unknown function
CIBE_3019	8up	-0.9	2.2	3.6	2.2	-	conserved protein of unknown function
CIBE_3504	8up	-1.1	0.8	3.4	4.0	-	conserved exported protein of unknown function
CIBE_1735	8up	-0.1	1.9	2.8	2.5	-	Spore coat protein
CIBE_2566	8up	0.3	2.0	2.8	2.0	-	conserved protein of unknown function
CIBE_1545	8up	0.3	1.8	2.8	2.2	-	conserved protein of unknown function
CIBE_1683	8up	0.2	2.2	2.7	2.0	-	conserved protein of unknown function
CIBE_3923	8up	0.1	1.6	2.7	2.6	-	Spore cortex-lytic protein
CIBE_1309	8up	-0.8	2.4	2.4	2.9	-	protein of unknown function
CIBE_5365	8up	-0.9	0.8	3.2	3.7	-	Methyl-accepting chemotaxis sensory transducer
CIBE_5656	8up	-1.3	2.5	3.0	2.6	-	Lipopolysaccharide biosynthesis protein
CIBE_5686	8up	-0.6	1.1	3.1	3.2	-	conserved protein of unknown function
CIBE_2493	8up	-0.3	1.8	2.7	2.5	-	Extracellular solute-binding protein, family 3
CIBE_5100	8up	-0.6	1.9	2.6	2.8	ydaM	putative glycosyltransferase associated to biofilm formation
CIBE_4957	8up	0.0	1.9	2.4	2.3	-	conserved protein of unknown function
CIBE_0510	8up	-0.9	1.9	3.0	2.7	-	Endothelin-converting enzyme 1
CIBE_3002	8up	-1.1	1.5	3.5	2.8	-	conserved protein of unknown function
CIBE_3935	8up	-0.3	1.3	2.9	2.7	-	Small, acid-soluble spore protein beta
CIBE_1670	8up	-0.2	1.6	2.8	2.4	-	Alpha-glucosidase 2
CIBE_3149	8up	-0.1	1.4	2.8	2.4	yodR	putative acyloate-acetoacetate CoA-transferase
CIBE_1312	8up	-0.4	0.8	2.8	3.2	-	Autolysin (fragment)
CIBE_4642	8up	0.0	3.3	1.4	1.7	-	conserved membrane protein of unknown function
CIBE_5644	8up	0.0	2.1	2.3	1.9	-	Glycosyl transferase, family 2
CIBE_3150	8up	-0.2	1.4	2.8	2.4	atoA	acetoacetyl CoA-transferase (subunit A)
CIBE_4958	8up	-0.2	1.7	2.7	2.2	-	conserved protein of unknown function
CIBE_0741	8up	0.2	1.8	2.3	2.1	-	conserved protein of unknown function
CIBE_2744	8up	-1.0	2.2	2.9	2.2	-	protein of unknown function
CIBE_1671	8up	0.1	1.6	2.7	2.0	malL	Oligo-1,6-glucosidase
CIBE_2745	8up	-0.7	2.2	3.1	1.7	rbr3A	Reverse rubrerythrin-1
CIBE_0064	8up	0.1	1.8	2.6	1.8	-	conserved protein of unknown function
CIBE_6033	8up	-1.1	1.6	3.1	2.5	-	Phosphohydrolase
CIBE_2316	8up	0.0	2.0	2.2	1.8	-	CarD family transcriptional regulator
CIBE_4956	8up	0.1	1.7	2.3	2.0	-	Amine oxidase
CIBE_1748	8up	-0.8	1.7	3.4	1.7	-	conserved exported protein of unknown function
CIBE_4402	8up	-0.8	1.7	2.6	2.5	-	Dual specificity protein phosphatase
CIBE_5066	8up	0.2	2.2	2.4	1.3	-	protein of unknown function
CIBE_3516	8up	0.1	1.6	2.4	1.9	-	conserved protein of unknown function
CIBE_5436	8up	-0.8	1.6	2.7	2.3	-	Amino acid permease-associated region
CIBE_3517	8up	-0.1	1.6	2.6	1.8	-	Rubrerythrin
CIBE_2560	8up	-0.5	1.1	2.9	2.4	-	conserved exported protein of unknown function
CIBE_2662	8up	-0.1	2.7	2.1	1.0	-	protein of unknown function
CIBE_1668	8up	-0.6	1.6	2.7	2.0	amyD	putative starch degradation products transport system permease protein AmyD
CIBE_5692	8up	-0.7	1.7	2.5	2.3	-	Glycosyl transferase
CIBE_2939	8up	-0.1	1.6	2.3	2.0	-	D-galactose-binding protein
CIBE_3567	8up	0.3	1.8	2.1	1.4	-	Ni/Fe hydrogenase
CIBE_2039	8up	-1.1	1.7	2.6	2.5	spoIVB	regulatory membrane-associated serine protease
CIBE_3924	8up	-0.2	1.5	2.4	2.0	-	Methyltransferase type 11
CIBE_0742	8up	0.1	1.8	2.2	1.6	-	conserved protein of unknown function
CIBE_3256	8up	0.1	1.8	2.1	1.7	-	Sugar transporter
CIBE_1500	8up	-0.5	1.2	3.1	2.0	-	Ferredoxin
CIBE_2196	8up	-0.9	1.1	2.8	2.7	nifJ	Pyruvate-flavodoxin oxidoreductase
CIBE_5643	8up	0.0	1.8	2.3	1.6	-	Glycosyl transferase, group 1
CIBE_4055	8up	-1.1	1.5	2.6	2.7	-	putative galactoside ABC transporter
CIBE_2661	8up	-0.1	2.6	2.0	1.1	-	protein of unknown function
CIBE_1667	8up	-0.9	1.4	2.9	2.2	-	ABC transporter substrate-binding protein
CIBE_4880	8up	-0.6	1.4	2.7	2.2	-	Pyruvate flavodoxin/ferredoxin oxidoreductase domain protein
CIBE_0641	8up	-0.6	0.7	3.0	2.4	ssp	Small, acid-soluble spore protein 1
CIBE_0047	8up	0.0	1.9	2.0	1.4	-	conserved protein of unknown function
CIBE_0738	8up	-0.1	1.3	2.3	1.8	-	conserved protein of unknown function
CIBE_1081	8up	-1.4	1.5	2.7	2.4	-	conserved exported protein of unknown function
CIBE_4034	8up	-0.4	2.1	2.3	1.3	-	conserved membrane protein of unknown function
CIBE_0740	8up	-0.2	1.5	2.2	1.8	rbr	Rubrerythrin
CIBE_5000	8up	0.2	1.7	2.2	1.1	-	conserved protein of unknown function
CIBE_0773	8up	-0.1	1.6	2.4	1.4	-	conserved protein of unknown function
CIBE_4879	8up	-0.5	1.4	2.4	1.9	-	Pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit
CIBE_1807	8up	-0.2	1.2	2.2	1.9	-	Sporulation protein
CIBE_0231	8up	-0.6	1.3	2.5	1.9	-	conserved protein of unknown function
CIBE_2101	8up	0.1	1.6	2.0	1.3	-	Lactate utilization protein B/C
CIBE_3953	8up	-0.1	1.9	1.6	1.6	-	conserved exported protein of unknown function
CIBE_0739	8up	-0.2	1.3	2.2	1.6	-	Stage V sporulation protein R
CIBE_5688	8up	-0.9	0.4	2.4	3.0	-	conserved protein of unknown function
CIBE_5774	8up	-0.7	1.1	3.0	1.5	-	putative manganese catalase
CIBE_3314	8up	0.0	1.5	2.0	1.4	-	conserved protein of unknown function
CIBE_0737	8up	-0.4	1.2	2.3	1.7	prkA	serine protein kinase
CIBE_2348	8up	-1.7	1.6	3.1	1.8	-	conserved protein of unknown function
CIBE_2879	8up	-0.5	1.0	2.2	2.0	-	Cytochrome b5
CIBE_5642	8up	-0.7	1.7	1.7	1.8	-	Polysaccharide biosynthesis protein
CIBE_2769	8up	-0.3	1.6	2.0	1.3	-	conserved protein of unknown function
CIBE_4807	8up	-0.3	1.6	1.7	1.6	-	exported protein of unknown function
CIBE_0538	8up	-0.3	1.3	1.7	1.8	yabG	sporulation-specific protease
CIBE_2224	8up	-0.1	0.3	2.1	2.2	-	conserved protein of unknown function
CIBE_1771	8up	0.0	1.9	1.6	0.8	-	Membrane protein
CIBE_4865	8up	-1.9	1.8	2.3	2.2	-	Glycosyl transferase
CIBE_5903	8up	-0.9	1.5	2.4	1.4	-	conserved protein of unknown function
CIBE_1043	8up	-0.2	1.4	1.8	1.3	-	Peptidase S8 and S53, subtilisin, kexin, sedolisin
CIBE_3965	8up	-0.6	0.7	2.4	1.7	-	Spore protein
CIBE_4722	8up	-0.5	0.6	2.6	1.6	-	putative galactoside ABC transporter
CIBE_5648	8up	-0.5	1.3	1.7	1.8	-	Glycosyl transferase family 1
CIBE_1232	8up	-0.8	1.0	2.2	1.9	-	Calcium-transporting ATPase 1
CIBE_2198	8up	-0.3	2.4	1.7	0.3	-	protein of unknown function

CIBE_3011	8up	-0.6	1.0	2.4	1.3	-	conserved exported protein of unknown function
CIBE_3600	8up	-0.3	1.4	1.8	1.3	fda	Fructose-bisphosphate aldolase class 1
CIBE_0206	8up	-0.8	0.8	2.0	1.9	-	N-acetylmuramoyl-L-alanine amidase CwlD
CIBE_3070	8up	-0.5	0.5	2.2	1.7	-	Serine acetyltransferase-related protein
CIBE_3462	8up	-0.1	1.5	1.3	1.1	-	Sodium:proton antiporter
CIBE_2293	8up	0.0	0.1	1.7	1.9	-	FAD-dependent oxidoreductase
CIBE_0419	8up	-0.3	1.4	1.4	1.1	nfsB	NAD(P)H-flavin oxidoreductase (nitroreductase)
CIBE_3541	8up	0.1	0.1	1.6	1.8	yrkC	putative dioxygenase; cupin family
CIBE_2065	8up	-0.7	1.3	2.0	0.9	azoR	FMN-dependent NADH-azoreductase
CIBE_4640	8up	-0.1	1.8	1.1	0.7	-	conserved protein of unknown function
CIBE_0807	8up	-1.1	1.1	2.6	1.0	-	conserved protein of unknown function
CIBE_1557	8up	-0.4	1.7	1.5	0.5	-	conserved protein of unknown function
CIBE_4641	8up	-0.1	2.2	0.7	0.6	yvrH	two-component response regulator YvrH involved in cell wall processes [YvrG]
CIBE_5966	8up	0.0	1.6	1.3	0.5	-	conserved protein of unknown function
CIBE_0428	8up	-0.6	1.0	1.9	1.0	-	conserved protein of unknown function
CIBE_5684	8up	-0.7	0.2	2.3	1.5	-	conserved protein of unknown function
CIBE_3428	8up	-0.2	1.5	1.5	0.5	-	conserved protein of unknown function
CIBE_3620	8up	-0.7	1.2	1.6	0.9	-	Uncharacterized NAD(P)H oxidoreductase HI_1544
CIBE_0581	8up	-0.8	1.2	1.8	0.8	-	conserved protein of unknown function
CIBE_2121	8up	-1.0	0.7	2.1	1.1	-	conserved membrane protein of unknown function
CIBE_3649	8up	-1.2	0.5	1.8	1.8	-	Small acid-soluble spore protein, alpha/beta type
CIBE_0042	8up	0.0	1.9	0.8	0.3	-	conserved membrane protein of unknown function
CIBE_1741	8up	-0.5	0.1	1.6	1.8	-	conserved protein of unknown function
CIBE_0040	8up	-0.5	0.0	1.7	1.8	-	Peptidoglycan-binding domain 1 protein
CIBE_1558	8up	-0.3	1.6	1.3	0.4	-	Lysophospholipase
CIBE_3057	8up	-0.8	-0.1	1.6	2.0	-	Glycosyl transferase, family 2
CIBE_0672	8up	-0.2	1.5	0.9	0.5	-	Peptidase M50
CIBE_1544	8up	-0.9	0.9	1.4	1.1	-	Lipase
CIBE_5092	8up	-0.5	1.1	1.2	0.8	-	Sporulation protein YunB
CIBE_0547	8up	-0.8	0.8	1.3	1.2	ispE	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase
CIBE_0754	8up	-0.2	1.4	1.0	0.2	mntP	putative manganese efflux pump MntP
CIBE_1646	8up	-0.4	1.2	1.1	0.5	-	Permease
CIBE_1682	8up	-0.7	0.9	1.2	0.7	-	Peptidase S8 and S53, subtilisin, kexin, sedolisin
CIBE_5685	8up	-1.4	0.0	2.2	1.1	-	conserved protein of unknown function
CIBE_2775	8up	-1.3	0.3	1.7	1.3	-	Small, acid-soluble spore protein beta
CIBE_4959	8up	-0.6	1.2	1.2	0.2	mntR	Transcriptional regulator MntR
CIBE_3698	8up	-0.8	-0.1	1.7	0.8	-	Small acid-soluble spore protein, alpha/beta type
CIBE_0673	8up	-0.4	1.3	0.5	-0.1	-	conserved protein of unknown function
CIBE_2216	8up	-0.4	1.2	1.3	-0.9	-	conserved protein of unknown function
CIBE_5060	8up	-0.9	1.1	0.8	0.2	-	Abortive infection protein
CIBE_2258	8down	-0.7	-0.5	-2.3	-2.6	-	conserved protein of unknown function
CIBE_4352	8down	0.1	-2.0	-2.1	-2.8	-	Pyruvate flavodoxin/ferredoxin oxidoreductase domain protein
CIBE_5053	8down	0.6	-1.3	-1.9	-4.3	-	Ferrous iron transport protein B
CIBE_5055	8down	0.4	-1.6	-1.5	-4.9	-	FeoA family protein
CIBE_5054	8down	0.4	-2.1	-1.8	-4.7	-	FeoA family protein
CIBE_1056	11up	-0.9	-0.3	1.8	2.3	yhxC	putative oxidoreductase
CIBE_2329	11up	-0.8	-0.2	1.7	2.1	-	conserved protein of unknown function
CIBE_4882	11up	-0.5	-0.2	1.6	1.7	-	Metallophosphoesterase
CIBE_1066	11up	-0.5	-0.5	1.4	1.9	-	putative ABC transporter, periplasmic-binding
CIBE_5950	11up	-1.0	-0.2	1.7	1.6	-	conserved protein of unknown function
CIBE_0536	11up	-0.9	-0.3	1.3	1.4	-	Glycosyl transferase, group 1
CIBE_0532	11up	-1.4	-0.5	1.5	1.9	-	Glycosyl transferase, group 1
CIBE_5516	11up	-1.0	-0.3	2.1	0.6	tlp	Protein Tlp homolog
CIBE_0533	11up	-1.0	-0.5	1.5	1.4	-	Spore coat protein
CIBE_4006	11up	-1.1	-0.6	1.5	1.6	-	conserved protein of unknown function
CIBE_4742	11up	-1.1	-0.8	1.4	1.5	yisY	AB hydrolase superfamily protein YisY
CIBE_3050	11up	-1.5	-0.6	1.0	1.9	fdtB	dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase
CIBE_0736	11up	-1.5	-0.4	1.3	0.9	-	conserved protein of unknown function
CIBE_3951	11up	-1.2	-0.8	1.4	0.7	-	Spore protein
CIBE_2913	11up	-1.7	-0.2	1.2	0.7	-	Small, acid-soluble spore protein beta
CIBE_1674	11up	-1.3	-0.9	1.2	0.3	-	Small, acid-soluble spore protein beta
CIBE_3604	11up	-2.6	-1.5	1.3	1.5	-	Ferrous iron transport protein B homolog (fragment)
CIBE_tRNA28	11up	-1.7	-0.9	0.1	0.6	-	Gly tRNA
CIBE_4841	11up	-1.6	-0.8	0.1	0.0	buk	branched-chain fatty-acid kinase
CIBE_3605	11up	-3.0	-1.7	0.6	1.0	-	Ferrous iron transport protein B homolog (fragment)
CIBE_3603	11up	-2.9	-1.7	0.2	1.0	-	Iron transporter FeoA
CIBE_4869	11up	-1.5	-2.5	0.2	-0.4	-	Beta-ketoacyl-acyl-carrier-protein synthase I
CIBE_4341	Unclassified	4.7	3.0	1.9	2.1	-	Sugar-binding protein
CIBE_3250	Unclassified	4.2	2.5	1.5	2.3	-	conserved protein of unknown function
CIBE_3258	Unclassified	-1.6	2.4	4.7	3.9	-	PTS maltose transporter subunit IIBC
CIBE_3259	Unclassified	-2.1	1.6	4.4	3.8	-	putative PTS IIA-like nitrogen-regulatory protein PtsN
CIBE_0988	Unclassified	0.1	1.7	0.5	-0.8	-	TspO
CIBE_0920	Unclassified	-0.5	1.3	0.3	-0.2	-	conserved protein of unknown function
CIBE_0080	Unclassified	-0.8	1.0	0.3	0.3	ykoT	putative glycosyltransferase
CIBE_5443	Unclassified	-1.0	0.9	0.3	-0.3	-	Transcription antiterminator BglG
CIBE_0107	Unclassified	1.1	0.8	-1.0	-1.3	-	Sporulation protein
CIBE_0308	Unclassified	1.5	-0.3	-0.7	-0.8	-	Signal transduction histidine kinase regulating citrate/malate metabolism
CIBE_5197	Unclassified	0.7	0.9	-1.1	-1.6	-	conserved exported protein of unknown function
CIBE_0919	Unclassified	-0.8	1.4	-0.6	-1.3	-	protein of unknown function
CIBE_2260	Unclassified	0.0	0.2	-1.5	-1.4	-	conserved protein of unknown function
CIBE_2839	Unclassified	0.2	0.6	-2.1	-1.7	-	protein of unknown function
CIBE_2277	Unclassified	-0.3	0.1	-1.6	-1.2	xkdU	putative phage protein XkdU
CIBE_0350	Unclassified	-4.1	-4.7	-1.5	-1.4	guaB	inosine-monophosphate dehydrogenase
CIBE_2740	Unclassified	-1.2	-3.2	-4.6	-5.0	treA	trehalose-6-phosphate hydrolase
CIBE_2739	Unclassified	-1.0	-3.4	-5.3	-5.1	treP	phosphotransferase system (PTS) trehalose-specific enzyme IIBC component
CIBE_0034	Unclassified	-3.2	-4.6	-6.5	-4.5	-	conserved protein of unknown function