

TABLE S1. Expression ratios (log₂FC) for all *P. alcaliphila* 34 genes exhibiting statistically significant ($p < 0.05$) change in expression and classified according to RAST annotation

peg ID	Subsystem	Role	Mean (K ₂ CrO ₄ /control) ^a at time <i>t</i> (min) ^b					Mean (biofilm/plank) ^c at 7-h
			Cr5min	Cr30min	Cr60min	Cr90min	Cr120min	
Amino Acids and Derivatives								
23630.peg.1163	A Hypothetical Protein Related to Proline Metabolism	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)		0.6		0.9		
23630.peg.439	Alanine biosynthesis	Chaperone protein HscA				1.0		1.5
23630.peg.441	Alanine biosynthesis	Iron binding protein IscA for iron-sulfur cluster assembly						1.6
23630.peg.3842	Alanine biosynthesis	Cysteine desulfurase (EC 2.8.1.7)		-0.8			-0.8	
23630.peg.2352	Alanine biosynthesis	Alanine racemase (EC 5.1.1.1)	-0.7			-1.1		
23630.peg.442	Alanine biosynthesis	Iron-sulfur cluster assembly scaffold protein IscU				0.9		
23630.peg.444	Alanine biosynthesis	Iron-sulfur cluster regulator IscR		0.6		1.1		
23630.peg.1922	Alanine biosynthesis	Alanine racemase (EC 5.1.1.1)	-0.8					
23630.peg.1669	Arginine and Ornithine Degradation	Ornithine cyclodeaminase (EC 4.3.1.12)	-1.4	-1.5				-1.2
23630.peg.1075	Arginine and Ornithine Degradation	Agmatinase (EC 3.5.3.11)	-0.9	-1.2	1.0			
23630.peg.3649	Arginine Biosynthesis extended	Predicted arginine uptake transporter					-1.4	
23630.peg.2679	Arginine Biosynthesis extended	Glutamate N-acetyltransferase (EC 2.3.1.35) / N-acetylglutamate synthase (EC 2.3.1.1)	0.8	0.7		0.9	0.8	
23630.peg.1957	Arginine Biosynthesis extended	Argininosuccinate lyase (EC 4.3.2.1)		0.8			0.9	
23630.peg.4366	Arginine Biosynthesis extended	Ornithine carbamoyltransferase (EC 2.1.3.3)		0.8				
23630.peg.4365	Arginine Deiminase Pathway	Arginine deiminase (EC 3.5.3.6)		0.8				
23630.peg.114	Aromatic amino acid degradation	Phenylalanine hydroxylase transcriptional activator PhhR		-0.7				
23630.peg.3404	Aromatic amino acid degradation	Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28)	-0.8	-0.6				
23630.peg.4721	Aromatic amino acid interconversions with aryl acids	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits			1.0		0.7	
23630.peg.4722	Branched-Chain Amino Acid Biosynthesis	Leucine dehydrogenase (EC 1.4.1.9)	1.1					1.7
23630.peg.553	Branched-Chain Amino Acid Biosynthesis	Acetolactate synthase large subunit (EC 2.2.1.6)			-0.6			
23630.peg.1232	Branched-Chain Amino Acid Biosynthesis	Dihydroxy-acid dehydratase (EC 4.2.1.9)		0.8				
23630.peg.3589	Chorismate Synthesis	Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.1.51)	-0.9				-0.8	
23630.peg.3156	Chorismate Synthesis	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase II (EC 2.5.1.54)		0.8	0.8		0.7	
23630.peg.482	Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.	Isochorismatase (EC 3.3.2.1)						-1.0
23630.peg.1699	Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.	Tryptophan synthase beta chain (EC 4.2.1.20)		0.7			0.7	
23630.peg.4850	Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.	Isochorismatase (EC 3.3.2.1)			0.6			
23630.peg.513	Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more.	Isochorismatase (EC 3.3.2.1)	0.8					
23630.peg.4374	Cyanophycin Metabolism	Secreted cyanophycinase CphE (EC 3.4.15.6)		-1.3				
23630.peg.4636	Cyanophycin Metabolism	Deblocking aminopeptidase (EC 3.4.11.-) @ Cyanophycinase 2 (EC 3.4.15.6)	-0.9					
23630.peg.4378	Cyanophycin Metabolism	Secreted cyanophycinase CphE (EC 3.4.15.6)	0.7					

23630.peg.1373	Cysteine Biosynthesis	Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25)				1.1		1.7
23630.peg.1697	Cysteine Biosynthesis	Sulfate permease	-1.5	-1.0	1.0		-1.1	
23630.peg.3588	Cysteine Biosynthesis	Adenylylsulfate kinase (EC 2.7.1.25)	-0.9	-0.7			-0.9	
23630.peg.67	Cysteine Biosynthesis	Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2)			-0.4		0.6	
23630.peg.2635	Cysteine Biosynthesis	Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)	1.4				0.6	
23630.peg.2636	Cysteine Biosynthesis	Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) / Adenylylsulfate kinase (EC 2.7.1.25)	0.7		0.5		0.7	
23630.peg.2992	Cysteine Biosynthesis	Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)	1.1	1.1		0.9	0.7	
23630.peg.1371	Cysteine Biosynthesis	Sulfate transport system permease protein CysT	0.8	0.9			0.7	
23630.peg.1333	Cysteine Biosynthesis	Sulfate and thiosulfate binding protein CysP	0.8	0.8			0.8	
23630.peg.3551	Cysteine Biosynthesis	Cys regulon transcriptional activator CysB	0.9	1.1	0.7		1.4	
23630.peg.1370	Cysteine Biosynthesis	Sulfate and thiosulfate binding protein CysP	1.8	1.7		1.6	1.6	
23630.peg.1372	Cysteine Biosynthesis	Sulfate transport system permease protein CysW			-0.5	1.0		
23630.peg.1331	Cysteine Biosynthesis	Sulfate transport system permease protein CysW			-0.6			
23630.peg.504	Glutamate and Aspartate uptake in Bacteria	Glutamate Aspartate periplasmic binding protein precursor GltI (TC 3.A.1.3.4)						1.9
23630.peg.1134	Glutamate and Aspartate uptake in Bacteria	Glutamate Aspartate transport system permease protein GltK (TC 3.A.1.3.4)		0.5			-1.2	
23630.peg.1753	Glutamate and Aspartate uptake in Bacteria	Sodium/glutamate symport protein	0.8	1.0	1.6	1.4	0.6	
23630.peg.503	Glutamate and Aspartate uptake in Bacteria	Glutamate Aspartate transport system permease protein GltJ (TC 3.A.1.3.4)				-0.9		
23630.peg.1133	Glutamate and Aspartate uptake in Bacteria	Glutamate Aspartate transport system permease protein GltJ (TC 3.A.1.3.4)		-1.2				
23630.peg.502	Glutamate and Aspartate uptake in Bacteria	Glutamate Aspartate transport system permease protein GltK (TC 3.A.1.3.4)		-0.7				
23630.peg.3683	Glutamate dehydrogenases	NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	1.0				0.7	1.5
23630.peg.754	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)				-1.2		-1.2
23630.peg.1752	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Aspartate ammonia-lyase (EC 4.3.1.1)				1.8		-1.1
23630.peg.2213	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)	-1.0		-0.6		-1.0	
23630.peg.4738	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	glutamine synthetase family protein		-0.7	-0.7	-1.1		
23630.peg.3106	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)			-0.6			
23630.peg.3290	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)			-0.5			
23630.peg.1387	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	glutamine synthetase family protein			0.7			
23630.peg.2889	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system	0.9	0.8	0.9			
23630.peg.2390	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	glutamine synthetase family protein	0.8					

23630.peg.2860	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	Glutamine amidotransferase class-I (EC 6.3.5.2)	0.9					
23630.peg.2023	Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis	glutamine synthetase family protein	1.0					
23630.peg.4143	Glycine and Serine Utilization	Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)			-0.9			1.9
23630.peg.1566	Glycine and Serine Utilization	L-serine dehydratase (EC 4.3.1.17)		1.0		0.5		
23630.peg.4141	Glycine and Serine Utilization	Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2)			-1.9			
23630.peg.243	Glycine and Serine Utilization	D-serine dehydratase (EC 4.3.1.18)	0.8					
23630.peg.3783	Glycine Biosynthesis	Low-specificity L-threonine aldolase (EC 4.1.2.5)	-0.6					
23630.peg.2011	Glycine cleavage system	Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)						1.3
23630.peg.142	Glycine cleavage system	Glycine cleavage system transcriptional activator GcvA	0.7					
23630.peg.2179	Histidine Biosynthesis	Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)						-1.5
23630.peg.2630	Histidine Biosynthesis	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	-1.2		-1.4			
23630.peg.1086	Histidine Degradation	Formiminoglutamate (EC 3.5.3.8)						0.9
23630.peg.1083	Histidine Degradation	Histidine ammonia-lyase (EC 4.3.1.3)	0.7					1.0
23630.peg.1084	Histidine Degradation	Urocanate hydratase (EC 4.2.1.49)	0.7	-0.5				1.8
23630.peg.1088	Histidine Degradation	Conserved hypothetical protein (perhaps related to histidine degradation)	-1.6			0.6		
23630.peg.1087	Histidine Degradation	Imidazolonepropiionase (EC 3.5.2.7)	-1.3					
23630.peg.1082	Histidine Degradation	Histidine utilization repressor	0.6					
23630.peg.2880	HMG CoA Synthesis	Methylglutaconyl-CoA hydratase (EC 4.2.1.18)	1.5		1.0			1.3
23630.peg.2884	HMG CoA Synthesis	Predicted transcriptional regulator LiuR of leucine degradation pathway, MerR family	0.6	1.2				2.9
23630.peg.2878	HMG CoA Synthesis	Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)	1.0	-0.5	0.9			
23630.peg.424	Leucine Biosynthesis	2-isopropylmalate synthase (EC 2.3.3.13)	1.0					
23630.peg.2883	Leucine Degradation and HMG-CoA Metabolism	Isovaleryl-CoA dehydrogenase (EC 1.3.99.10)	0.7					2.7
23630.peg.2879	Leucine Degradation and HMG-CoA Metabolism	Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)	1.0		0.3			
23630.peg.4333	Leucine Degradation and HMG-CoA Metabolism	Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5)	0.7		1.0			
23630.peg.4332	Leucine Degradation and HMG-CoA Metabolism	Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)			1.2			
23630.peg.3515	Leucine Degradation and HMG-CoA Metabolism	Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4)	-0.7					
23630.peg.2881	Leucine Degradation and HMG-CoA Metabolism	Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4)	0.8					
23630.peg.3781	Lysine Biosynthesis DAP Pathway, GJO scratch	Aspartokinase (EC 2.7.2.4)		0.6				
23630.peg.1022	Lysine degradation	Outer membrane porin, OprD family	-2.3	-1.6	-1.1		-1.7	-0.8
23630.peg.1909	Lysine degradation	Glutarate-semialdehyde dehydrogenase (EC 1.2.1.20); Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)			-0.9	-0.9		1.6
23630.peg.1904	Lysine degradation	Glutarate-semialdehyde dehydrogenase (EC 1.2.1.20); Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)					0.6	2.3
23630.peg.1034	Lysine degradation	Outer membrane porin, OprD family	-1.7				-1.5	

23630.peg.4376	Lysine degradation	Outer membrane porin, OprD family			0.5		-0.7	
23630.peg.1352	Lysine degradation	Outer membrane porin, OprD family		1.1			1.0	
23630.peg.1913	Lysine degradation	L-lysine permease	-0.9	-0.7		-0.9		
23630.peg.650	Lysine degradation	L-lysine permease	0.8	0.6				
23630.peg.3714	Lysine degradation	Outer membrane porin, OprD family	0.6					
23630.peg.2842	Methionine Biosynthesis	Methionine ABC transporter permease protein	1.1	0.7				-2.0
23630.peg.1528	Methionine Biosynthesis	Methionine ABC transporter permease protein	1.0	1.1	0.6		1.3	0.9
23630.peg.884	Methionine Biosynthesis	Methionine ABC transporter ATP-binding protein					0.7	
23630.peg.3140	Methionine Biosynthesis	O-acetylhomoserine sulfhydrylase (EC 2.5.1.49)					0.7	
23630.peg.4714	Methionine Biosynthesis	Transcriptional activator MetR	0.8	0.7			0.8	
23630.peg.1527	Methionine Biosynthesis	Methionine ABC transporter ATP-binding protein	0.8	1.2		1.5	1.0	
23630.peg.2828	Methionine Biosynthesis	Methionine ABC transporter substrate-binding protein	2.0	1.7	1.1	1.5	2.0	
23630.peg.2844	Methionine Biosynthesis	Methionine ABC transporter substrate-binding protein				0.6		
23630.peg.2107	Methionine Biosynthesis	S-adenosylmethionine synthetase (EC 2.5.1.6)				0.6		
23630.peg.2100	Methionine Biosynthesis	Adenosylhomocysteinase (EC 3.3.1.1)				0.8		
23630.peg.3132	Methionine Biosynthesis	5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)	0.7		0.8			
23630.peg.2843	Methionine Biosynthesis	Methionine ABC transporter ATP-binding protein		0.8				
23630.peg.2027	Polyamine Metabolism	Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)	1.1				0.7	1.5
23630.peg.3924	Polyamine Metabolism	Agmatine deiminase (EC 3.5.3.12)					0.6	
23630.peg.2021	Polyamine Metabolism	Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)			0.6		0.7	
23630.peg.2026	Polyamine Metabolism	Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)					0.7	
23630.peg.2549	Polyamine Metabolism	Ornithine decarboxylase (EC 4.1.1.17) / Arginine decarboxylase (EC 4.1.1.19)			1.0			
23630.peg.1076	Polyamine Metabolism	Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)	-1.0		1.1			
23630.peg.977	Polyamine Metabolism	Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1)	-0.8					
23630.peg.1216	Polyamine Metabolism	Spermidine Putrescine ABC transporter permease component potC (TC_3.A.1.11.1)	0.9					
23630.peg.1214	Polyamine Metabolism	ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1)	0.9					
23630.peg.1215	Polyamine Metabolism	Spermidine Putrescine ABC transporter permease component PotB (TC 3.A.1.11.1)	1.0					
23630.peg.798	Proline Synthesis	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	1.0	0.9			0.7	
23630.peg.1596	Proline, 4-hydroxyproline uptake and utilization	L-Proline/Glycine betaine transporter ProP	-1.2	-1.4		-0.5	-1.1	-0.8
23630.peg.1546	Proline, 4-hydroxyproline uptake and utilization	Predicted regulator PutR for proline utilization, GntR family						1.7
23630.peg.1888	Proline, 4-hydroxyproline uptake and utilization	Ketoglutarate semialdehyde dehydrogenase (EC 1.2.1.26)			-0.6			
23630.peg.1905	Putrescine utilization pathways	5-aminovalerate aminotransferase (EC 2.6.1.48) / Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase (EC 2.6.1.19)			-1.0			1.8
23630.peg.2771	Putrescine utilization pathways	Gamma-glutamyl-putrescine oxidase (EC1.4.3.-)			-0.8	-0.9		
23630.peg.4946	Putrescine utilization pathways	Gamma-glutamyl-putrescine oxidase (EC1.4.3.-)			-0.8	-0.9		

23630.peg.3952	Threonine and Homoserine Biosynthesis	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)	-0.9				-0.3
23630.peg.2420	Threonine and Homoserine Biosynthesis	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)				0.5	
23630.peg.1754	Threonine and Homoserine Biosynthesis	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)	-1.0	-1.5			
23630.peg.3492	Threonine and Homoserine Biosynthesis	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)		0.8			
23630.peg.69	Threonine and Homoserine Biosynthesis	Transcriptional regulator, GntR family domain / Aspartate aminotransferase (EC 2.6.1.1)	-0.9				
23630.peg.2993	Threonine and Homoserine Biosynthesis	Homoserine kinase (EC 2.7.1.39)	0.8				
23630.peg.755	Threonine degradation	Threonine dehydratase (EC 4.3.1.19)	0.7	1.1		0.9	
23630.peg.2430	Urea carboxylase and Allophanate hydrolase cluster	Allophanate hydrolase (EC 3.5.1.54)				0.8	
23630.peg.3071	Urea carboxylase and Allophanate hydrolase cluster	Biotin carboxylase (EC 6.3.4.14)	-1.5	-0.8			
23630.peg.859	Urea carboxylase and Allophanate hydrolase cluster	Biotin carboxylase (EC 6.3.4.14)	1.4	-0.6			
23630.peg.4674	Urea carboxylase and Allophanate hydrolase cluster	Allophanate hydrolase 2 subunit 2 (EC 3.5.1.54)		0.8			
23630.peg.4126	Urea carboxylase and Allophanate hydrolase cluster	Urea carboxylase (EC 6.3.4.6)	-1.6				
23630.peg.2426	Urea decomposition	Urea ABC transporter, permease protein UrtB	-1.1	-1.2		-1.5	-1.9
23630.peg.2539	Urea decomposition	Urea ABC transporter, permease protein UrtB	-2.3	-2.8		-1.0	-1.4
23630.peg.2423	Urea decomposition	Urea ABC transporter, ATPase protein UrtE					-1.2
23630.peg.4119	Urea decomposition	Urea carboxylase-related ABC transporter, ATPase protein	-1.0			-1.3	
23630.peg.4125	Urea decomposition	Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10)	-1.7			-1.0	
23630.peg.2424	Urea decomposition	Urea ABC transporter, ATPase protein UrtD				-0.7	
23630.peg.2541	Urea decomposition	Urea ABC transporter, ATPase protein UrtD	-1.5	-1.3		-0.7	
23630.peg.2429	Urea decomposition	Urea carboxylase (EC 6.3.4.6)	-1.3	-2.1		-0.3	
23630.peg.2409	Urea decomposition	Urease beta subunit (EC 3.5.1.5)	0.9	0.7		0.7	
23630.peg.4123	Urea decomposition	Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein				-0.6	
23630.peg.2407	Urea decomposition	Urease alpha subunit (EC 3.5.1.5)		0.6			
23630.peg.4117	Urea decomposition	Urea carboxylase-related ABC transporter, periplasmic substrate-binding protein	-1.4	0.9			
23630.peg.4816	Urea decomposition	Eukaryotic-type low-affinity urea transporter		-0.7			
23630.peg.2540	Urea decomposition	Urea ABC transporter, permease protein UrtC	-1.1				
23630.peg.2376	Urea decomposition	HupE-UreJ family metal transporter	0.9				
23630.peg.2377	Urease subunits	Urease accessory protein UreG	1.0	1.5		0.8	
23630.peg.2408	Urease subunits	Urease alpha subunit (EC 3.5.1.5)			-0.8		
23630.peg.2413	Urease subunits	Urease accessory protein UreD		1.1			
23630.peg.2378	Urease subunits	Urease accessory protein UreF	-1.6				
23630.peg.2412	Urease subunits	Urease gamma subunit (EC 3.5.1.5)	1.0				
Carbohydrates							
23630.peg.2153	Acetyl-CoA fermentation to Butyrate	Electron transfer flavoprotein, alpha subunit	-1.3		-1.2	-0.8	-1.3
23630.peg.3780	Carbon storage regulator	Carbon storage regulator				-0.7	
23630.p.4819	D-galactarate, D-glucarate and D-glycerate catabolism - gjo	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)		-1.3	-0.8	-1.1	
23630.p.4280	D-galactarate, D-glucarate and D-glycerate catabolism - gjo	D-galactarate permease	-1.4	-0.6		-1.0	

23630.peg.4282	D-galactarate, D-glucarate and D-glycerate catabolism - gjo	5-dehydro-4-deoxyglucarate dehydratase (EC 4.2.1.41)			-0.8		-0.6
23630.peg.4279	D-galactarate, D-glucarate and D-glycerate catabolism - gjo	D-galactarate dehydratase (EC 4.2.1.42)	0.7			0.9	0.6
23630.peg.1877	D-galactarate, D-glucarate and D-glycerate catabolism - gjo	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)		0.7		0.7	
23630.peg.4281	D-galactarate, D-glucarate and D-glycerate catabolism - gjo	Glucarate dehydratase (EC 4.2.1.40)		-0.7	-1.0		
23630.peg.4286	D-galactarate, D-glucarate and D-glycerate catabolism - gjo	Glucarate dehydratase (EC 4.2.1.40)			-0.8		
23630.peg.4043	D-galactarate, D-glucarate and D-glycerate catabolism - gjo	Sugar diacid utilization regulator SdaR	-0.9				
23630.peg.1694	D-gluconate and ketogluconates metabolism	Methylglyoxal reductase, acetol producing (EC 1.1.1.-) / 2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)				1.0	
23630.peg.2972	D-gluconate and ketogluconates metabolism	Gluconate utilization system Gnt-I transcriptional repressor	-0.7				
23630.peg.726	Entner-Doudoroff Pathway	Gluconolactonase (EC 3.1.1.17)					-1.5
23630.peg.4818	Entner-Doudoroff Pathway	D-glycerate 2-kinase (EC 2.7.1.-)	2.0	0.5	0.4	0.7	0.9
23630.peg.287	Entner-Doudoroff Pathway	Gluconolactonase (EC 3.1.1.17)			-0.7	-1.0	
23630.peg.4176	Entner-Doudoroff Pathway	Phosphogluconate dehydratase (EC 4.2.1.12)			-0.5		
23630.peg.126	Entner-Doudoroff Pathway	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)	-1.0				
23630.peg.4201	Fermentations: Lactate	Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9); Fructose-6-phosphate phosphoketolase (EC 4.1.2.22)				-1.3	
23630.peg.2611	Fructose utilization	Phosphotransferase system, phosphocarrier protein HPr					-1.7
23630.peg.2532	Fructose utilization	1-phosphofructokinase (EC 2.7.1.56)			-0.8	-1.0	1.3
23630.peg.2531	Fructose utilization	Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) / Fructose-specific phosphocarrier protein HPr (EC 2.7.1.69) / PTS system, fructose-specific IIA component (EC 2.7.1.69)				-0.9	
23630.peg.2533	Fructose utilization	PTS system, fructose-specific IIB component (EC 2.7.1.69) / PTS system, fructose-specific IIC component (EC 2.7.1.69)			-0.6		
23630.peg.4820	Glycerate metabolism	Hydroxypyruvate isomerase (EC 5.3.1.22)			-1.6	-1.8	-0.8
23630.peg.4821	Glycerate metabolism	Glyoxylate carboligase (EC 4.1.1.47)			-0.7	-1.3	
23630.peg.182	Glycerate metabolism	Hydroxypyruvate isomerase (EC 5.3.1.22)			-0.5		
23630.peg.2895	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)	1.2	-0.7		0.2	1.7
23630.peg.2893	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3)	1.5	-0.6		0.5	1.8
23630.peg.2897	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerol-3-phosphate ABC transporter, permease protein UgpA (TC 3.A.1.1.3)	1.8		-0.5	0.8	2.0
23630.peg.1237	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)			1.2	1.1	0.3
23630.peg.337	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerol-3-phosphate regulon repressor, DeoR family				-0.8	
23630.peg.3082	Glycogen metabolism	4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)	-1.4			-0.6	

23630.peg.3079	Glycogen metabolism	Glycogen debranching enzyme (EC 3.2.1.-)			-0.5			
23630.peg.1828	Glycolate, glyoxylate interconversions	Hypothetical protein GlcG in glycolate utilization operon	2.2	1.8		0.0	1.2	0.9
23630.peg.968	Glycolate, glyoxylate interconversions	Phosphoglycolate phosphatase (EC 3.1.3.18)	0.9	0.7			0.7	
23630.peg.1830	Glycolate, glyoxylate interconversions	Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE	0.8		-0.6	-2.0		
23630.peg.1829	Glycolate, glyoxylate interconversions	Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF			-0.9	-2.0		
23630.peg.1831	Glycolate, glyoxylate interconversions	Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD	0.8			-1.5		
23630.peg.4822	Glycolate, glyoxylate interconversions	Transcriptional regulator, LysR family, in glycolate utilization operon			-0.7			
23630.peg.2113	Glycolysis and Gluconeogenesis	Phosphoglycerate kinase (EC 2.7.2.3)						-1.3
23630.peg.4817	Glycolysis and Gluconeogenesis	Pyruvate kinase (EC 2.7.1.40)	2.2		0.8	0.5	1.2	0.2
23630.peg.1827	Glyoxylate bypass	Malate synthase G (EC 2.3.3.9)	3.2	2.1	0.9		2.3	1.1
23630.peg.2957	Glyoxylate bypass	Citrate synthase (si) (EC 2.3.3.1)	1.2	1.2	1.1	0.9	0.9	1.9
23630.peg.1109	Glyoxylate bypass	Malate synthase G (EC 2.3.3.9)	1.2	1.0			0.8	
23630.peg.3654	Glyoxylate bypass	Isocitrate dehydrogenase phosphatase (EC 2.7.11.5)/kinase (EC 3.1.3.-)				-0.9		
23630.peg.3299	Glyoxylate bypass	Isocitrate lyase (EC 4.1.3.1)	0.9	0.6				
23630.peg.2154	Lactate utilization	Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF	-2.0	-0.9			-0.8	-1.3
23630.peg.1826	Lactate utilization	L-lactate permease	3.0	1.9	0.7	0.6	2.5	1.6
23630.peg.621	Lactate utilization	Lactate-responsive regulator LldR in Enterobacteria, GntR family			-0.8			
23630.peg.2552	Lactate utilization	L-lactate dehydrogenase (EC 1.1.2.3)			-0.6			
23630.peg.624	Lactate utilization	D-Lactate dehydrogenase (EC 1.1.2.5)	-1.6		-0.5			
23630.peg.1851	Malonate decarboxylase	Malonate decarboxylase alpha subunit	1.0	1.5		0.9	1.0	1.6
23630.peg.1855	Malonate decarboxylase	Malonate decarboxylase gamma subunit	2.0	0.6		1.0	0.7	1.6
23630.peg.1856	Malonate decarboxylase	Phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.-)	1.0			-0.6		2.0
23630.peg.1857	Malonate decarboxylase	Malonyl CoA acyl carrier protein transacylase (EC 2.3.1.39)					-1.3	
23630.peg.1853	Malonate decarboxylase	Malonate decarboxylase delta subunit					0.5	
23630.peg.1852	Malonate decarboxylase	Triphosphoribosyl-dephospho-CoA synthetase (EC 2.7.8.25)	2.2		-0.6		0.6	
23630.peg.1859	Malonate decarboxylase	Malonate transporter, MadM subunit	0.9		-0.6			
23630.peg.1854	Malonate decarboxylase	Malonate decarboxylase beta subunit	1.2	-0.6				
23630.peg.3081	Maltose and Maltodextrin Utilization	Malto-oligosyltrehalose synthase (EC 5.4.99.15)	-1.4	-1.3	1.0	-1.0		
23630.peg.70	Maltose and Maltodextrin Utilization	Maltoporin (maltose/maltodextrin high-affinity receptor, phage lambda receptor protein)	0.9		0.7			
23630.peg.1401	Mannose Metabolism	Phosphomannomutase (EC 5.4.2.8) / Phosphoglucomutase (EC 5.4.2.2)		0.6	0.7			
23630.peg.4450	Mannose Metabolism	Mannose-6-phosphate isomerase (EC 5.3.1.8) / Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)		-0.9				
23630.peg.3002	Methylcitrate cycle	2-methylcitrate synthase (EC 2.3.3.5)						-1.4
23630.peg.3001	Methylcitrate cycle	Methylisocitrate lyase (EC 4.1.3.30)		0.8				
23630.peg.1234	Methylglyoxal Metabolism	Lactoylglutathione lyase (EC 4.4.1.5)		0.9			0.6	
23630.peg.128	Pentose phosphate pathway	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	1.1	0.9	0.8		0.7	1.1
23630.peg.4416	Pentose phosphate pathway	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	0.9		1.0			1.7
23630.peg.3822	Pentose phosphate pathway	Transketolase, N-terminal section (EC 2.2.1.1)	1.1	0.9			-0.8	

23630.peg.74	Peripheral Glucose Catabolism Pathways	Glucose ABC transport system, periplasmic sugar-binding protein			-0.9	-1.2		0.6
23630.peg.72	Peripheral Glucose Catabolism Pathways	Glucose ABC transport system, inner membrane component 2	0.4	-0.8			-1.1	1.1
23630.peg.71	Peripheral Glucose Catabolism Pathways	Glucose ABC transporter, ATP-binding subunit (EC 3.6.3.-)	1.0		1.0	0.3	0.9	
23630.peg.73	Peripheral Glucose Catabolism Pathways	Glucose ABC transport system, inner membrane component 1	0.9	-0.6				
23630.peg.77	Peripheral Glucose Catabolism Pathways	Glucokinase (EC 2.7.1.2)	0.8					
23630.peg.686	Pyruvate Alanine Serine Interconversions	Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)			0.8		0.8	
23630.peg.2024	Pyruvate Alanine Serine Interconversions	Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)					0.8	
23630.peg.1920	Pyruvate Alanine Serine Interconversions	D-amino acid dehydrogenase small subunit (EC 1.4.99.1)	0.4		2.0	-0.8	2.1	
23630.peg.2130	Pyruvate Alanine Serine Interconversions	Alanine dehydrogenase (EC 1.4.1.1)			-0.8			
23630.peg.1507	Pyruvate metabolism I: anaplerotic reactions, PEP	Pyruvate carboxyl transferase subunit A (EC 6.4.1.1)	1.7	1.0	1.7		1.4	1.3
23630.peg.235	Pyruvate metabolism I: anaplerotic reactions, PEP	Pyruvate kinase (EC 2.7.1.40)						2.1
23630.peg.1506	Pyruvate metabolism I: anaplerotic reactions, PEP	Pyruvate carboxyl transferase subunit B (EC 6.4.1.1)					0.8	
23630.peg.3772	Pyruvate metabolism I: anaplerotic reactions, PEP	Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3)			-0.5			
23630.peg.2964	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4) / Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4)						1.4
23630.peg.631	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	Phosphate acetyltransferase (EC 2.3.1.8)		0.7	1.2		0.9	
23630.peg.1115	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	Acetate permease ActP (cation/acetate symporter)	0.8		-0.8	-1.2		
23630.peg.99	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	Acetyl-coenzyme A synthetase (EC 6.2.1.1)			-0.6			
23630.peg.630	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	Acetate kinase (EC 2.7.2.1)		-1.0				
23630.peg.4873	Serine-glyoxylate cycle	Aconitate hydratase (EC 4.2.1.3)		0.7	0.7		0.8	
23630.peg.1880	Serine-glyoxylate cycle	Malate dehydrogenase (EC 1.1.1.37)	1.9				1.1	
23630.peg.63	TCA Cycle	Malate:quinone oxidoreductase (EC 1.1.99.16)		-1.1	0.6		-0.7	-1.2
23630.peg.4369	TCA Cycle	Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4)	1.1					
23630.peg.3067	Trehalose Biosynthesis	Trehalose synthase (EC 5.4.99.16)	-1.0	-1.8	-0.7		-1.2	
23630.peg.3083	Trehalose Biosynthesis	Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141)		-0.6	1.6		-0.8	
23630.peg.1501	Xylose utilization	Xylulose kinase (EC 2.7.1.17)		-0.9				
Cell Division and Cell Cycle								
23630.peg.3275	Bacterial Cytoskeleton	Cell division protein FtsK	-0.9					-1.7
23630.peg.2603	Bacterial Cytoskeleton	Rod shape-determining protein MreD						1.9
23630.peg.2660	Bacterial Cytoskeleton	Cell division protein MraZ	-0.8	-0.7	-0.6		-0.9	
23630.peg.2672	Bacterial Cytoskeleton	Cell division protein FtsQ		-0.8	-0.8		-0.9	
23630.peg.4844	Bacterial Cytoskeleton	Cell division protein ZipA					-0.9	
23630.peg.2700	Bacterial Cytoskeleton	Chromosome (plasmid) partitioning protein ParA				0.9	0.6	
23630.peg.4253	Bacterial Cytoskeleton	Septum site-determining protein MinC	1.3	1.0	1.0	1.1	1.0	

23630.peg.13	Bacterial Cytoskeleton	Cell division protein DivIC (FtsB), stabilizes FtsL against RasP cleavage					-0.8	
23630.peg.4255	Bacterial Cytoskeleton	Cell division topological specificity factor MinE	0.8	0.7			0.9	
23630.peg.2600	Bacterial Cytoskeleton	Rod shape-determining protein MreB	1.1			0.9	1.2	
23630.peg.3856	Bacterial Cytoskeleton	Septum formation protein Maf				-0.7		
23630.peg.2663	Bacterial Cytoskeleton	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)				-0.6		
23630.peg.2668	Bacterial Cytoskeleton	Cell division protein FtsW				-0.5		
23630.peg.2674	Bacterial Cytoskeleton	Cell division protein FtsZ (EC 3.4.24.-)			-0.8			
23630.peg.308	Bacterial Cytoskeleton	Cell division protein DivIC (FtsB), stabilizes FtsL against RasP cleavage			0.8			
23630.peg.999	Macromolecular synthesis operon	SSU ribosomal protein S21p	1.1			1.2	1.4	
23630.peg.609	Macromolecular synthesis operon	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	0.8			0.9		
23630.peg.4591	MukBEF Chromosome Condensation	Chromosome partition protein MukE	-0.8	-1.1	-0.6	-1.0	-0.8	
23630.peg.4590	MukBEF Chromosome Condensation	Chromosome partition protein MukB	-0.9	-1.0		-1.3	-0.8	
23630.peg.4592	MukBEF Chromosome Condensation	Chromosome partition protein MukF		-1.0				
Cell Wall and Capsule								
23630.peg.4702	Alginate metabolism	Probable poly(beta-D-mannuronate) O-acetylase (EC 2.3.1.-)	-1.1	-1.1		-0.8		-2.0
23630.peg.4701	Alginate metabolism	Alginate biosynthesis protein AlgJ		0.8	0.9	0.9	0.3	-0.7
23630.peg.4012	Alginate metabolism	RNA polymerase sigma-H factor AlgT	-0.8	-1.0			-1.2	
23630.peg.4696	Alginate metabolism	Alginate lyase precursor (EC 4.2.2.3)			-0.5		-0.8	
23630.peg.4703	Alginate metabolism	Outer membrane protein AlgE	-1.4	-1.1			-0.8	
23630.peg.3770	Alginate metabolism	Alginate biosynthesis transcriptional activator		-0.7			-0.7	
23630.peg.4443	Alginate metabolism	Outer membrane protein AlgE	0.8	1.2			1.1	
23630.peg.4442	Alginate metabolism	Alginate biosynthesis protein AlgK precursor				-1.1		
23630.peg.4706	Alginate metabolism	Alginate biosynthesis protein Alg8				0.9		
23630.peg.4699	Alginate metabolism	Alginate biosynthesis protein AlgX		0.8	0.7	1.0		
23630.peg.4439	Alginate metabolism	GDP-mannose 6-dehydrogenase (EC 1.1.1.132)				1.1		
23630.peg.4708	Alginate metabolism	GDP-mannose 6-dehydrogenase (EC 1.1.1.132)				1.3		
23630.peg.4698	Alginate metabolism	Alginate lyase precursor (EC 4.2.2.3)			0.7			
23630.peg.4700	Alginate metabolism	Alginate o-acetyltransferase AlgF		-1.0				
23630.peg.2117	Alginate metabolism	Alginate lyase precursor (EC 4.2.2.3)		-0.7				
23630.peg.4704	Alginate metabolism	Alginate biosynthesis protein AlgK precursor		0.7				
23630.peg.4444	Alginate metabolism	Poly (beta-D-mannuronate) C5 epimerase precursor (EC 5.1.3.-)	-1.2					
23630.peg.4705	Alginate metabolism	Alginate biosynthesis protein Alg44	-1.2					
23630.peg.4446	Alginate metabolism	Alginate lyase precursor (EC 4.2.2.3)	-1.0					
23630.peg.3578	CMP-N-acetylneuraminate Biosynthesis	N-Acetylneuraminate cytidyltransferase (EC 2.7.7.43)		-0.7				
23630.peg.2296	Core Oligosaccharide Glycosylation in Pseudomonas	Hypothetical protein FIG015671 in large core OS assembly cluster						-1.3
23630.peg.2289	Core Oligosaccharide Glycosylation in Pseudomonas	Glycosyl transferase in large core OS assembly cluster				-0.6		-1.3
23630.peg.2287	Core Oligosaccharide Glycosylation in Pseudomonas	Glycosyl transferase in large core OS assembly cluster	-0.9	-0.7	-0.9		-1.1	
23630.peg.2290	Core Oligosaccharide Glycosylation in Pseudomonas	alpha-1,3-rhamnosyltransferase		-0.7			-0.7	
23630.peg.24	KDO2-Lipid A biosynthesis	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-)						-1.8
23630.peg.1658	KDO2-Lipid A biosynthesis	Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-)			0.7		0.7	
23630.peg.4252	KDO2-Lipid A biosynthesis	Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.-)	0.8		0.8			

23630.peg.2675	KDO2-Lipid A biosynthesis	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (EC 3.5.1.-)	0.6				
23630.peg.4617	Lipid A modifications	Transcriptional regulatory protein PhoP	-0.7		0.8		
23630.peg.2810	Lipid A modifications	Sensor protein PhoQ (EC 2.7.13.3)	0.6				
23630.peg.25	Lipopolysaccharide assembly	Outer membrane protein H precursor			0.9		-0.9
23630.peg.616	Lipopolysaccharide assembly	Outer membrane lipoprotein SmpA, a component of the essential YaeT outer-membrane protein assembly complex					-0.7
23630.peg.26	Lipopolysaccharide assembly	Outer membrane protein assembly factor YaeT precursor				-0.9	
23630.peg.2621	Lipopolysaccharide assembly	Uncharacterized ABC transporter, ATP-binding protein YrbF	0.8		0.9		
23630.peg.2282	LOS core oligosaccharide biosynthesis	Lipopolysaccharide core biosynthesis protein WaaP (EC 2.7.-.), heptosyl-I-kinase		0.9	0.6		
23630.peg.2280	LOS core oligosaccharide biosynthesis	Lipopolysaccharide heptosyltransferase I (EC 2.4.1.-)			-0.6		
23630.peg.2918	Murein Hydrolases	Membrane-bound lytic murein transglycosylase D precursor (EC 3.2.1.-)	0.9		1.2		
23630.peg.2458	Peptidoglycan Biosynthesis	Penicillin-insensitive transglycosylase (EC 2.4.2.-) & transpeptidase PBP-1C	0.8	0.7		0.9	1.1
23630.peg.1692	Peptidoglycan Biosynthesis	Murein-DD-endopeptidase (EC 3.4.99.-)	0.8		0.7	0.8	
23630.peg.2664	Peptidoglycan Biosynthesis	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (EC 6.3.2.13)			-0.6		
23630.peg.4577	Peptidoglycan Biosynthesis	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)		0.6			
23630.peg.786	Peptidoglycan Biosynthesis	Membrane-bound lytic murein transglycosylase B precursor (EC 3.2.1.-)		0.7			
23630.peg.794	Peptidoglycan Biosynthesis	Penicillin-binding protein 2 (PBP-2)	-0.8				
23630.peg.1598	Recycling of Peptidoglycan Amino Acids	AmpG permease		-1.4			
23630.peg.1702	Rhamnose containing glycans	UDP-glucose 4-epimerase (EC 5.1.3.2)	0.9			0.8	1.0
23630.peg.286	Rhamnose containing glycans	UDP-glucose 4-epimerase (EC 5.1.3.2)			-1.2	-1.1	2.4
23630.peg.1305	Rhamnose containing glycans	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)			0.7		
23630.peg.895	Rhamnose containing glycans	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)		0.6			
23630.peg.289	Sialic Acid Metabolism	TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter				-0.8	
23630.peg.1874	Sialic Acid Metabolism	TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter	0.7		1.2	0.7	
23630.peg.2386	Sialic Acid Metabolism	TRAP-type transport system, small permease component, predicted N-acetylneuraminate transporter		-1.2	-0.9		
23630.peg.2971	Sialic Acid Metabolism	TRAP-type transport system, periplasmic component, predicted N-acetylneuraminate-binding protein	-0.9				
23630.peg.288	Sialic Acid Metabolism	TRAP-type transport system, periplasmic component, predicted N-acetylneuraminate-binding protein	0.7				
23630.peg.2627	UDP-N-acetylmuramate from Fructose-6-phosphate Biosynthesis	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)		0.8	1.0		0.6
Cofactors, Vitamins, Prosthetic Groups, Pigments							
23630.peg.299	5-FCL-like protein	Formyltetrahydrofolate deformylase (EC 3.5.1.10)	1.3	0.6	0.8	0.6	1.2
23630.peg.770	5-FCL-like protein	Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)		1.1		0.7	
23630.peg.752	5-FCL-like protein	Alcohol dehydrogenase (EC 1.1.1.1)		0.6		0.7	
23630.peg.2392	5-FCL-like protein	Alcohol dehydrogenase (EC 1.1.1.1)	1.2			0.8	
23630.peg.1741	5-FCL-like protein	Alcohol dehydrogenase (EC 1.1.1.1)			-1.2		

23630.peg.2435	5-FCL-like protein	IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)					1.1
23630.peg.972	5-FCL-like protein	Alcohol dehydrogenase (EC 1.1.1.1)	-1.1		-0.5		
23630.peg.4595	5-FCL-like protein	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)			0.9		
23630.peg.2898	5-FCL-like protein	Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	0.8		0.9		
23630.peg.2498	5-FCL-like protein	Serine hydroxymethyltransferase (EC 2.1.2.1)		0.6			
23630.peg.2887	5-FCL-like protein	Butyryl-CoA dehydrogenase (EC 1.3.99.2)		0.7			
23630.peg.4727	Biotin biosynthesis	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	-1.0	-1.4	-0.8		-1.7
23630.peg.1099	Biotin biosynthesis	Biotin synthase (EC 2.8.1.6)			0.6	0.5	
23630.peg.816	Biotin biosynthesis	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)	1.4	0.6		1.0	0.6
23630.peg.253	Biotin biosynthesis	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)		0.7	2.2		1.4
23630.peg.3898	Biotin biosynthesis	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)			-0.8		
23630.peg.507	Biotin biosynthesis	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)			-0.6		
23630.peg.1097	Biotin biosynthesis	Biotin synthesis protein BioH	-1.7	-1.2			
23630.peg.1095	Biotin biosynthesis	Dethiobiotin synthetase (EC 6.3.3.3)				0.9	
23630.peg.3130	Biotin biosynthesis Experimental	NfuA Fe-S protein maturation		0.6			
23630.peg.1098	Biotin synthesis cluster	8-amino-7-oxononanoate synthase (EC 2.3.1.47)		0.8		1.0	0.6
23630.peg.210	Biotin synthesis cluster	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)		0.5			0.9
23630.peg.3359	Biotin synthesis cluster	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)			-1.0		
23630.peg.4537	Biotin synthesis cluster	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	-0.7		-0.7		
23630.peg.1590	Cobalamin synthesis	Cobalamin biosynthesis protein CbiG / Cobalt-precorrin-3b C17-methyltransferase				0.8	
23630.peg.3704	Cobalamin synthesis	Cob(I)alamin adenosyltransferase (EC 2.5.1.17)	-1.2				
23630.peg.2685	Coenzyme A Biosynthesis	2-dehydropantoate 2-reductase (EC 1.1.1.169)				-0.8	
23630.peg.706	Coenzyme B12 biosynthesis	Optional hypothetical component of the B12 transporter BtuN			1.1	-0.7	
23630.peg.1585	Coenzyme B12 biosynthesis	Cobalt-precorrin-6x reductase (EC 1.3.1.54)		0.9			0.7
23630.peg.1611	Coenzyme B12 biosynthesis	CobN component of cobalt chelatase involved in B12 biosynthesis				0.9	
23630.peg.1588	Coenzyme B12 biosynthesis	Cobalt-precorrin-8x methylmutase (EC 5.4.1.2)		0.7		1.0	
23630.peg.1609	Coenzyme B12 biosynthesis	ChlD component of cobalt chelatase involved in B12 biosynthesis				1.2	
23630.peg.707	Coenzyme B12 biosynthesis	Outer membrane vitamin B12 receptor BtuB			-0.9		
23630.peg.3701	Coenzyme B12 biosynthesis	Adenosylcobinamide-phosphate synthase			-0.6		
23630.peg.1608	Coenzyme B12 biosynthesis	Precorrin-6A synthase (EC 2.1.1.152)			-0.6		
23630.peg.864	Coenzyme B12 biosynthesis	Outer membrane vitamin B12 receptor BtuB	0.8		0.9		
23630.peg.3695	Coenzyme B12 biosynthesis	Cobalamin synthase		-1.2			
23630.peg.1587	Coenzyme B12 biosynthesis	Cobalamin biosynthesis protein CobG		0.6			
23630.peg.865	Coenzyme B12 biosynthesis	Vitamin B12 ABC transporter, B12-binding component BtuF		0.7			

23630.peg.1586	Coenzyme B12 biosynthesis	Cobalt-precorrin-6y C5-methyltransferase (EC 2.1.1.-) / Cobalt-precorrin-6y C15-methyltransferase [decarboxylating] (EC 2.1.1.-)	0.9			
23630.peg.3702	Coenzyme B12 biosynthesis	Cobalamin biosynthesis protein BluB @ 5,6-dimethylbenzimidazole synthase, flavin destructase family	-1.0			
23630.peg.4952	Coenzyme PQQ synthesis	Coenzyme PQQ synthesis protein E		-0.9		-0.8
23630.peg.2762	Coenzyme PQQ synthesis	Coenzyme PQQ synthesis protein B		-1.2		
23630.peg.4955	Coenzyme PQQ synthesis	Coenzyme PQQ synthesis protein B		-1.2		
23630.peg.2763	Coenzyme PQQ synthesis	Coenzyme PQQ synthesis protein C		-0.8		
23630.peg.4954	Coenzyme PQQ synthesis	Coenzyme PQQ synthesis protein C		-0.8		
23630.peg.1560	Folate Biosynthesis	GTP cyclohydrolase I (EC 3.5.4.16) type 2	-0.8	-0.6		
23630.peg.274	Folate Biosynthesis	FolM Alternative dihydrofolate reductase 1		0.8		
23630.peg.966	Folate Biosynthesis	Anthranilate synthase, amidotransferase component (EC 4.1.3.27) @ Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85)	-0.8			
23630.peg.3435	Heme and Siroheme Biosynthesis	Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22)		0.6	-1.0	
23630.peg.3270	Heme and Siroheme Biosynthesis	Siroheme synthase / Precorrin-2 oxidase (EC 1.3.1.76) / Sirohydrochlorin ferrochelatase (EC 4.99.1.4) / Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)		-0.5		
23630.peg.954	Heme and Siroheme Biosynthesis	Protoporphyrinogen IX oxidase, novel form, HemJ (EC 1.3.-.-)	-0.8			
23630.peg.4434	Molybdenum cofactor biosynthesis	Molybdenum cofactor biosynthesis protein MoaD				0.6
23630.peg.1366	Molybdenum cofactor biosynthesis	Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1)	0.4	0.7	1.0	0.8
23630.peg.1103	Molybdenum cofactor biosynthesis	DNA-binding domain of ModE / Molybdate-binding domain of ModE	0.9	0.6	0.9	
23630.peg.3840	Molybdenum cofactor biosynthesis	Molybdenum cofactor biosynthesis protein MoaA		0.7		
23630.peg.1364	Molybdenum cofactor biosynthesis	Molybdenum ABC transporter, periplasmic molybdenum-binding protein ModA (TC 3.A.1.8.1)	0.9	1.1		
23630.peg.1365	Molybdenum cofactor biosynthesis	Molybdenum transport system permease protein ModB (TC 3.A.1.8.1)	0.9	1.1		
23630.peg.4910	Molybdenum cofactor biosynthesis	Molybdenum transport ATP-binding protein ModC (TC 3.A.1.8.1)	-0.8			
23630.peg.2308	NAD and NADP cofactor biosynthesis global	ADP-ribose pyrophosphatase (EC 3.6.1.13)				-1.2
23630.peg.3122	NAD and NADP cofactor biosynthesis global	Ribosyl nicotinamide transporter, PnuC-like				1.3
23630.peg.3926	NAD and NADP cofactor biosynthesis global	Nicotinamide-nucleotide adenyltransferase, NadR family (EC 2.7.7.1) / Ribosylnicotinamide kinase (EC 2.7.1.22)	-0.6	0.7		-0.7
23630.peg.2523	NAD and NADP cofactor biosynthesis global	Quinolate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)	0.8	0.8		0.8
23630.peg.4072	NAD and NADP cofactor biosynthesis global	Nicotinamidase (EC 3.5.1.19)			-2.5	0.9
23630.peg.4073	NAD and NADP cofactor biosynthesis global	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)	-1.0		-1.2	
23630.peg.4071	NAD and NADP cofactor biosynthesis global	Nudix-related transcriptional regulator NrtR	-0.9		-0.8	
23630.peg.2520	NAD and NADP cofactor biosynthesis global	Quinolate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)	0.8	0.7		
23630.peg.3927	NAD and NADP cofactor biosynthesis global	Ribosyl nicotinamide transporter, PnuC-like	0.8			

23630.peg.797	NAD and NADP cofactor biosynthesis global	Nicotinate-nucleotide adenyltransferase (EC 2.7.7.18)	0.9					
23630.peg.3743	Pterin carbinolamine dehydratase	Homogentisate 1,2-dioxygenase (EC 1.13.11.5)		0.9	-0.6	0.8		1.4
23630.peg.3742	Pterin carbinolamine dehydratase	Fumarylacetoacetase (EC 3.7.1.2)		1.2		1.0	0.7	1.9
23630.peg.3744	Pterin carbinolamine dehydratase	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)		1.1		0.7		2.9
23630.peg.1885	Pterin carbinolamine dehydratase	Fumarylacetoacetate hydrolase family protein				0.9	0.8	
23630.peg.3741	Pterin carbinolamine dehydratase	Maleylacetoacetate isomerase (EC 5.2.1.2) @ Glutathione S-transferase, zeta (EC 2.5.1.18)	-0.7	1.1		0.5		
23630.peg.1878	Pterin carbinolamine dehydratase	Fumarylacetoacetate hydrolase family protein			0.7	0.7		
23630.peg.3565	Pterin carbinolamine dehydratase	Biosynthetic Aromatic amino acid aminotransferase alpha (EC 2.6.1.57) @ Aromatic-amino-acid aminotransferase (EC 2.6.1.57)			0.7			
23630.peg.115	Pterin carbinolamine dehydratase	Phenylalanine-4-hydroxylase (EC 1.14.16.1)		0.7				
23630.peg.3678	Pyridoxin (Vitamin B6) Biosynthesis	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)						-1.3
23630.peg.4517	Pyridoxin (Vitamin B6) Biosynthesis	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)			0.7		0.7	
23630.peg.651	Pyridoxin (Vitamin B6) Biosynthesis	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	1.0	0.9	0.8	0.9	0.7	
23630.peg.3590	Pyridoxin (Vitamin B6) Biosynthesis	Phosphoserine aminotransferase (EC 2.6.1.52)				0.9		
23630.peg.1260	Pyridoxin (Vitamin B6) Biosynthesis	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)			0.7			
23630.peg.2848	Pyridoxin (Vitamin B6) Biosynthesis	Pyridoxal kinase (EC 2.7.1.35)	0.8					
23630.peg.986	Pyridoxin (Vitamin B6) Biosynthesis	4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)	0.8					
23630.peg.4177	Pyridoxin (Vitamin B6) Biosynthesis	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	1.2					
23630.peg.2765	Pyrroloquinoline Quinone biosynthesis	Coenzyme PQQ synthesis protein E				-0.9	-0.8	
23630.peg.2764	Pyrroloquinoline Quinone biosynthesis	Coenzyme PQQ synthesis protein D			-0.6			
23630.peg.4953	Pyrroloquinoline Quinone biosynthesis	Coenzyme PQQ synthesis protein D			-0.6			
23630.peg.875	Riboflavin, FMN and FAD metabolism	Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)	0.9					1.3
23630.peg.212	Riboflavin, FMN and FAD metabolism in plants	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61) / FAD-dependent cmnm(5)s(2)U34 oxidoreductase						1.7
23630.peg.4569	Riboflavin, FMN and FAD metabolism in plants	C-terminal domain of CinA type S; Protein Implicated in DNA repair function with RecA and MutS	0.8					
23630.peg.4160	Thiamin biosynthesis	Thiamin ABC transporter, transmembrane component	-0.7	-1.0	-0.7	-0.8	-0.7	
23630.peg.1151	Thiamin biosynthesis	tRNA S(4)U 4-thiouridine synthase (former ThiI) / Rhodanese-like domain required for thiamine synthesis	1.0		0.6			
23630.peg.1179	Thiamin biosynthesis	Sulfur carrier protein ThiS	0.9		0.8			
23630.peg.2007	Ubiquinone Biosynthesis	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase (EC 1.14.13.-)		0.7				
23630.peg.2183	Ubiquinone Biosynthesis - gjo	Ubiquinone/menaquinone biosynthesis methyltransferase UbiE (EC 2.1.1.-)					0.8	
23630.peg.78	Ubiquinone Biosynthesis - gjo	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase (EC 1.14.13.-)		-0.7		-0.9		
23630.peg.1431	Ubiquinone Biosynthesis - gjo	Chorismate--pyruvate lyase (EC 4.1.3.40)			0.6	1.1		
DNA Metabolism								
23630.peg.3595	2-phosphoglycolate salvage	Similar to phosphoglycolate phosphatase, clustered with ubiquinone biosynthesis SAM-dependent O-methyltransferase		0.7		1.3	0.6	

23630.peg.3858	2-phosphoglycolate salvage	Similar to phosphoglycolate phosphatase, clustered with ribosomal large subunit pseudouridine synthase C	-0.9		-0.9	
23630.peg.3464	DNA processing cluster	FIG000557: hypothetical protein co-occurring with RecR	-0.8		-0.6	-0.7
23630.peg.4861	DNA Repair Base Excision	DNA-3-methyladenine glycosylase II (EC 3.2.2.21)				1.2
23630.peg.301	DNA Repair Base Excision	Exodeoxyribonuclease I (EC 3.1.11.1)			-0.8	-0.8
23630.peg.1656	DNA Repair Base Excision	DNA-3-methyladenine glycosylase (EC 3.2.2.20)	1.4	1.6	0.8	1.2
23630.peg.1784	DNA Repair Base Excision	DNA polymerase I (EC 2.7.7.7)			-0.6	
23630.peg.799	DNA Repair Base Excision	DNA-3-methyladenine glycosylase II (EC 3.2.2.21)	1.0		0.9	
23630.peg.420	DNA repair, bacterial	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)		1.0		1.2
23630.peg.3892	DNA repair, bacterial	SOS-response repressor and protease LexA (EC 3.4.21.88)	1.4	1.3		1.2
23630.peg.3219	DNA repair, bacterial	DNA repair protein RadC			1.4	-1.9
23630.peg.2579	DNA repair, bacterial	ADA regulatory protein / Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)				-0.6
23630.peg.2494	DNA repair, bacterial	DNA repair protein RadaA			0.8	
23630.peg.1286	DNA repair, bacterial	A/G-specific adenine glycosylase (EC 3.2.2.-)		0.9		
23630.peg.2707	DNA repair, bacterial	DNA repair protein RadC	-1.2			
23630.peg.1123	DNA repair, bacterial DinG and relatives	DinG family ATP-dependent helicase CPE1197		-0.7	-1.1	-1.2
23630.peg.4492	DNA repair, bacterial MutL-MutS system	DNA mismatch repair protein MutS		-0.7		-0.7
23630.peg.4398	DNA repair, bacterial photolyase	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)		0.6		1.1
23630.peg.2804	DNA repair, bacterial RecBCD pathway	Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)	-0.9	-0.7		-0.8
23630.peg.2802	DNA repair, bacterial RecBCD pathway	Exodeoxyribonuclease V gamma chain (EC 3.1.11.5)	-0.8		-0.7	
23630.peg.4570	DNA repair, bacterial RecFOR pathway	RecA protein	1.0	0.7		0.9
23630.peg.2784	DNA repair, bacterial UvrD and related helicases	ATP-dependent DNA helicase pcrA (EC 3.6.1.-)		-0.7		-0.6
23630.peg.4933	DNA repair, bacterial UvrD and related helicases	ATP-dependent DNA helicase pcrA (EC 3.6.1.-)		-0.7		-0.6
23630.peg.1928	DNA repair, bacterial UvrD and related helicases	ATP-dependent DNA helicase Rep			-0.7	
23630.peg.4301	DNA repair, UvrABC system	Excinuclease cho (excinuclease ABC alternative C subunit)				-1.1
23630.peg.2778	DNA structural proteins, bacterial	Integration host factor alpha subunit	-0.8			-0.8
23630.peg.4939	DNA structural proteins, bacterial	Integration host factor alpha subunit	-0.8			-0.8
23630.peg.4843	DNA structural proteins, bacterial	Chromosome partition protein smc	-1.1		-0.8	-0.8
23630.peg.3474	DNA structural proteins, bacterial	DNA-binding protein HU-beta			0.7	1.1
23630.peg.2436	DNA structural proteins, bacterial	DNA-binding protein Fis	0.9		0.7	
23630.peg.1423	DNA structural proteins, bacterial	DNA-binding protein HU ## PA5348 type	0.9			
23630.peg.4600	DNA-replication	Chromosomal replication initiator protein DnaA				0.9
23630.peg.1419	DNA-replication	ATP-dependent DNA helicase RecG (EC 3.6.1.-)				-1.0
23630.peg.2803	DNA-replication	Exodeoxyribonuclease V beta chain (EC 3.1.11.5)	-1.0			-0.9
23630.peg.1112	DNA-replication	DNA polymerase III epsilon subunit (EC 2.7.7.7)			-1.1	-0.9
23630.peg.471	DNA-replication	DNA polymerase III chi subunit (EC 2.7.7.7)				0.6
23630.peg.3103	DNA-replication	DNA polymerase III alpha subunit (EC 2.7.7.7)	-1.2	-0.8		
23630.peg.3886	DNA-replication	Transcription-repair coupling factor		0.7		
23630.peg.2781	Restriction-Modification System	Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	-1.1	-0.9		-1.5
23630.peg.4936	Restriction-Modification System	Type I restriction-modification system, DNA-methyltransferase subunit M (EC 2.1.1.72)	-1.1	-0.9		-1.5
23630.peg.2782	Restriction-Modification System	Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)				-1.0

23630.peg.4935	Restriction-Modification System	Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)					-1.0
23630.peg.2780	Restriction-Modification System	Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)					-0.6
23630.peg.4937	Restriction-Modification System	Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)					-0.6
23630.peg.641	Restriction-Modification System	Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	-0.9				
23630.peg.2716	Type I Restriction-Modification	Type I restriction-modification system, specificity subunit S (EC 3.1.21.3)	-1.4	-0.7			-1.3
23630.peg.1159	Uracil-DNA glycosylase	Domain often clustered or fused with uracil-DNA glycosylase		0.5			
<i>Dormancy and Sporulation</i>							
23630.peg.272	Persister Cells	Cell division inhibitor					0.6
23630.peg.4419	Sporulation-associated proteins with broader functions	Peptidyl-tRNA hydrolase (EC 3.1.1.29)			1.1		
<i>Fatty Acids, Lipids, and Isoprenoids</i>							
23630.peg.3850	Fatty Acid Biosynthesis FASII	Acyl carrier protein					-0.8
23630.peg.3820	Fatty Acid Biosynthesis FASII	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	1.2	1.0			0.9
23630.peg.198	Fatty Acid Biosynthesis FASII	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)			-0.5		
23630.peg.3365	Fatty Acid Biosynthesis FASII	3-oxoacyl-[acyl-carrier-protein] synthase, KASI (EC 2.3.1.41)			-0.5		
23630.peg.2469	Fatty Acid Biosynthesis FASII	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)			-0.5		
23630.peg.3542	Fatty Acid Biosynthesis FASII	Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)			0.7		
23630.peg.3851	Fatty Acid Biosynthesis FASII	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)		-0.7			
23630.peg.2061	Fatty acid metabolism cluster	Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)					1.4
23630.peg.4561	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Diacylglycerol kinase (EC 2.7.1.107)					-1.3
23630.peg.2793	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Aldehyde dehydrogenase (EC 1.2.1.3)	-1.2				-0.4
23630.peg.2761	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Aldehyde dehydrogenase (EC 1.2.1.3)			-0.8	-1.1	-0.3
23630.peg.4956	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Aldehyde dehydrogenase (EC 1.2.1.3)			-0.8	-1.1	-0.3
23630.peg.3260	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)					1.1
23630.peg.3911	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	-1.7		-0.6	-0.8	-1.0
23630.peg.3076	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Cardiolipin synthetase (EC 2.7.8.-)		-1.0	-0.6		-0.4
23630.peg.3406	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)					0.8
23630.peg.338	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	0.9	-1.2		-0.8	0.8

23630.peg.2391	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Aldehyde dehydrogenase (EC 1.2.1.3)	0.9			-1.0	
23630.peg.3372	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Diacylglycerol kinase (EC 2.7.1.107)				0.4	
23630.peg.3910	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Glycerol kinase (EC 2.7.1.30)	-1.5		-0.9		
23630.peg.1652	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)			-0.8		
23630.peg.132	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)			-0.7		
23630.peg.4041	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Glycerate kinase (EC 2.7.1.31)			-0.7		
23630.peg.1651	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)	0.9		0.7		
23630.peg.4347	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)			0.8		
23630.peg.2725	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Aldehyde dehydrogenase (EC 1.2.1.3)	-0.7	-1.1			
23630.peg.870	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Phosphatidylglycerophosphatase A (EC 3.1.3.27)			-0.8		
23630.peg.29	Glycerolipid and Glycerophospholipid Metabolism in Bacteria	Phosphatidate cytidyltransferase (EC 2.7.7.41)			1.0		
23630.peg.12	Isoprenoid Biosynthesis	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.60)		0.7	0.7		0.6
23630.peg.3289	Isoprenoid Biosynthesis	Hydroxymethylglutaryl-CoA reductase (EC 1.1.1.34)			-0.6		
23630.peg.28	Nonmevalonate Branch of Isoprenoid Biosynthesis	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)	-1.2				-1.4
23630.peg.4415	Nonmevalonate Branch of Isoprenoid Biosynthesis	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)	1.2		1.0		
23630.peg.2241	Phospholipid and Fatty acid biosynthesis related cluster	FIG022199: FAD-binding protein					-1.0
23630.peg.2244	Phospholipid and Fatty acid biosynthesis related cluster	FIG027190: Putative transmembrane protein	-1.0				-1.0
23630.peg.2242	Phospholipid and Fatty acid biosynthesis related cluster	FIG064705: cation/hydrogen antiporter					-0.9
23630.peg.3616	Phospholipid and Fatty acid biosynthesis related cluster	FIG027190: Putative transmembrane protein	1.3			0.8	1.1
23630.peg.2237	Phospholipid and Fatty acid biosynthesis related cluster	3-hydroxydecanoyl-[ACP] dehydratase (EC 4.2.1.60)	-1.1	-0.8	-0.5		-0.9
23630.peg.2247	Phospholipid and Fatty acid biosynthesis related cluster	Lysophospholipid acyltransferase		-0.9			-0.8
23630.peg.2226	Phospholipid and Fatty acid biosynthesis related cluster	3-oxoacyl-[ACP] synthase (EC 2.3.1.41) FabV like		0.8	0.6	0.9	
23630.peg.2254	Phospholipid and Fatty acid biosynthesis related cluster	3-oxoacyl-[ACP] synthase		0.6	1.1		
23630.peg.2243	Phospholipid and Fatty acid biosynthesis related cluster	FIG021862: membrane protein, exporter		0.5			
23630.peg.2248	Phospholipid and Fatty acid biosynthesis related cluster	FIG143263: Glycosyl transferase	-1.0				
23630.peg.1073	Polyhydroxybutyrate metabolism	D-beta-hydroxybutyrate permease	-2.2	-0.6	-1.6	-1.2	-2.5
23630.peg.2185	Polyhydroxybutyrate metabolism	polyhydroxyalkanoate granule-associated protein PhaI	-1.1				-0.8
23630.peg.4334	Polyhydroxybutyrate metabolism	Acetyl-CoA acetyltransferase (EC 2.3.1.9)		0.6			0.7
23630.peg.2983	Polyhydroxybutyrate metabolism	D-beta-hydroxybutyrate permease				-0.8	
23630.peg.1650	Triacylglycerol metabolism	Putative lipase in cluster with Phosphatidate cytidyltransferase				0.9	
Iron acquisition and metabolism							
23630.peg.1579	ABC transporter [iron.B12.siderophore.hemin]	ABC transporter (iron.B12.siderophore.hemin) , permease component					1.4

23630.peg.1580	ABC transporter [iron.B12.siderophore.hemin]	ABC transporter (iron.B12.siderophore.hemin) , periplasmic substrate-binding component	-2.2	-2.8		-2.2	-2.2	
23630.peg.1583	ABC transporter [iron.B12.siderophore.hemin]	Outer membrane (iron.B12.siderophore.hemin) receptor	-1.3	-1.8			-1.2	
23630.peg.1582	ABC transporter [iron.B12.siderophore.hemin]	ABC transporter (iron.B12.siderophore.hemin) , ATP-binding component		-0.9				
23630.peg.4736	Heme, hemin uptake and utilization systems in GramNegatives	Ferrichrome transport ATP-binding protein FhuC (TC 3.A.1.14.3)	2.2	1.6	1.1		1.5	1.5
23630.peg.766	Heme, hemin uptake and utilization systems in GramNegatives	Ferrichrome transport ATP-binding protein FhuC (TC 3.A.1.14.3)	-1.8		0.7		-0.9	
23630.peg.544	Heme, hemin uptake and utilization systems in GramNegatives	Paraquat-inducible protein B		-0.8			-0.9	
23630.peg.703	Heme, hemin uptake and utilization systems in GramNegatives	Outer membrane receptor proteins, mostly Fe transport				-0.7		
23630.peg.564	Heme, hemin uptake and utilization systems in GramNegatives	ABC-type hemin transport system, ATPase component				-0.6		
23630.peg.673	Heme, hemin uptake and utilization systems in GramNegatives	Putative heme iron utilization protein		-0.7				
23630.peg.545	Heme, hemin uptake and utilization systems in GramNegatives	Paraquat-inducible protein A		-0.7				
23630.peg.1531	Heme, hemin uptake and utilization systems in GramNegatives	Heme oxygenase HemO, associated with heme uptake	0.9					
23630.peg.1530	Heme, hemin uptake and utilization systems in GramPositives	FIG039061: hypothetical protein related to heme utilization	1.6	0.7	0.9		0.9	
23630.peg.3632	Heme, hemin uptake and utilization systems in GramPositives	FIG039061: hypothetical protein related to heme utilization		0.9				
23630.peg.566	Hemin transport system	Periplasmic hemin-binding protein	-1.0	-0.7	1.0	-1.5	-1.9	
23630.peg.888	Hemin transport system	Ferric siderophore transport system, periplasmic binding protein TonB				1.1		
23630.peg.2008	Iron acquisition in Streptococcus	Ferric iron ABC transporter, iron-binding protein	1.3	1.7	0.6		1.2	
23630.peg.4641	Siderophore Pyoverdine	ABC transporter in pyoverdin gene cluster, permease component	-1.2	-0.6	0.8			-1.5
23630.peg.4646	Siderophore Pyoverdine	FIG139991: Putative thiamine pyrophosphate-requiring enzyme	-2.6		0.8			-1.3
23630.peg.4723	Siderophore Pyoverdine	Sigma factor PvdS, controlling pyoverdin biosynthesis		-0.5			-0.7	
23630.peg.4725	Siderophore Pyoverdine	L-ornithine 5-monooxygenase (EC 1.13.12.-), PvdA of pyoverdin biosynthesis	1.1	0.6		1.0	0.7	
23630.peg.4642	Siderophore Pyoverdine	ABC transporter in pyoverdin gene cluster, ATP-binding component				1.1	1.1	
23630.peg.4647	Siderophore Pyoverdine	FIG137594: Putative iron-regulated membrane protein	0.9	1.4	1.1	1.3	1.2	
23630.peg.4645	Siderophore Pyoverdine	FIG137877: Hypothetical protein in pyoverdin gene cluster		0.6		1.2		
23630.peg.4643	Siderophore Pyoverdine	FIG014801: Cation ABC transporter, periplasmic cation-binding protein	-0.1	0.9	0.9	2.1		
23630.peg.4732	Siderophore Pyoverdine	FIG006220: Hypothetical MbtH-like protein		-0.7				
23630.peg.4734	Siderophore Pyoverdine	Hypothetical protein PvdY		-0.7				
23630.peg.4640	Siderophore Pyoverdine	ABC transporter in pyoverdin gene cluster, periplasmic component	-1.1					

Membrane Transport

23630.peg.1573	A TRAP transporter and a hypothetical	TRAP transporter, 4TM/12TM fusion protein, unknown substrate 1					0.6	
23630.peg.1574	A TRAP transporter and a hypothetical	TRAP transporter solute receptor, unknown substrate 1	1.4				0.9	
23630.peg.1572	A TRAP transporter and a hypothetical	DUF1850 domain-containing protein	1.0					
23630.peg.3767	ABC transporter alkylphosphonate (TC 3.A.1.9.1)	Phosphonate ABC transporter permease protein phnE (TC 3.A.1.9.1)	-1.2					-1.3
23630.peg.3768	ABC transporter alkylphosphonate (TC 3.A.1.9.1)	Phosphonate ABC transporter phosphate-binding periplasmic component (TC 3.A.1.9.1)	-1.4					-0.9
23630.peg.3769	ABC transporter alkylphosphonate (TC 3.A.1.9.1)	Phosphonate ABC transporter ATP-binding protein (TC 3.A.1.9.1)		0.9	1.7		0.5	
23630.peg.837	ABC transporter branched-chain amino acid (TC 3.A.1.4.1)	High-affinity branched-chain amino acid transport system permease protein LivH (TC 3.A.1.4.1)	0.8				0.6	
23630.peg.2585	ABC transporter dipeptide (TC 3.A.1.5.2)	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)						2.0
23630.peg.2583	ABC transporter dipeptide (TC 3.A.1.5.2)	Dipeptide transport system permease protein DppC (TC 3.A.1.5.2)		0.8				
23630.peg.2589	ABC transporter dipeptide (TC 3.A.1.5.2)	Dipeptide-binding ABC transporter, periplasmic substrate-binding component (TC 3.A.1.5.2)		0.8				
23630.peg.1186	Bacterial signal recognition particle (SRP)	Signal recognition particle receptor protein FtsY (=alpha subunit) (TC 3.A.5.1.1)	0.8		0.7			
23630.peg.3249	Conjugative transfer	Conjugative transfer protein TrbB		0.7				-0.4
23630.peg.4501	Conjugative transfer	Conjugative transfer protein TrbL	-1.5	-1.1	-0.4		-1.5	
23630.peg.4503	Conjugative transfer	Conjugative transfer protein TrbJ			-0.5		0.6	
23630.peg.3253	Conjugative transfer	Conjugative transfer protein TrbJ					0.7	
23630.peg.4504	Conjugative transfer	Conjugative transfer protein TrbE			0.9		0.7	
23630.peg.3250	Conjugative transfer	Conjugative transfer protein TrbC				-0.9		
23630.peg.4497	Conjugative transfer	Conjugative transfer protein TrbI		0.7				
23630.peg.4507	Conjugative transfer	Conjugative transfer protein TrbB	-2.5					
23630.peg.4500	Conjugative transfer	Conjugative transfer protein TrbF	0.7					
23630.peg.3802	General Secretion Pathway	General secretion pathway protein G					-0.7	
23630.peg.3796	General Secretion Pathway	General secretion pathway protein M			-0.8			
23630.peg.4306	Magnesium transport	Mg/Co/Ni transporter MgtE / CBS domain		-0.8		-1.4		
23630.peg.3064	Magnesium transport	Mg(2+) transport ATPase protein C				0.9		
23630.peg.3010	Magnesium transport	Magnesium and cobalt transport protein CorA			-0.6			
23630.peg.4056	Multi-subunit cation antiporter	Na(+) H(+) antiporter subunit G	0.8					-1.3
23630.peg.4052	Multi-subunit cation antiporter	Na(+) H(+) antiporter subunit C					0.7	
23630.peg.4051	Multi-subunit cation antiporter	Na(+) H(+) antiporter subunit A; Na(+) H(+) antiporter subunit B			-0.8	-1.0		
23630.peg.4053	Multi-subunit cation antiporter	Na(+) H(+) antiporter subunit D	0.6					
23630.peg.1207	NhaA, NhaD and Sodium-dependent phosphate transporters	Sodium-dependent phosphate transporter		0.7				
23630.peg.2854	sigma-Fimbriae	Sigma-fimbriae uncharacterized paralogous subunit					-0.7	
23630.peg.2852	sigma-Fimbriae	Sigma-fimbriae chaperone protein			-1.0			
23630.peg.2850	sigma-Fimbriae	Sigma-fimbriae tip adhesin			0.7			
23630.peg.2851	sigma-Fimbriae	Sigma-fimbriae usher protein	1.0		0.9			
23630.peg.354	Ton and Tol transport systems	Outer membrane lipoprotein omp16 precursor		0.7		0.5	0.8	2.0
23630.peg.1603	Ton and Tol transport systems	TonB-dependent receptor	-1.0		1.2		-0.8	
23630.peg.2968	Ton and Tol transport systems	TonB-dependent receptor					0.7	

23630.peg.3867	Ton and Tol transport systems	MotA/TolQ/ExbB proton channel family protein	0.8				0.7	
23630.peg.1602	Ton and Tol transport systems	TonB-dependent receptor					0.7	
23630.peg.892	Ton and Tol transport systems	TonB system biopolymer transport component; Chromosome segregation ATPase	1.2	0.8			1.0	
23630.peg.1597	Ton and Tol transport systems	Outer membrane receptor proteins, likely involved in siderophore uptake @ TonB-dependent siderophore receptor			1.4	-0.7		
23630.peg.889	Ton and Tol transport systems	Biopolymer transport protein ExbD/TolR	-0.8	-0.7	-0.6		0.7	
23630.peg.887	Ton and Tol transport systems	TPR domain protein, putative component of TonB system					0.8	
23630.peg.891	Ton and Tol transport systems	MotA/TolQ/ExbB proton channel family protein					0.8	
23630.peg.3825	Ton and Tol transport systems	TonB-dependent receptor			-0.7			
23630.peg.1570	Ton and Tol transport systems	Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid		-0.6				
23630.peg.2967	Ton and Tol transport systems	TonB-dependent receptor	0.8	0.6				
23630.peg.2553	Ton and Tol transport systems	TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins		1.1				
23630.peg.3723	Ton and Tol transport systems	TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins	-1.2					
23630.peg.2631	Transport of Nickel and Cobalt	Additional periplasmic component NikK of nickel ECF transporter	-0.9				-1.1	
23630.peg.106	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, periplasmic component	1.1				0.9	1.6
23630.peg.1848	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, periplasmic component	-1.0	-1.3	0.7		-1.4	
23630.peg.290	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, large permease component		-0.8	-0.8		-1.1	
23630.peg.2389	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, periplasmic component	1.6				0.9	
23630.peg.102	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, periplasmic component			-1.3	-1.2		
23630.peg.2970	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, large permease component				-1.0		
23630.peg.2641	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, large permease component	-0.6			-0.5		
23630.peg.2387	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, large permease component			-0.9			
23630.peg.3818	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, small permease component	0.8		-0.7			
23630.peg.100	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, large permease component			-0.6			
23630.peg.1313	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, large permease component			-0.6			
23630.peg.1070	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, periplasmic component			-0.6			
23630.peg.1068	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, large permease component	0.8	0.7				

23630.peg.3819	TRAP Transporter collection	TRAP-type C4-dicarboxylate transport system, periplasmic component	0.8						
23630.peg.4677	TRAP Transporter unknown substrate 5	TRAP transporter solute receptor, unknown substrate 5			0.8				-2.2
23630.peg.4683	TRAP Transporter unknown substrate 5	TRAP dicarboxylate transporter, DctM subunit, unknown substrate 5			0.7				
23630.peg.1711	TRAP Transporter unknown substrate 6	TRAP dicarboxylate transporter, DctM subunit, unknown substrate 6			-0.8				
23630.peg.1764	TRAP Transporter unknown substrate 7	TRAP dicarboxylate transporter, DctQ subunit, unknown substrate 6	-0.9	-1.2	-0.7				
23630.peg.1765	TRAP Transporter unknown substrate 7	TRAP dicarboxylate transporter, DctM subunit, unknown substrate 6			-0.6				
23630.peg.1763	TRAP Transporter unknown substrate 9	TRAP transporter solute receptor, unknown substrate 6		-1.1					
23630.peg.4983	Tricarboxylate transport system	Tricarboxylate porin OpdH	-1.6	-0.8					-0.7
23630.peg.1881	Tricarboxylate transport system	Tricarboxylate transport membrane protein TctA	1.1						0.6
23630.peg.4323	Tricarboxylate transport system	Tricarboxylate transport membrane protein TctA	-0.9	0.6	0.8			-1.2	
23630.peg.1321	Tricarboxylate transport system	Tricarboxylate porin OpdH		-0.9	-0.9	-0.9		-0.8	
23630.peg.4019	Tricarboxylate transport system	Tricarboxylate transport sensor protein TctE		0.8				0.6	
23630.peg.4324	Tricarboxylate transport system	Tricarboxylate transport protein TctB		-1.0		-0.9			
23630.peg.4021	Tricarboxylate transport system	Tricarboxylate porin OpdH			-1.3	-0.3			
23630.peg.4022	Tricarboxylate transport system	Tricarboxylate transport protein TctC	0.7			0.9			
23630.peg.4289	Tricarboxylate transport system	Tricarboxylate transport membrane protein TctA			-0.6				
23630.peg.4679	Tricarboxylate transport system	Tricarboxylate porin OpdH			1.1				
23630.peg.4025	Tricarboxylate transport system	Ammonia monooxygenase		-1.2					
23630.peg.4024	Tricarboxylate transport system	Tricarboxylate transport membrane protein TctA		-0.6					
23630.peg.4288	Tricarboxylate transport system	Tricarboxylate transport protein TctB	0.4						
23630.peg.4287	Tricarboxylate transport system	Tricarboxylate transport protein TctC	0.5						
23630.peg.4326	Tricarboxylate transport system	Tricarboxylate porin OpdH	0.9						
23630.peg.1883	Tricarboxylate transport system	Tricarboxylate transport protein TctC	0.9						
23630.peg.2178	Twin-arginine translocation system	Twin-arginine translocation protein TatA	-0.8						
23630.peg.4474	Type IV pilus	Type IV pilus biogenesis protein PilE							-1.4
23630.peg.2204	Type IV pilus	Type IV pilus biogenesis protein PilN		-0.9	-0.6	-0.8		-1.0	
23630.peg.2207	Type IV pilus	Type IV pilus biogenesis protein PilQ		-1.2	-0.8	-1.2		-0.9	
23630.peg.2205	Type IV pilus	Type IV pilus biogenesis protein PilO		-1.0		-0.9		-0.9	
23630.peg.4469	Type IV pilus	type 4 fimbrial biogenesis protein FimU						-0.7	
23630.peg.2206	Type IV pilus	Type IV pilus biogenesis protein PilP			-0.7			-0.7	
23630.peg.1160	Type IV pilus	Twitching motility protein PilT	0.8					0.8	
23630.peg.2873	Type IV pilus	Twitching motility protein PilT				-1.0			
23630.peg.2513	Type IV pilus	Type IV fimbrial assembly protein PilC		-0.8		-0.8			
23630.peg.4466	Type IV pilus	Two-component sensor PilS	0.8	0.6		1.2			
23630.peg.2512	Type IV pilus	Leader peptidase (Prepilin peptidase) (EC 3.4.23.43) / N-methyltransferase (EC 2.1.1.-)			0.6				
23630.peg.4472	Type IV pilus	Type IV fimbrial biogenesis protein PilX	0.9						
23630.peg.1716	Type VI secretion systems	Uncharacterized protein similar to VCA0109	-1.0	-0.9	0.8	1.1			-1.3
23630.peg.625	Type VI secretion systems	ClpB protein							-1.2
23630.peg.1726	Type VI secretion systems	Uncharacterized protein ImpJ/VasE		-0.5		1.3			1.8
23630.peg.1719	Type VI secretion systems	Protein ImpG/VasA	-1.3	-1.2				-1.1	
23630.peg.3175	Type VI secretion systems	Uncharacterized protein homologous to Paeru. PA2364		-0.8				-0.8	
23630.peg.3171	Type VI secretion systems	Uncharacterized protein ImpA						-0.8	

23630.peg.3174	Type VI secretion systems	Uncharacterized protein ImpJ/VasE		-0.6	-0.8		-0.7
23630.peg.2564	Type VI secretion systems	VgrG protein	-0.9				-0.5
23630.peg.1714	Type VI secretion systems	Uncharacterized protein ImpB		1.0		1.4	0.4
23630.peg.3176	Type VI secretion systems	Uncharacterized protein ImpB	1.0			0.9	0.7
23630.peg.1517	Type VI secretion systems	VgrG protein	1.1	1.2	0.7	1.4	0.7
23630.peg.3177	Type VI secretion systems	Uncharacterized protein ImpC	0.9				0.8
23630.peg.3180	Type VI secretion systems	Protein ImpG/VasA	1.2				0.9
23630.peg.3179	Type VI secretion systems	Uncharacterized protein ImpF	1.5	0.8	0.9		1.3
23630.peg.2546	Type VI secretion systems	ClpB protein		-1.5		-1.0	
23630.peg.1728	Type VI secretion systems	IcmF-related protein	-1.3			-0.2	
23630.peg.1722	Type VI secretion systems	Sigma-54 dependent transcriptional regulator				0.7	
23630.peg.3182	Type VI secretion systems	ClpB protein	0.6			1.0	
23630.peg.1516	Type VI secretion systems	Secreted protein Hcp				1.0	
23630.peg.1720	Type VI secretion systems	Uncharacterized protein ImpH/VasB		-0.8	-0.6		
23630.peg.1713	Type VI secretion systems	Uncharacterized protein ImpA			0.7		
23630.peg.1727	Type VI secretion systems	Outer membrane protein ImpK/VasF, OmpA/MotB domain		-0.8			
23630.peg.1724	Type VI secretion systems	Uncharacterized protein ImpI/VasC		0.7			
23630.peg.3181	Type VI secretion systems	Uncharacterized protein ImpH/VasB	0.8				
Metabolism of Aromatic Compounds							
23630.peg.847	Benzoate degradation	Benzoate 1,2-dioxygenase beta subunit (EC 1.14.12.10)	0.8		-0.8		-0.5
23630.peg.3499	Benzoate degradation	Benzoate transport protein		0.8	0.7		0.9
23630.peg.844	Benzoate degradation	benzoate MFS transporter BenK		0.8		0.8	
23630.peg.845	Benzoate degradation	1,2-dihydroxycyclohexa-3,5-diene-1-carboxylate dehydrogenase (EC 1.3.1.25)	0.8	0.9		0.9	
23630.peg.848	Benzoate degradation	Benzoate 1,2-dioxygenase alpha subunit (EC 1.14.12.10)	0.7		-0.6		
23630.peg.839	Benzoate degradation	benzoate-specific porin		1.0			
23630.peg.846	Benzoate degradation	Benzoate 1,2-dioxygenase, ferredoxin reductase component	1.1				
23630.peg.3052	Biphenyl Degradation	biphenyl-2,3-diol 1,2-dioxygenase III-related protein			-0.6		
23630.peg.4339	Biphenyl Degradation	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1.-)		1.0			
23630.peg.842	Catechol branch of beta-ketoadipate pathway	Muconolactone isomerase (EC 5.3.3.4)	0.8	0.9			0.7
23630.peg.831	Catechol branch of beta-ketoadipate pathway	3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6); Glutaconate CoA-transferase subunit B (EC 2.8.3.12)	-1.3	-1.0		-1.3	
23630.peg.841	Catechol branch of beta-ketoadipate pathway	Catechol 1,2-dioxygenase (EC 1.13.11.1)		0.7			
23630.peg.843	Catechol branch of beta-ketoadipate pathway	Muconate cycloisomerase (EC 5.5.1.1)		0.9			
23630.peg.2064	Gentisare degradation	putative 4-hydroxybenzoyl-CoA thioesterase	1.0				
23630.peg.3983	n-Phenylalkanoic acid degradation	enoyl-CoA hydratase, R-specific					1.8
23630.peg.4147	Protocatechuate branch of beta-ketoadipate pathway	PhaK-like protein		-1.0	-0.7		-0.8
23630.peg.2131	Protocatechuate branch of beta-ketoadipate pathway	Protocatechuate 3,4-dioxygenase beta chain (EC 1.13.11.3)			-0.9		
23630.peg.2594	Protocatechuate branch of beta-ketoadipate pathway	4-carboxymuconolactone decarboxylase (EC 4.1.1.44)		0.7			
Miscellaneous							
23630.peg.3606	Broadly distributed proteins not in subsystems	YciL protein			0.8		0.7
23630.peg.2330	Scaffold proteins for [4Fe-4S] cluster assembly (MRP family)	Epoxyqueuosine (oQ) reductase QueG			-0.8		-0.5

23630.peg.2340 Scaffold proteins for [4Fe-4S] cluster assembly (MRP family) HflC protein -0.6

Motility and Chemotaxis

23630.peg.1228	Bacterial Chemotaxis	Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)						-1.6
23630.peg.2444	Bacterial Chemotaxis	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	-1.1		1.1		-0.9	
23630.peg.1437	Bacterial Chemotaxis	Flagellar motor switch protein FliG	-1.0		-0.5		-0.8	
23630.peg.1441	Bacterial Chemotaxis	Flagellar motor switch protein FliM	1.0	0.9	2.4	0.7	0.7	
23630.peg.4745	Bacterial Chemotaxis	Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)			-0.6	-0.7		
23630.peg.3342	Bacterial Chemotaxis	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)		-1.2		-0.7		
23630.peg.125	Bacterial Chemotaxis	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)	-2.4		0.9	1.2		
23630.peg.731	Bacterial Chemotaxis	Chemotaxis protein CheC -- inhibitor of MCP methylation			-0.8			
23630.peg.3120	Bacterial Chemotaxis	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)			-0.8			
23630.peg.1442	Bacterial Chemotaxis	Flagellar motor switch protein FliN			1.1			
23630.peg.2527	Bacterial Chemotaxis	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)		-0.8				
23630.peg.4789	Flagellar motility	RNA polymerase sigma factor for flagellar operon			-0.8		-0.9	
23630.peg.3110	Flagellar motility	Chemotaxis protein CheV (EC 2.7.3.-)	-0.8		-0.8		-0.8	
23630.peg.1211	Flagellar motility	Predicted signal transduction protein					-0.7	
23630.peg.1836	Flagellar motility	Flagellar basal-body rod modification protein FlgD		1.1	0.7	0.7	-0.7	
23630.peg.4772	Flagellar motility	Flagellum-specific ATP synthase FliI		-0.7	-0.7		-0.7	
23630.peg.1447	Flagellar motility	Flagellar biosynthesis protein FlhA				-0.9		
23630.peg.2325	Flagellar motility	Flagellar motor rotation protein MotA			0.6			
23630.peg.1840	Flagellar motility	Flagellar L-ring protein FlgH			0.7			
23630.peg.1819	Flagellum	RNA polymerase sigma factor for flagellar operon						-1.0
23630.peg.4743	Flagellum	Flagellar basal-body P-ring formation protein FlgA						1.2
23630.peg.4780	Flagellum	Flagellar motor switch protein FliN						1.7
23630.peg.4750	Flagellum	Flagellar basal-body rod protein FlgF						2.0
23630.peg.1835	Flagellum	Flagellar basal-body rod protein FlgC				0.8	-1.0	
23630.peg.1820	Flagellum	Flagellar motor rotation protein MotA		-0.8			-0.8	
23630.peg.1841	Flagellum	Flagellar P-ring protein FlgI					-0.8	
23630.peg.4760	Flagellum	Flagellin protein FlaG		-1.0	-0.6		-0.8	
23630.peg.4771	Flagellum	Flagellar assembly protein FliH			-1.3		-0.8	
23630.peg.1844	Flagellum	Flagellar hook-associated protein FlgL					-0.8	
23630.peg.1824	Flagellum	Flagellin protein FlaA	0.8		1.1		0.6	
23630.peg.4753	Flagellum	Flagellar P-ring protein FlgI	0.8	0.6			0.7	
23630.peg.4770	Flagellum	Flagellar motor switch protein FliG			-0.8	-1.4		
23630.peg.1443	Flagellum	Flagellar biosynthesis protein FliP				-1.2		
23630.peg.4767	Flagellum	Flagellar regulatory protein FleQ				-0.9		
23630.peg.4773	Flagellum	Flagellar protein FliJ				-0.8		
23630.peg.1838	Flagellum	Flagellar basal-body rod protein FlgF		0.6		0.7		
23630.peg.1440	Flagellum	Flagellar regulatory protein FleQ	0.9		1.6	0.7		
23630.peg.2326	Flagellum	Flagellar motor rotation protein MotB			-0.8			
23630.peg.4782	Flagellum	Flagellar biosynthesis protein FliP	-0.9		-0.7			

23630.peg.4755	Flagellum	Flagellar hook-associated protein FlgK						-0.7
23630.peg.4754	Flagellum	Flagellar protein FlgJ [peptidoglycan hydrolase] (EC 3.2.1.-)						-0.7
23630.peg.4795	Flagellum	Flagellar motor rotation protein MotB	-0.8	-0.8				-0.6
23630.peg.4091	Flagellum	Sodium-type flagellar protein motY precursor						-0.6
23630.peg.4781	Flagellum	Flagellar biosynthesis protein FliQ						-0.6
23630.peg.1438	Flagellum	Flagellar M-ring protein FliF	-0.7					-0.3
23630.peg.1436	Flagellum	Flagellar assembly protein FliH	-0.4					-0.2
23630.peg.1818	Flagellum	Flagellar biosynthesis protein FliL						0.7
23630.peg.1843	Flagellum	Flagellar hook-associated protein FlgK						0.8
23630.peg.1839	Flagellum	Flagellar basal-body rod protein FlgG		0.9				0.8
23630.peg.1439	Flagellum	Flagellar hook-basal body complex protein FliE						0.9
23630.peg.1837	Flagellum	Flagellar hook protein FlgE		1.2				0.9
23630.peg.1435	Flagellum	Flagellum-specific ATP synthase FliI						1.0
23630.peg.4741	Flagellum	Flagellar biosynthesis protein FlgN		-0.7				
23630.peg.4777	Flagellum	Flagellar hook-length control protein FliK	0.8	0.6				
23630.peg.4768	Flagellum in Campylobacter	Flagellar hook-basal body complex protein FliE						1.9
23630.peg.1834	Flagellum in Campylobacter	Flagellar basal-body rod protein FlgB		0.6		0.7	-1.0	
23630.peg.4759	Flagellum in Campylobacter	Flagellin protein FlaB	-1.0	-0.7	-0.6			
Nitrogen Metabolism								
23630.peg.2277	Ammonia assimilation	Glutamate-ammonia-ligase adenylyltransferase (EC 2.7.7.42)						-0.6
23630.peg.4589	Ammonia assimilation	Ammonium transporter		-0.9		0.7		
23630.peg.4680	Cyanate hydrolysis	Cyn operon transcriptional activator		-0.7		-0.9	-0.8	-0.9
23630.peg.2215	Cyanate hydrolysis	Cyanate ABC transporter, substrate binding protein	-1.3			1.3		-0.9
23630.peg.3974	Cyanate hydrolysis	Cyn operon transcriptional activator						0.6
23630.peg.679	Cyanate hydrolysis	Carbonic anhydrase (EC 4.2.1.1)	2.2	1.9		1.1	0.7	0.8
23630.peg.3978	Cyanate hydrolysis	Cyanate transport protein CynX	1.3	2.8		1.0	0.9	1.3
23630.peg.2216	Cyanate hydrolysis	Cyanate ABC transporter, permease protein		-0.8				
23630.peg.3017	Nitrate and nitrite ammonification	Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4)		-1.6				-1.5
23630.peg.979	Nitrate and nitrite ammonification	Nitrate/nitrite sensor protein (EC 2.7.3.-)	-1.1			-1.0	-0.9	-0.9
23630.peg.3021	Nitrate and nitrite ammonification	Nitrate/nitrite transporter		-0.8				-1.1
23630.peg.2748	Nitrate and nitrite ammonification	Nitrate/nitrite sensor protein (EC 2.7.3.-)				-0.7	-1.2	0.7
23630.peg.4969	Nitrate and nitrite ammonification	Nitrate/nitrite sensor protein (EC 2.7.3.-)				-0.7	-1.2	0.7
23630.peg.3402	Nitrate and nitrite ammonification	Nitrate ABC transporter, nitrate-binding protein	0.9			0.7		0.7
23630.peg.3016	Nitrate and nitrite ammonification	Assimilatory nitrate reductase large subunit (EC:1.7.99.4)						0.9
23630.peg.4613	Nitrate and nitrite ammonification	Periplasmic nitrate reductase component NapD					-0.9	
23630.peg.4614	Nitrate and nitrite ammonification	Periplasmic nitrate reductase component NapE		-0.7			-0.8	
23630.peg.3403	Nitrate and nitrite ammonification	Response regulator NasT					-0.8	
23630.peg.3018	Nitrate and nitrite ammonification	Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)	-1.3	-1.5				
23630.peg.1367	Nitrosative stress	Anaerobic nitric oxide reductase transcription regulator NorR	1.7	1.1			1.5	1.8
23630.peg.531	Nitrosative stress	Anaerobic nitric oxide reductase transcription regulator NorR	-0.9	-0.7				
23630.peg.535	Nitrosative stress	NnrS protein involved in response to NO		0.8				
Nucleosides and Nucleotides								
23630.peg.1740	De Novo Purine Biosynthesis	Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)	1.0	0.8	0.8			0.9

23630.peg.2433	De Novo Purine Biosynthesis	Phosphoribosylamine--glycine ligase (EC 6.3.4.13)				0.8		
23630.peg.2078	De Novo Pyrimidine Synthesis	Uracil phosphoribosyltransferase (EC 2.4.2.9) / Pyrimidine operon regulatory protein PyrR					0.7	
23630.peg.3502	De Novo Pyrimidine Synthesis	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)			1.0			
23630.peg.4827	Hydantoin metabolism	Hydantoin permease	0.8					
23630.peg.3285	Nudix proteins (nucleoside triphosphate hydrolases)	Nudix-like NDP and NTP phosphohydrolase YmfB						1.7
23630.peg.167	Nudix proteins (nucleoside triphosphate hydrolases)	Nudix hydrolase family protein PA3470	0.7	0.4	1.2		0.7	
23630.peg.757	Purine conversions	AMP nucleosidase (EC 3.2.2.4)		0.6			0.6	
23630.peg.298	Purine conversions	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)			-0.6			
23630.peg.436	Purine conversions	Nucleoside diphosphate kinase (EC 2.7.4.6)	0.7		1.0			
23630.peg.4839	Purine Utilization	Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)				-0.8		
23630.peg.4835	Purine Utilization	Xanthine/uracil/thiamine/ascorbate permease family protein			-0.6			
23630.peg.696	Purine Utilization	Guanine deaminase (EC 3.5.4.3); Hydroxydechloroatrazine ethylaminohydrolase (EC 3.5.99.3)			0.7			
23630.peg.3746	pyrimidine conversions	CTP synthase (EC 6.3.4.2)			-0.6	-1.0		-1.2
23630.peg.2502	pyrimidine conversions	Thymidine phosphorylase (EC 2.4.2.4)	-0.7	-0.6	-1.1		-0.9	
23630.peg.4455	pyrimidine conversions	Thioredoxin reductase (EC 1.8.1.9)	0.9	1.0	0.8	0.9	1.2	
23630.peg.3585	pyrimidine conversions	Cytidylate kinase (EC 2.7.4.14)	-0.9					
23630.peg.2524	pyrimidine conversions	Thymidine phosphorylase (EC 2.4.2.4)	-0.8					
23630.peg.4526	Xanthine dehydrogenase subunits	Xanthine-uracil permease	-1.6	-0.8				1.0
23630.peg.1791	Xanthine Metabolism in Bacteria	Xanthine permease	1.1	1.0		1.2		1.6
23630.peg.688	Xanthine Metabolism in Bacteria	Xanthine permease	0.9	1.1	0.6		0.7	
Phages, Prophages, Transposable elements, Plasmids								
23630.peg.53	Integrans	Integron integrase IntIPac		-1.3	0.6			
Phosphorus Metabolism								
23630.peg.3762	Alkylphosphonate utilization	PhnJ protein	-1.8					-1.0
23630.peg.3764	Alkylphosphonate utilization	PhnH protein	-1.7					-0.8
23630.peg.3759	Alkylphosphonate utilization	Metal-dependent hydrolase involved in phosphonate metabolism	-1.6					-0.2
23630.peg.3763	Alkylphosphonate utilization	PhnI protein	-1.5				-0.7	-0.2
23630.peg.4915	Alkylphosphonate utilization	PhnG protein		0.7			0.6	
23630.peg.3760	Alkylphosphonate utilization	Phosphonates transport ATP-binding protein PhnL	-1.2			0.8		
23630.peg.3766	Alkylphosphonate utilization	Transcriptional regulator PhnF		-1.0	0.7			
23630.peg.4389	Alkylphosphonate utilization	Alkylphosphonate utilization operon protein PhnA			0.8			
23630.peg.4911	Alkylphosphonate utilization	Phosphonates transport ATP-binding protein PhnK		0.6				
23630.peg.4912	Alkylphosphonate utilization	PhnJ protein		0.6				
23630.peg.3761	Alkylphosphonate utilization	Phosphonates transport ATP-binding protein PhnK		0.8				
23630.peg.3765	Alkylphosphonate utilization	PhnG protein	-1.0	0.8				
23630.peg.1809	High affinity phosphate transporter and control of PHO regulon	Phosphate transport system permease protein PstA (TC 3.A.1.7.1)	-1.0	0.7				
23630.peg.1810	High affinity phosphate transporter and control of PHO regulon	Phosphate transport ATP-binding protein PstB (TC 3.A.1.7.1)	-1.2					
23630.peg.1808	High affinity phosphate transporter and control of PHO regulon	Phosphate transport system permease protein PstC (TC 3.A.1.7.1)	-0.4					

23630.peg.1807	Phosphate metabolism	Phosphate ABC transporter, periplasmic phosphate-binding protein PstS (TC 3.A.1.7.1)	0.6	0.7	1.3	-2.1
23630.peg.4239	Phosphate metabolism	Pyrophosphate-specific outer membrane porin OprO	-1.9			-1.8
23630.peg.4237	Phosphate metabolism	Inorganic pyrophosphatase (EC 3.6.1.1)	-1.7			-1.4
23630.peg.1811	Phosphate metabolism	Phosphate transport system regulatory protein PhoU	-1.3			-1.2
23630.peg.825	Phosphate metabolism	Inorganic pyrophosphatase (EC 3.6.1.1)	0.9	0.7		1.0
23630.peg.4436	Phosphate metabolism	Predicted ATPase related to phosphate starvation-inducible protein PhoH	0.6			1.4
23630.peg.2448	Phosphate metabolism	Alkaline phosphatase (EC 3.1.3.1)	-0.9	-0.6		-1.0
23630.peg.1454	Phosphate metabolism	NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)				0.6
23630.peg.1453	Phosphate metabolism	NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)	1.0			1.0
23630.peg.1455	Phosphate metabolism	NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)	-0.8	-0.9	-0.6	
23630.peg.1427	Phosphate metabolism	Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)			1.4	
23630.peg.1428	Phosphate metabolism	Phosphate regulon transcriptional regulatory protein PhoB (SphR)			1.7	
Potassium metabolism						
23630.peg.1969	Glutathione-regulated potassium-efflux system and associated functions	Glutathione-regulated potassium-efflux system ATP-binding protein				-0.8
23630.peg.3188	Glutathione-regulated potassium-efflux system and associated functions	Glutathione-regulated potassium-efflux system protein KefB	-1.3	-0.7		
23630.peg.1347	Potassium homeostasis	Potassium-transporting ATPase A chain (EC 3.6.3.12) (TC 3.A.3.7.1)	-1.7	-2.1	-0.5	-1.1
23630.peg.1345	Potassium homeostasis	Potassium-transporting ATPase C chain (EC 3.6.3.12) (TC 3.A.3.7.1)	1.1	1.6	1.0	0.9
23630.peg.3614	Potassium homeostasis	Potassium uptake protein TrkH			-0.7	
23630.peg.1346	Potassium homeostasis	Potassium-transporting ATPase B chain (EC 3.6.3.12) (TC 3.A.3.7.1)	0.9	0.7		
Protein Metabolism						
23630.peg.1558	G3E family of P-loop GTPases (metallocenter biosynthesis)	Putative metal chaperone, involved in Zn homeostasis, GTPase of COG0523 family	-1.1			0.7
23630.peg.676	GroEL GroES	Heat shock protein 60 family chaperone GroEL		0.7		
23630.peg.3568	N-linked Glycosylation in Bacteria	Lipid carrier : UDP-N-acetylgalactosaminyltransferase (EC 2.4.1.-)				-0.8
23630.peg.3572	N-linked Glycosylation in Bacteria	UDP-N-acetylglucosamine 4,6-dehydratase (EC 4.2.1.-)		-0.8		-0.7
23630.peg.2271	Peptide methionine sulfoxide reductase	Peptide methionine sulfoxide reductase MsrA (EC 1.8.4.11)	0.9	0.6		0.8
23630.peg.4476	Peptidyl-prolyl cis-trans isomerase	FKBP-type peptidyl-prolyl cis-trans isomerase SlpA (EC 5.2.1.8)		-0.6		-0.8
23630.peg.159	Peptidyl-prolyl cis-trans isomerase	Peptidyl-prolyl cis-trans isomerase PpiC (EC 5.2.1.8)	0.7	0.7	0.7	1.0
23630.peg.3395	Peptidyl-prolyl cis-trans isomerase	Peptidyl-prolyl cis-trans isomerase PpiB (EC 5.2.1.8)	0.7			0.6
23630.peg.744	Periplasmic disulfide interchange	Cytochrome c-type biogenesis protein CcmG/DsbE, thiol:disulfide oxidoreductase	-1.1			
23630.peg.4272	Proteasome bacterial	ATP-dependent protease La (EC 3.4.21.53) Type I	0.8	1.1		0.7
23630.peg.440	Protein chaperones	Chaperone protein HscB				0.9
23630.peg.2729	Protein degradation	Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP- specific)	-1.6	-1.2	-0.6	-1.4
						-0.6

23630.peg.1670	Protein degradation	Aminopeptidase YpdF (MP-, MA-, MS-, AP-, NP- specific)	-1.8	-2.0	0.1	-1.5	-1.4	
23630.peg.2194	Proteolysis in bacteria, ATP-dependent	ATP-dependent protease HslV (EC 3.4.25.-)				1.1	0.6	
23630.peg.2633	Proteolysis in bacteria, ATP-dependent	Outer membrane stress sensor protease DegS			0.7		0.7	
23630.peg.2193	Proteolysis in bacteria, ATP-dependent	ATP-dependent hsl protease ATP-binding subunit HslU	1.2	0.9			0.7	
23630.peg.3190	Proteolysis in bacteria, ATP-dependent	ATP-dependent Clp protease ATP-binding subunit ClpA			0.7			
23630.peg.3732	Ribosomal protein S12p Asp methylthiotransferase	Ribosomal protein S12p Asp88 (E. coli) methylthiotransferase		-0.7				
23630.peg.1640	Ribosome LSU bacterial	LSU ribosomal protein L34p	1.8	1.2	1.5	1.6	1.1	0.7
23630.peg.911	Ribosome LSU bacterial	LSU ribosomal protein L18p (L5e)						1.4
23630.peg.922	Ribosome LSU bacterial	LSU ribosomal protein L22p (L17e)				0.7		1.6
23630.peg.925	Ribosome LSU bacterial	LSU ribosomal protein L23p (L23Ae)				0.7		1.6
23630.peg.938	Ribosome LSU bacterial	LSU ribosomal protein L11p (L12e)						1.7
23630.peg.1395	Ribosome LSU bacterial	LSU ribosomal protein L33p @ LSU ribosomal protein L33p, zinc-independent	0.9		0.8			1.9
23630.peg.920	Ribosome LSU bacterial	LSU ribosomal protein L16p (L10e)				0.5		
23630.peg.919	Ribosome LSU bacterial	LSU ribosomal protein L29p (L35e)				0.8		
23630.peg.906	Ribosome LSU bacterial	LSU ribosomal protein L36p				0.9		
23630.peg.2198	Ribosome LSU bacterial	LSU ribosomal protein L31p @ LSU ribosomal protein L31p, zinc-dependent	1.0		0.9	0.9		
23630.peg.937	Ribosome LSU bacterial	LSU ribosomal protein L1p (L10Ae)				1.0		
23630.peg.1396	Ribosome LSU bacterial	LSU ribosomal protein L28p	1.1		1.2	1.0		
23630.peg.924	Ribosome LSU bacterial	LSU ribosomal protein L2p (L8e)				1.2		
23630.peg.909	Ribosome LSU bacterial	LSU ribosomal protein L30p (L7e)				1.2		
23630.peg.936	Ribosome LSU bacterial	LSU ribosomal protein L10p (P0)				1.3		
23630.peg.2350	Ribosome LSU bacterial	LSU ribosomal protein L9p				1.4		
23630.peg.3854	Ribosome LSU bacterial	LSU ribosomal protein L32p	0.9			1.5		
23630.peg.916	Ribosome LSU bacterial	LSU ribosomal protein L24p (L26e)			-0.6			
23630.peg.2648	Ribosome LSU bacterial	LSU ribosomal protein L13p (L13Ae)	0.8		1.0			
23630.peg.1390	Selenocysteine metabolism	NADH dehydrogenase-like protein / Selenide,water dikinase (EC 2.7.9.3)						-1.0
23630.peg.1680	Translation initiation factors bacterial	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	0.7				0.6	
23630.peg.2452	Translation initiation factors bacterial	Translation initiation factor SUI1-related protein	0.9		0.7			
23630.peg.35	Translation termination factors bacterial	Methionine aminopeptidase (EC 3.4.11.18)					0.7	
23630.peg.363	Translation termination factors bacterial	Peptide chain release factor 2; programmed frameshift-containing			0.8			
23630.peg.2196	tRNA aminoacylation, Arg	Arginyl-tRNA synthetase (EC 6.1.1.19)						2.2
23630.peg.4218	tRNA aminoacylation, Asp and Asn	Aspartyl-tRNA synthetase (EC 6.1.1.12) @ Aspartyl-tRNA(Asn) synthetase (EC 6.1.1.23)					0.7	
23630.peg.2599	tRNA aminoacylation, Asp and Asn	Aspartyl-tRNA(Asn) amidotransferase subunit C (EC 6.3.5.6) @ Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.7)	0.9		0.9			
23630.peg.1655	tRNA aminoacylation, Gly	Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)						1.7
23630.peg.782	tRNA aminoacylation, Leu	Leucyl-tRNA synthetase (EC 6.1.1.4)		0.6				
23630.peg.2777	tRNA aminoacylation, Phe	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)					-0.7	
23630.peg.4940	tRNA aminoacylation, Phe	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)					-0.7	
23630.peg.4227	tRNA aminoacylation, Pro	Prolyl-tRNA synthetase (EC 6.1.1.15), bacterial type	0.9	0.7	1.0		1.0	
23630.peg.818	tRNA aminoacylation, Pro	tRNA proofreading protein STM4549			0.7			

23630.peg.2772	tRNA aminoacylation, Thr	Threonyl-tRNA synthetase (EC 6.1.1.3)		-0.6		
23630.peg.4945	tRNA aminoacylation, Thr	Threonyl-tRNA synthetase (EC 6.1.1.3)		-0.6		
23630.peg.2337	Universal GTPases	GTP-binding protein HflX		-0.7		-0.8
23630.peg.1150	Universal GTPases	GTP-binding protein TypA/BipA			1.4	
23630.peg.428	Universal GTPases	GTP-binding protein EngA		0.6		
Regulation and Cell signaling						
23630.peg.1111	cAMP signaling in bacteria	Predicted signal-transduction protein containing cAMP-binding and CBS domains				-0.8
23630.peg.3210	cAMP signaling in bacteria	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases			-1.0	
23630.peg.2487	cAMP signaling in bacteria	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17)	-1.3			
23630.peg.4193	DNA-binding regulatory proteins, strays	LysR family transcriptional regulator PA3398				-1.1
23630.peg.4331	DNA-binding regulatory proteins, strays	LysR family transcriptional regulator near succinyl-CoA:3-ketoacid-coenzyme A transferase	-0.9	-1.2		
23630.peg.4115	DNA-binding regulatory proteins, strays	LysR family transcriptional regulator PA0739	-1.9	-0.7		
23630.peg.1508	DNA-binding regulatory proteins, strays	LysR family transcriptional regulator PA5437	-1.5			
23630.peg.1865	Extracellular matrix proteins (PEL) involved in glucose-rich biofilm formation in Pseudomonas	Extracellular Matrix protein PelA		-0.9	-1.0	
23630.peg.1869	Extracellular matrix proteins (PEL) involved in glucose-rich biofilm formation in Pseudomonas	Extracellular Matrix protein PelE			-0.6	
23630.peg.1870	Extracellular matrix proteins (PEL) involved in glucose-rich biofilm formation in Pseudomonas	Extracellular matrix protein PelF, glycosyltransferase, group 1		-0.9		
23630.peg.1867	Extracellular matrix proteins (PEL) involved in glucose-rich biofilm formation in Pseudomonas	Extracellular Matrix protein PelC		-0.7		
23630.peg.1866	Extracellular matrix proteins (PEL) involved in glucose-rich biofilm formation in Pseudomonas	Extracellular Matrix protein PelB		-0.7		
23630.peg.2592	Global Two-component Regulator PrrBA in Proteobacteria	Dna binding response regulator PrrA (RegA)				1.8
23630.peg.4328	LysR-family proteins in Escherichia coli	LysR family transcriptional regulator YbhD		-0.6		-0.8
23630.peg.419	LysR-family proteins in Salmonella enterica Typhimurium	LysR-family transcriptional regulator STM3020	1.0	0.8		
23630.peg.257	Orphan regulatory proteins	Two-component system response regulator QseB		0.7		0.6
23630.peg.258	Orphan regulatory proteins	Sensory histidine kinase QseC		0.9		0.6
23630.peg.135	Orphan regulatory proteins	Transcriptional regulatory protein RstA			-1.5	
23630.peg.1452	Orphan regulatory proteins	Glycine cleavage system transcriptional activator	0.0	0.7	0.8	
23630.peg.3925	Orphan regulatory proteins	Glycine cleavage system transcriptional activator		-0.8		
23630.peg.134	Orphan regulatory proteins	Sensory histidine kinase in two-component regulatory system with RstA	-0.8			
23630.peg.4693	Phd-Doc, YdcE-YdcD toxin-antitoxin (programmed cell death) systems	Death on curing protein, Doc toxin			-1.0	
23630.peg.4695	Phd-Doc, YdcE-YdcD toxin-antitoxin (programmed cell death) systems	Prevent host death protein, Phd antitoxin		0.6		
23630.peg.1412	Stringent Response, (p)ppGpp metabolism	GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase II / Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase (EC 3.1.7.2)				-0.7
23630.peg.1559	Zinc regulated enzymes	C4-type zinc finger protein, DksA/TraR family	0.8	-0.6		-1.1
23630.peg.2805	Zinc regulated enzymes	Queuosine biosynthesis QueD, PTPS-I		0.9		

Respiration

23630.peg.4530	Anaerobic respiratory reductases	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1; Vanillate O-demethylase oxidoreductase (EC 1.14.13.-)	-1.4	-1.4		-0.9	-1.8	
23630.peg.4804	Biogenesis of c-type cytochromes	ABC transporter involved in cytochrome c biogenesis, CcmB subunit			0.8			1.6
23630.peg.4807	Biogenesis of c-type cytochromes	Cytochrome c-type biogenesis protein CcmE, heme chaperone		0.7	0.7			
23630.peg.4810	Biogenesis of c-type cytochromes	Cytochrome c heme lyase subunit CcmL	-1.2					
23630.peg.1774	Biogenesis of cytochrome c oxidases	Cytochrome oxidase biogenesis protein Cox11-CtaG, copper delivery to Cox1	1.9			-0.9	0.7	
23630.peg.1777	Biogenesis of cytochrome c oxidases	Cytochrome oxidase biogenesis protein Surf1, facilitates heme A insertion	1.3			-1.1		
23630.peg.1780	Biogenesis of cytochrome c oxidases	Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX10-CtaB	0.7			-0.9		
23630.peg.3961	Biogenesis of cytochrome c oxidases	Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX10-CtaB	-1.2			1.0		
23630.peg.4192	Biogenesis of cytochrome c oxidases	Ferredoxin--NADP(+) reductase (EC 1.18.1.2)	0.9					
23630.peg.1779	Biogenesis of cytochrome c oxidases	Heme A synthase, cytochrome oxidase biogenesis protein Cox15-CtaA	1.3					
23630.peg.1622	F0F1-type ATP synthase	ATP synthase epsilon chain (EC 3.6.3.14)						0.1
23630.peg.1629	F0F1-type ATP synthase	ATP synthase A chain (EC 3.6.3.14)			0.8		0.7	
23630.peg.1623	F0F1-type ATP synthase	ATP synthase beta chain (EC 3.6.3.14)			-0.6			
23630.peg.1630	F0F1-type ATP synthase	ATP synthase protein I	0.7					
23630.peg.2068	Formate hydrogenase	Putative formate dehydrogenase oxidoreductase protein	1.0		-0.4	0.0	0.6	2.0
23630.peg.3882	Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	Na(+)-translocating NADH-quinone reductase subunit C (EC 1.6.5.-)						1.0
23630.peg.3879	Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)	-1.1		-0.7		-0.7	
23630.peg.3877	Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	probable exported protein YPO3233	-0.8	-0.7	-0.6		-0.7	
23630.peg.4085	Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	Electron transport complex protein RnfE					0.6	
23630.peg.4084	Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	Electron transport complex protein RnfG		0.9	0.8		0.8	
23630.peg.3880	Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	Na(+)-translocating NADH-quinone reductase subunit E (EC 1.6.5.-)				0.8		
23630.peg.3881	Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	Na(+)-translocating NADH-quinone reductase subunit D (EC 1.6.5.-)				1.0		
23630.peg.4080	Na(+)-translocating NADH-quinone oxidoreductase and rnf-like group of electron transport complexes	Electron transport complex protein RnfA			0.8	1.3		
23630.peg.179	Quinone oxidoreductase family	Putative oxidoreductase SMC00968			-0.7			2.2
23630.peg.1993	Quinone oxidoreductase family	Quinone oxidoreductase (EC 1.6.5.5)		0.6			0.7	
23630.peg.3310	Respiratory Complex I	NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)						-1.5
23630.peg.3303	Respiratory Complex I	NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)	-0.7	-1.0	-0.7		-1.1	
23630.peg.3107	Respiratory dehydrogenases 2	NADH dehydrogenase (EC 1.6.99.3)	0.9	1.0			0.9	
23630.peg.3828	Respiratory dehydrogenases 3	NADH dehydrogenase (EC 1.6.99.3)		-1.0		-0.8		
23630.peg.2754	Soluble cytochromes and functionally related electron carriers	Cytochrome C550 (Soluble cytochrome C)			-0.6			1.8

23630.peg.4963	Soluble cytochromes and functionally related electron carriers	Cytochrome C550 (Soluble cytochrome C)	-0.6				1.8
23630.peg.1787	Soluble cytochromes and functionally related electron carriers	Cytochrome c4				0.7	
23630.peg.3423	Terminal cytochrome C oxidases	Cytochrome c oxidase subunit CcoO (EC 1.9.3.1)					-1.1
23630.peg.3422	Terminal cytochrome C oxidases	Cytochrome c oxidase subunit CcoN (EC 1.9.3.1)					-0.9
23630.peg.3425	Terminal cytochrome C oxidases	Cytochrome c oxidase subunit CcoP (EC 1.9.3.1)	-1.2				-0.9
23630.peg.3424	Terminal cytochrome C oxidases	Cytochrome c oxidase subunit CcoQ (EC 1.9.3.1)	-1.4			-0.7	-0.8
23630.peg.1775	Terminal cytochrome C oxidases	Cytochrome c oxidase polypeptide III (EC 1.9.3.1)	1.3	-0.8		-1.4	2.5
23630.peg.3093	Terminal cytochrome C oxidases	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)		-0.7			-0.9
23630.peg.68	Terminal cytochrome C oxidases	Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in Cu oxidation					0.6
23630.peg.3430	Terminal cytochrome C oxidases	Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in Cu oxidation	-0.7	0.8		0.7	
23630.peg.1773	Terminal cytochrome C oxidases	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)	1.7				0.9
23630.peg.3428	Terminal cytochrome C oxidases	Cytochrome c oxidase subunit CcoQ (EC 1.9.3.1)				0.9	
23630.peg.1772	Terminal cytochrome C oxidases	Cytochrome c oxidase polypeptide II (EC 1.9.3.1)			-0.6		
23630.peg.2471	Terminal cytochrome d ubiquinol oxidases	putative Cytochrome bd2, subunit I / Cyanide insensitive terminal oxidase, subunit I				1.4	
23630.peg.3965	Terminal cytochrome O ubiquinol oxidase	Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-)	-1.1			0.8	
23630.peg.3964	Terminal cytochrome oxidases	Cytochrome O ubiquinol oxidase subunit I (EC 1.10.3.-)	-1.7	-0.7			1.7
23630.peg.3963	Terminal cytochrome oxidases	Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-)	-1.2	-0.9			
23630.peg.3962	Terminal cytochrome oxidases	Cytochrome O ubiquinol oxidase subunit IV (EC 1.10.3.-)	-1.8	-0.9			
23630.peg.2472	Terminal cytochrome oxidases	putative Cytochrome bd2, subunit II	-1.0				
23630.peg.2651	Ubiquinone Menaquinone-cytochrome c reductase complexes	Ubiquinol--cytochrome c reductase, cytochrome B subunit (EC 1.10.2.2)					0.6
23630.peg.2652	Ubiquinone Menaquinone-cytochrome c reductase complexes	ubiquinol cytochrome C oxidoreductase, cytochrome C1 subunit	-0.6				
RNA Metabolism							
23630.peg.2661	16S rRNA modification within P site of ribosome	rRNA small subunit methyltransferase H	-0.9				-1.4
23630.peg.2096	ATP-dependent RNA helicases, bacterial	ATP-dependent RNA helicase RhlE					1.5
23630.peg.510	ATP-dependent RNA helicases, bacterial	ATP-dependent RNA helicase RhlB				0.7	
23630.peg.775	Methylthiotransferases	tRNA-i(6)A37 methylthiotransferase	1.2	1.2		0.8	
23630.peg.1635	mnm5U34 biosynthesis bacteria	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA		0.7			
23630.peg.577	Polyadenylation bacterial	Poly(A) polymerase (EC 2.7.7.19)					1.5
23630.peg.994	Polyadenylation bacterial	tRNA nucleotidyltransferase (EC 2.7.7.21) (EC 2.7.7.25)	1.1	0.9		0.7	
23630.peg.4565	Polyadenylation bacterial	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)				0.8	
23630.peg.4386	Queuosine-Archaeosine Biosynthesis	Permease of the drug/metabolite transporter (DMT) superfamily	-0.8	-0.3			
23630.peg.162	Queuosine-Archaeosine Biosynthesis	Permease of the drug/metabolite transporter (DMT) superfamily				0.7	
23630.peg.1674	Queuosine-Archaeosine Biosynthesis	Putative preQ0 transporter	1.1			0.7	
23630.peg.4196	Queuosine-Archaeosine Biosynthesis	Permease of the drug/metabolite transporter (DMT) superfamily	1.3			0.7	
23630.peg.213	Queuosine-Archaeosine Biosynthesis	Permease of the drug/metabolite transporter (DMT) superfamily	-1.0	0.7			

23630.peg.2890	Queuosine-Archaeosine Biosynthesis	Permease of the drug/metabolite transporter (DMT) superfamily	-1.0				
23630.peg.4206	Queuosine-Archaeosine Biosynthesis	Queuosine Biosynthesis QueE Radical SAM	0.9				
23630.peg.455	Ribonuclease H	Ribonuclease HI (EC 3.1.26.4)				0.7	
23630.peg.4202	Ribonucleases in Bacillus	Metallo-beta-lactamase family protein, RNA-specific				-1.4	
23630.peg.3581	Ribonucleases in Bacillus	Metallo-beta-lactamase family protein, RNA-specific	-1.8	-1.0		-1.0	
23630.peg.2092	RNA methylation	Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.-)					-1.3
23630.peg.4922	RNA methylation	23S rRNA (guanine-N-2-) -methyltransferase rlmG (EC 2.1.1.-)	-1.9			-0.9	
23630.peg.3136	RNA methylation	Probable RNA methyltransferase PA1839	0.8		0.9	0.8	0.8
23630.peg.1679	RNA methylation	16S rRNA (cytosine(967)-C(5))-methyltransferase (EC 2.1.1.176)			-0.8	0.8	
23630.peg.2488	RNA methylation	23S rRNA (guanine-N-2-) -methyltransferase rlmG (EC 2.1.1.-)	0.7		0.7		
23630.peg.1269	RNA methylation	tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207) ### TrmL			0.7		
23630.peg.3291	RNA methylation	tRNA-specific 2-thiouridylase MnmA			0.8		
23630.peg.604	RNA methylation	Cell division protein FtsJ / Ribosomal RNA large subunit methyltransferase E (EC 2.1.1.-)		-0.8			
23630.peg.4576	RNA methylation	23S rRNA (guanine-N-2-) -methyltransferase rlmL EC 2.1.1.-)		-0.6			
23630.peg.46	RNA methylation	Ribosomal RNA large subunit methyltransferase A (EC 2.1.1.51)		0.6			
23630.peg.4026	RNA pseudouridine syntheses	Similar to ribosomal large subunit pseudouridine synthase A					1.9
23630.peg.751	RNA pseudouridine syntheses	Ribosomal large subunit pseudouridine synthase E (EC 4.2.1.70)	1.3	1.2	0.7	0.9	
23630.peg.4463	RNA pseudouridine syntheses	Ribosomal large subunit pseudouridine synthase D (EC 4.2.1.70)	0.8		1.0		
23630.peg.4129	RNA pseudouridine syntheses	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70)	0.9				
23630.peg.607	Transcription factors bacterial	Transcription elongation factor GreA	-0.9		-0.7		
23630.peg.939	Transcription factors bacterial	Transcription antitermination protein NusG		-1.2			
23630.peg.2976	Transcription factors bacterial	Transcription elongation factor GreB	1.3				
23630.peg.4009	Transcription initiation, bacterial sigma factors	Sigma factor RpoE regulatory protein RseC	-0.9	-0.7	-0.6		-0.8
23630.peg.3919	Transcription initiation, bacterial sigma factors	RNA polymerase sigma factor RpoE				-1.2	
23630.peg.4256	tRNA modification Bacteria	Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70)					2.1
23630.peg.4875	tRNA modification Bacteria	tRNA 5-methylaminomethyl-2-thiouridine synthase TusA				-1.1	
23630.peg.437	tRNA modification Bacteria	Believed to be involved in assembly of Fe-S clusters	-0.9				-0.9
23630.peg.2335	tRNA modification Bacteria	tRNA dimethylallyltransferase (EC 2.5.1.75)		-1.1			-0.8
23630.peg.3605	tRNA modification Bacteria	COG0613, Predicted metal-dependent phosphoesterases (PHP family)	1.0		0.9		0.6
23630.peg.2437	tRNA modification Bacteria	tRNA dihydrouridine synthase B (EC 1.-.-)	1.0	0.7	0.7		0.7
23630.peg.2575	tRNA modification Bacteria	tRNA (uracil(54)-C5)-methyltransferase (EC 2.1.1.35)	0.9		0.8	0.8	
23630.peg.3397	tRNA modification Bacteria	tRNA-(ms[2]io[6]A)-hydroxylase (EC 1.-.-)			0.6		

23630.peg.4893	tRNA modification Bacteria	NADPH-dependent 7-cyano-7-deazaguanine reductase (EC 1.7.1.-)	0.7				
23630.peg.4630	tRNA modification Bacteria	tRNA(Cytosine32)-2-thiocytidine synthetase	0.8		1.0		
23630.peg.113	tRNA processing	tRNA-specific adenosine-34 deaminase (EC 3.5.4.-)				-1.1	
23630.peg.1639	tRNA processing	Ribonuclease P protein component (EC 3.1.1.26.5)	0.8		0.7		
Stress Response							
23630.peg.528	Bacterial hemoglobins	Hemoglobin-like protein HbO		0.7	0.7		1.1
23630.peg.59	Bacterial hemoglobins	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	0.8				1.8
23630.peg.4169	Bacterial hemoglobins	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	-0.6	-1.0		1.2	-0.7
23630.peg.3208	Bacterial hemoglobins	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)					0.6
23630.peg.2042	Bacterial hemoglobins	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)			-0.6		
23630.peg.80	Bacterial hemoglobins	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	-1.0				
23630.peg.2724	Choline and Betaine Uptake and Betaine Biosynthesis	GbcA Glycine betaine demethylase subunit A	-0.9				-2.0
23630.peg.2146	Choline and Betaine Uptake and Betaine Biosynthesis	Glycine betaine ABC transport system, permease protein OpuAB					1.2
23630.peg.2149	Choline and Betaine Uptake and Betaine Biosynthesis	L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1)		-1.1	-0.8		-1.2
23630.peg.1690	Choline and Betaine Uptake and Betaine Biosynthesis	Choline-sulfatase (EC 3.1.6.6)	-1.2		-1.0		-0.8
23630.peg.1141	Choline and Betaine Uptake and Betaine Biosynthesis	Sarcosine oxidase alpha subunit (EC 1.5.3.1)	1.4	1.1			0.5
23630.peg.1143	Choline and Betaine Uptake and Betaine Biosynthesis	Sarcosine oxidase beta subunit (EC 1.5.3.1)				0.7	0.6
23630.peg.1142	Choline and Betaine Uptake and Betaine Biosynthesis	Sarcosine oxidase delta subunit (EC 1.5.3.1)	1.0	1.1			1.2
23630.peg.2732	Choline and Betaine Uptake and Betaine Biosynthesis	High-affinity choline uptake protein BetT	-1.7	-1.1		-1.0	
23630.peg.1147	Choline and Betaine Uptake and Betaine Biosynthesis	GbcB Glycine betaine demethylase subunit B			-0.8	-0.2	
23630.peg.365	Choline and Betaine Uptake and Betaine Biosynthesis	Choline dehydrogenase (EC 1.1.99.1)			-0.8		
23630.peg.2140	Choline and Betaine Uptake and Betaine Biosynthesis	Betaine aldehyde dehydrogenase (EC 1.2.1.8)			-0.6		
23630.peg.2145	Choline and Betaine Uptake and Betaine Biosynthesis	L-proline glycine betaine binding ABC transporter protein ProX (TC 3.A.1.12.1)		-0.7			
23630.peg.524	Choline and Betaine Uptake and Betaine Biosynthesis	Sarcosine oxidase beta subunit (EC 1.5.3.1)		1.0			
23630.peg.3282	Cold shock, CspA family of proteins	Cold shock protein CspD					-0.3
23630.peg.4222	Cold shock, CspA family of proteins	Cold shock protein CspC				0.6	
23630.peg.2174	D-tyrosyl-tRNA(Tyr) deacylase	D-tyrosyl-tRNA(Tyr) deacylase			-0.7		1.5
23630.peg.2857	Flavohaemoglobin	ABC-type Fe3+-siderophore transport system, permease 2 component			0.5		
23630.peg.1271	Glutaredoxins	Glutaredoxin 3 (Grx3)	0.8	0.7	0.8	1.0	
23630.peg.329	Glutaredoxins	Glutaredoxin-related protein	0.8	0.9		1.2	
23630.peg.2786	Glutathione: Non-redox reactions	Glutathione S-transferase (EC 2.5.1.18)	-1.0	-1.4		-1.0	-1.5
23630.peg.4931	Glutathione: Non-redox reactions	Glutathione S-transferase (EC 2.5.1.18)	-1.0	-1.4		-1.0	-1.5
23630.peg.4151	Glutathione: Non-redox reactions	Glutathione S-transferase (EC 2.5.1.18)	1.2	2.2		0.9	1.5
23630.peg.4529	Glutathione: Non-redox reactions	Glutathione S-transferase, unnamed subgroup (EC 2.5.1.18)	-2.6	-2.6	-0.8	-0.8	
23630.peg.3491	Glutathione: Non-redox reactions	Glutathione S-transferase, unnamed subgroup (EC 2.5.1.18)			0.8	1.0	
23630.peg.3269	Glutathione: Non-redox reactions	Glutathione S-transferase, omega (EC 2.5.1.18)			0.7		

23630.peg.627	Glutathione: Redox cycle	Glutathione peroxidase (EC 1.11.1.9)		-0.7			
23630.peg.9	Glutathione-dependent pathway of formaldehyde detoxification	S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284)	0.8		-0.1		
23630.peg.8	Glutathione-dependent pathway of formaldehyde detoxification	S-formylglutathione hydrolase (EC 3.1.2.12)	0.6				
23630.peg.10	Glutathione-dependent pathway of formaldehyde detoxification	Transcriptional regulator, LysR family, in formaldehyde detoxification operon	-1.2				
23630.peg.2082	Heat shock dnaK gene cluster extended	Glutathione synthetase (EC 6.3.2.3)		-0.6			
23630.peg.2439	Heat shock dnaK gene cluster extended	Ribosomal protein L11 methyltransferase (EC 2.1.1.-)	1.0	0.8			
23630.peg.4061	Osmoregulation	Outer membrane protein A precursor			-1.0		
23630.peg.591	Osmoregulation	Osmotically inducible protein OsmY			1.2		
23630.peg.3087	Oxidative stress	Catalase (EC 1.11.1.6)	-1.3			-1.7	
23630.peg.4145	Oxidative stress	Redox-sensitive transcriptional activator SoxR	0.9	0.9		-1.4	
23630.peg.615	Oxidative stress	Ferric uptake regulation protein FUR		-0.7		-0.9	
23630.peg.4220	Oxidative stress	Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase (EC 1.16.3.1)			0.9	0.6	
23630.peg.1341	Oxidative stress	Alkyl hydroperoxide reductase subunit C-like protein	1.8	1.1		1.7	1.7
23630.peg.385	Oxidative stress	Organic hydroperoxide resistance protein				1.4	
23630.peg.485	Oxidative stress	Phytochrome, two-component sensor histidine kinase (EC 2.7.3.-)		-0.8	-0.6		
23630.peg.1381	Oxidative stress	transcriptional regulator, Crp/Fnr family	0.9				
23630.peg.2017	Protection from Reactive Oxygen Species	Cytochrome c551 peroxidase (EC 1.11.1.5)			-1.4		-1.5
23630.peg.4139	Protection from Reactive Oxygen Species	Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)		0.8			
23630.peg.1825	Rubredoxin	Rubredoxin	1.0	0.9	0.8		
23630.peg.2726	Rubredoxin	Rubredoxin	-1.5	-1.3			
23630.peg.3193	Synthesis of osmoregulated periplasmic glucans	Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)	-2.1	-1.4		-0.7	-1.5
23630.peg.234	Universal stress protein family	Universal stress protein E		-0.8	-1.6		-1.6
23630.peg.3398	Universal stress protein family	Universal stress protein family 7			-0.9		-1.5
23630.peg.4555	Universal stress protein family	Universal stress protein family 4	-0.8				
23630.peg.2892	Uptake of selenate and selenite	Various polyols ABC transporter, ATP-binding component	1.4		-0.7	0.3	0.3
23630.peg.1496	Uptake of selenate and selenite	Various polyols ABC transporter, periplasmic substrate-binding protein			-1.3	-0.8	
23630.peg.1498	Uptake of selenate and selenite	Various polyols ABC transporter, permease component 2			0.9		
23630.peg.1497	Uptake of selenate and selenite	Various polyols ABC transporter, permease component 1	0.9				
Sulfur Metabolism							
23630.peg.1337	Alkanesulfonate assimilation	Alkanesulfonate monooxygenase (EC 1.14.14.5)	0.7				-1.8
23630.peg.2847	Alkanesulfonate assimilation	Acyl-CoA dehydrogenase; probable dibenzothiophene desulfurization enzyme				0.6	
23630.peg.2846	Alkanesulfonate assimilation	Acyl-CoA dehydrogenase; probable dibenzothiophene desulfurization enzyme	1.1	1.2		0.7	
23630.peg.1354	Alkanesulfonate assimilation	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	-0.3	0.8	0.8	0.8	
23630.peg.1351	Alkanesulfonate assimilation	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	1.3	0.8		1.8	1.1
23630.peg.1355	Alkanesulfonate assimilation	Acyl-CoA dehydrogenase; probable dibenzothiophene desulfurization enzyme	1.0	0.4		0.2	1.2

23630.peg.2831	Alkanesulfonate assimilation	Alpha-ketoglutarate-dependent taurine dioxygenase (EC 1.14.11.17)	2.2	1.5	0.5	1.0	1.3
23630.peg.2835	Alkanesulfonate assimilation	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components	1.2	2.0	0.7	0.9	1.5
23630.peg.1340	Alkanesulfonate assimilation	FMN reductase (EC 1.5.1.29)	1.6	1.4	0.6		1.8
23630.peg.1334	Alkanesulfonate assimilation	Organosulfonate utilization protein SsuF				1.0	
23630.peg.1349	Alkanesulfonate assimilation	Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter, ATP-binding subunit SsuB	-1.0				
23630.peg.1336	Alkanesulfonates Utilization	Alkanesulfonates transport system permease protein				1.3	
23630.peg.1335	Alkanesulfonates Utilization	Alkanesulfonates ABC transporter ATP-binding protein / Sulfonate ABC transporter, ATP-binding subunit SsuB		-0.8	-0.7		
23630.peg.1339	Alkanesulfonates Utilization	Alkanesulfonates-binding protein		0.8			
23630.peg.79	Galactosylceramide and Sulfatide metabolism	Arylsulfatase (EC 3.1.6.1)					1.4
23630.peg.66	Inorganic Sulfur Assimilation	Oxidoreductase probably involved in sulfite reduction	-1.2	-1.3		-1.2	-1.6
23630.peg.2834	Taurine Utilization	Taurine transport system permease protein TauC				-0.2	
23630.peg.2833	Taurine Utilization	Taurine transport ATP-binding protein TauB			-0.5		
23630.peg.2832	Taurine Utilization	Taurine-binding periplasmic protein TauA		0.7			
23630.peg.4166	Thioredoxin-disulfide reductase	Alkyl hydroperoxide reductase protein C (EC 1.6.4.-)				0.9	1.8
Virulence, Disease and Defense							
23630.peg.2827	Adaptation to d-cysteine	D-cysteine desulphydrase (EC 4.4.1.15)					-1.3
23630.peg.2824	Adaptation to d-cysteine	Cystine ABC transporter, ATP-binding protein		0.6			0.6
23630.peg.479	Arsenic resistance	Arsenic efflux pump protein					-0.9
23630.peg.3837	Arsenic resistance	Arsenical resistance operon repressor		-1.0			
23630.peg.3757	Beta-lactamase	Metal-dependent hydrolases of the beta-lactamase superfamily I; PhnP protein				0.9	
23630.peg.2888	Beta-lactamase	Beta-lactamase (EC 3.5.2.6)		1.1		1.2	
23630.peg.4908	Beta-lactamase	Beta-lactamase (EC 3.5.2.6)			0.8		
23630.peg.1007	Cobalt-zinc-cadmium resistance	Cobalt/zinc/cadmium efflux RND transporter, membrane fusion protein, CzcB family	-1.9				-1.2
23630.peg.3320	Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA		-1.1			-0.8
23630.peg.1006	Cobalt-zinc-cadmium resistance	Heavy metal RND efflux outer membrane protein, CzcC family	-1.6			-0.9	-1.0
23630.peg.1008	Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA	-2.4	-1.1	-1.2	-1.2	-1.9
23630.peg.747	Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein				1.7	1.8
23630.peg.1027	Cobalt-zinc-cadmium resistance	Heavy metal RND efflux outer membrane protein, CzcC family	-2.0	-1.6	-0.7		-2.4
23630.peg.1053	Cobalt-zinc-cadmium resistance	Copper-sensing two-component system response regulator CusR	-1.5	-0.7	-0.6	-1.6	-1.1
23630.peg.1054	Cobalt-zinc-cadmium resistance	Heavy metal sensor histidine kinase	-1.2				-1.1
23630.peg.1023	Cobalt-zinc-cadmium resistance	Cobalt-zinc-cadmium resistance protein CzcA; Cation efflux system protein CusA	-0.7		-0.6		-0.9
23630.peg.3318	Cobalt-zinc-cadmium resistance	Heavy metal RND efflux outer membrane protein, CzcC family	-1.5			-1.1	
23630.peg.3214	Cobalt-zinc-cadmium resistance	DNA-binding heavy metal response regulator	-0.9			-1.1	
23630.peg.1029	Cobalt-zinc-cadmium resistance	DNA-binding heavy metal response regulator				-0.9	
23630.peg.3456	Cobalt-zinc-cadmium resistance	Transcriptional regulator, MerR family		0.8			

23630.peg.1045	Copper homeostasis	Copper chaperone	-2.2	-1.1	-0.9	-2.1	-1.7
23630.peg.2565	Copper homeostasis	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)	-2.2	0.6		-1.8	-1.6
23630.peg.4812	Copper homeostasis	Cytochrome c heme lyase subunit CcmH					-1.5
23630.peg.2567	Copper homeostasis	Copper chaperone	-2.7	-1.6	-1.3	-2.6	-1.4
23630.peg.1037	Copper homeostasis	Copper resistance protein B	-1.2			-1.0	-0.7
23630.peg.1050	Copper homeostasis	Copper tolerance protein	-2.0			-1.7	
23630.peg.1038	Copper homeostasis	Multicopper oxidase	-1.7			-1.4	
23630.peg.1039	Copper homeostasis	Multicopper oxidase	-1.3	-0.6		-1.0	
23630.peg.1051	Copper homeostasis	Copper tolerance protein	-1.4			-0.7	
23630.peg.3477	Copper homeostasis	Multicopper oxidase	-1.0		-0.6	-0.7	
23630.peg.409	Copper homeostasis	Multicopper oxidase				-0.8	
23630.peg.4370	Copper homeostasis	Multidrug resistance transporter, Bcr/CflA family			-0.7		
23630.peg.4808	Copper homeostasis	Cytochrome c heme lyase subunit CcmF	-0.9		-0.6		
23630.peg.3476	Copper homeostasis	Copper tolerance protein		0.6			
23630.peg.3478	Copper homeostasis	Copper tolerance protein	-1.1				
23630.peg.2571	Copper homeostasis	Multidrug resistance transporter, Bcr/CflA family	1.0				
23630.peg.2822	Copper homeostasis: copper tolerance	Magnesium and cobalt efflux protein CorC				-1.4	
23630.peg.2490	Copper homeostasis: copper tolerance	Magnesium and cobalt efflux protein CorC		0.6			
23630.peg.779	Copper homeostasis: copper tolerance	Apolipoprotein N-acyltransferase (EC 2.3.1.-) / Copper homeostasis protein CutE		0.6			
23630.peg.1705	Lysozyme inhibitors	Inhibitor of vertebrate lysozyme precursor	-1.0			-0.9	1.3
23630.peg.3114	MexE-MexF-OprN Multidrug Efflux System	Multidrug efflux transporter MexF		-0.9	-0.9		-1.3
23630.peg.3115	MexE-MexF-OprN Multidrug Efflux System	Outer membrane protein OprN		-1.1	0.7	-0.9	
23630.peg.2445	Multidrug Resistance Efflux Pumps	Type I secretion outer membrane protein, TolC precursor					-1.2
23630.peg.716	Multidrug Resistance Efflux Pumps	RND efflux system, inner membrane transporter CmeB	-1.5				0.0
23630.peg.717	Multidrug Resistance Efflux Pumps	RND efflux system, outer membrane lipoprotein CmeC		1.0		0.1	
23630.peg.2570	Multidrug Resistance Efflux Pumps	RND efflux system, inner membrane transporter CmeB	1.3			0.6	
23630.peg.1930	Multidrug Resistance Efflux Pumps	Multidrug and toxin extrusion (MATE) family efflux pump YdhE/NorM, homolog		1.0		0.7	
23630.peg.4710	Multidrug Resistance Efflux Pumps	RND multidrug efflux transporter; Acriflavin resistance protein		-1.3		-0.9	
23630.peg.715	Multidrug Resistance Efflux Pumps	Membrane fusion protein of RND family multidrug efflux pump			0.8	1.2	
23630.peg.2569	Multidrug Resistance Efflux Pumps	Membrane fusion protein of RND family multidrug efflux pump			-0.8		
23630.peg.88	Multidrug Resistance Efflux Pumps	RND efflux system, membrane fusion protein CmeA		0.4	0.5		
23630.peg.713	Multidrug Resistance Efflux Pumps	Transcription repressor of multidrug efflux pump acrAB operon, TetR (AcrR) family			0.9		
23630.peg.4877	Multidrug Resistance Efflux Pumps	Multidrug and toxin extrusion (MATE) family efflux pump YdhE/NorM			1.1		
23630.peg.89	Multidrug Resistance Efflux Pumps	RND efflux system, inner membrane transporter CmeB	-1.5				
23630.peg.2775	Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)	LSU ribosomal protein L20p		-0.8		-1.1	
23630.peg.4942	Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)	LSU ribosomal protein L20p		-0.8		-1.1	

23630.peg.2774	Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)	LSU ribosomal protein L35p					1.0
23630.peg.4943	Mycobacterium virulence operon involved in protein synthesis (LSU ribosomal proteins)	LSU ribosomal protein L35p					1.0
23630.peg.942	Mycobacterium virulence operon involved in protein synthesis (SSU ribosomal proteins)	Translation elongation factor Tu					1.4
23630.peg.1120	Tolerance to colicin E2	Inner membrane protein CreD	-0.9	-1.0		-0.6	
DEGs non classified in RAST Categories							
23630.peg.4130		(R)-3-hydroxydecanoyl-ACP:CoA transacylase PhaG (3-hydroxyacyl-CoA-acyl carrier protein transferase) (EC 2.4.1.-)	-1.3		0.8		-1.2
23630.peg.3213		(Y14336) putative extracellular protein containing predicted 35aa signal peptide	-1.1				
23630.peg.3553		16 kDa heat shock protein A			0.8		
23630.peg.4460		2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34)			0.8	-0.4	0.8
23630.peg.4156		2-aminoethylphosphonate uptake and metabolism regulator				1.1	
23630.peg.3445		2-hydroxychromene-2-carboxylate isomerase family protein, glutathione-dependent			-0.8	-0.8	
23630.peg.4535		2-Oxobutyrate oxidase, putative	-1.6				-1.3
23630.peg.4121		2-Oxobutyrate oxidase, putative			-0.9	-0.7	
23630.peg.4528		2-Oxobutyrate oxidase, putative			-1.3		
23630.peg.699		2-Oxobutyrate oxidase, putative	0.9				
23630.peg.2048		33 kDa chaperonin (Heat shock protein 33) (HSP33)	1.3			0.9	
23630.peg.2465		3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64)			0.6		
23630.peg.4111		3-hydroxyisobutyryl-CoA hydrolase (EC 3.1.2.4)	1.7				
23630.peg.813		3-methylmercaptopropionyl-CoA ligase (DmdB)	0.8			-0.9	
23630.peg.1601		4-carboxymuconolactone decarboxylase domain/alkylhydroperoxidase AhpD family core domain protein			0.7		
23630.peg.834		ABC transporter ATP-binding protein					1.4
23630.peg.3904		ABC transporter ATP-binding protein			0.7	0.7	1.8
23630.peg.2053		ABC transporter ATP-binding protein USSDB6B					-0.9
23630.peg.2978		ABC transporter ATP-binding protein YvcR	1.0		0.7	0.8	0.8
23630.peg.2742		ABC transporter permease protein			-1.4		1.0
23630.peg.4975		ABC transporter permease protein			-1.4		
23630.peg.4257		ABC transporter, ATP-binding protein			-0.9		-0.9
23630.peg.2743		ABC transporter, ATP-binding protein	0.7				0.1
23630.peg.4974		ABC transporter, ATP-binding protein	0.7				0.1
23630.peg.3748		ABC transporter, ATP-binding/permease protein				-0.6	-1.2
23630.peg.2915		ABC transporter, periplasmic substrate-binding protein			1.0	0.6	0.8
23630.peg.43		ABC transporter, periplasmic substrate-binding protein-related protein			-0.7	-0.7	-0.9
23630.peg.2484		ABC transporter, permease protein	-0.6		-1.2		-0.8
23630.peg.695		ABC transporter, permease protein			-1.2	0.8	
23630.peg.3638		ABC transporter, transmembrane region:ABC transporter:Peptidase C39, bacteriocin processing				-0.7	-1.0

23630.peg.2228	ABC-2	1.1	0.8	1.1	0.7	
23630.peg.480	ABC-type amino acid transport/signal transduction system			-1.0		
23630.peg.3350	ABC-type antimicrobial peptide transport system, ATPase component	1.1	-0.6		0.7	
23630.peg.885	ABC-type antimicrobial peptide transport system, permease component		0.7			
23630.peg.835	ABC-type branched-chain amino acid transport systems, ATPase component	1.0	0.9		0.6	
23630.peg.2483	ABC-type Fe3+ transport system, periplasmic component		0.9	0.9	0.6	
23630.peg.2856	ABC-type Fe3+-siderophore transport system, ATPase component				0.6	
23630.peg.191	ABC-type multidrug transport system, ATPase and permease components			-0.5		
23630.peg.1995	ABC-type multidrug transport system, permease component	-1.0			-0.6	
23630.peg.1996	ABC-type multidrug transport system, permease component	-1.0	-0.7	-0.9		
23630.peg.417	ABC-type sugar transport systems, ATPase components	0.8			0.8	
23630.peg.2054	ABC-type transport system involved in resistance to organic solvents, permease component USSDB6A	-0.8	-0.8	-0.9	-0.7	
23630.peg.1925	Acetyl-CoA hydrolase		0.8			
23630.peg.2694	acetyltransferase		0.9	0.8		
23630.peg.3512	Acyclic terpenes utilization regulator AtuR, TetR family		-0.6	-0.6		
23630.peg.2227	acyl carrier protein					1.3
23630.peg.2062	Acyl-CoA dehydrogenase (EC 1.3.99.3)					1.7
23630.peg.815	Acyl-CoA dehydrogenase (EC 1.3.99.3)				0.6	
23630.peg.761	Acyl-CoA dehydrogenase (EC 1.3.99.3)	0.9	0.9	1.0	1.3	
23630.peg.83	Acyl-CoA dehydrogenase (EC 1.3.99.3)			0.5		
23630.peg.254	Acyl-CoA long-chain enzyme transcriptional related heme family		0.8	2.1	1.6	-1.0
23630.peg.4621	Aerobic C4-dicarboxylate transporter for fumarate, L-malate, D-malate, succinate		-0.9		-1.6	-1.6
23630.peg.3641	aerotaxis receptor, putative			-1.1		
23630.peg.3637	Agglutination protein	0.8		-0.7		
23630.peg.293	Aldose 1-epimerase	-1.4			-0.9	
23630.peg.4841	Alkane-1 monooxygenase (EC 1.14.15.3)		0.8			
23630.peg.4114	Alkyl sulfatase and related hydrolases	-1.7		0.4	-0.9	
23630.peg.3912	Alkyldihydroxyacetonephosphate synthase (EC 2.5.1.26)		0.7			
23630.peg.2385	alpha/beta hydrolase fold	1.1				
23630.peg.264	Alpha/beta hydrolase fold (EC 3.8.1.5)	0.9				
23630.peg.2457	Alpha-2-macroglobulin			-0.9		
23630.peg.1873	Altronate hydrolase (EC 4.2.1.7)	1.0				
23630.peg.2755	amino acid ABC transporter, periplasmic substrate-binding protein			-0.9		
23630.peg.4962	amino acid ABC transporter, periplasmic substrate-binding protein			-0.9		
23630.peg.1986	amino acid ABC transporter, permease protein		-0.7		0.7	

23630.peg.2417	Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine			-1.0		-0.9	
23630.peg.491	amino acid permease-associated region	-1.2				0.8	
23630.peg.2839	Antibiotic biosynthesis monooxygenase			-0.5		-0.9	
23630.peg.642	AraC-type DNA-binding domain-containing proteins	-1.0	-0.8	-0.6			1.7
23630.peg.683	Arylamine N-acetyltransferase (EC 2.3.1.5)			-0.7			
23630.peg.295	ATPase			-0.8			
23630.peg.2496	ATPase (PiIT family)	-0.8					-1.2
23630.peg.4653	ATPase involved in DNA repair		-0.9				
23630.peg.959	ATPase, AAA family				-0.8		
23630.peg.852	ATPase, AFG1 type			-0.6			
23630.peg.3968	ATP-dependent helicase HrpA			0.8			
23630.peg.1385	AttT protein					-1.0	
23630.peg.851	Auxin Efflux Carrier						-1.3
23630.peg.281	AzIC protein				-0.9		
23630.peg.2811	Azoreductase		0.7				
23630.peg.2371	Azurin	-1.1					
23630.peg.339	Bacterioferritin		-0.8			-0.9	-1.8
23630.peg.4094	Bacterioferritin-associated ferredoxin	2.9	1.9	0.7	1.3	1.7	
23630.peg.4670	BatA (Bacteroides aerotolerance operon)		-0.7				
23630.peg.2840	Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-); Similar to arginate lyase	-1.2	-1.5	1.0	-1.3	-0.6	0.3
23630.peg.4371	Bll1207 protein		0.9				
23630.peg.3475	Bll2208 protein	-1.0	-1.0	-0.6			
23630.peg.4536	bmp family protein	-1.1			-1.2		
23630.peg.698	bmp family protein	-0.7		-0.6			
23630.peg.4558	BNR/Asp-box repeat protein		-0.7			-1.4	
23630.peg.1747	BNR/Asp-box repeat protein	1.7	1.5	2.6	1.2	1.3	
23630.peg.2699	Bsl0049 protein				-1.3		
23630.peg.1577	C4-dicarboxylate transport sensor protein	0.8				0.7	
23630.peg.4349	Ca ion P-type ATPase			0.5	-1.1		
23630.peg.539	Carboxynorspermidine decarboxylase	1.2		1.0			
23630.peg.538	Carboxynorspermidine dehydrogenase			0.7	1.3		1.8
23630.peg.394	CcsA-related protein			1.1			
23630.peg.4344	CDP-abequose synthase (Fragment)		-0.7	0.8	-0.7		
23630.peg.3893	Cell division inhibitor-related protein	1.3	1.3			1.1	0.6
23630.peg.1184	Cell division protein FtsX			-0.7		-0.8	
23630.peg.2904	Cell division trigger factor (EC 5.2.1.8)						0.9
23630.peg.1677	Chaperone protein YscY (Yop proteins translocation protein Y)		-0.6				
23630.peg.4579	Chemotactic transducer-related protein	0.9				0.6	
23630.peg.2719	chemotaxis protein MotB-related protein	-1.7	-1.1	-0.7	-0.8	-1.2	-1.2
23630.peg.2291	Chloramphenicol acetyltransferase (EC 2.3.1.28)		-0.8				
23630.peg.4185	Chloramphenicol-sensitive protein rarD						1.8
23630.peg.4894	Chromosome segregation ATPases						-1.1
23630.peg.543	Chromosome segregation ATPases	-0.8		-0.6			

23630.peg.3085	CinA domain protein			-0.6	-0.9		
23630.peg.107	Citrate lyase beta chain (EC 4.1.3.6)	2.0		1.0			
23630.peg.2845	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases	-1.6	-1.2				
23630.peg.223	COG0553: Superfamily II DNA/RNA helicases, SNF2 family				1.0		
23630.peg.1056	COG0582: Integrase	-1.0					
23630.peg.3855	COG1399 protein, clustered with ribosomal protein L32p			0.7	0.9		
23630.peg.4396	COG1683: Uncharacterized conserved protein / FIG143828: Hypothetical protein YbgA				-0.9		
23630.peg.4401	COG2907: Amine oxidase, flavin-containing	1.2			1.1	1.3	2.0
23630.peg.2686	COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain		-0.7				
23630.peg.2518	COG3744: Uncharacterized protein conserved in bacteria					-1.0	
23630.peg.2853	COG5430: Uncharacterized secreted protein	1.5		0.6		1.1	1.1
23630.peg.111	COGs COG3777				1.1		
23630.peg.466	cold acclimation protein B	-0.9	-1.2	-0.8		-1.6	
23630.peg.2801	competence protein ComEA helix-hairpin-helix repeat	-0.7	-0.8	-1.0		-1.1	
23630.peg.3566	protein						
	competence protein ComEA helix-hairpin-helix repeat		-0.7	-0.6		-1.0	
	protein						
23630.peg.3055	Conidiation-specific protein 10		0.6	0.6			
23630.peg.2984	Conserved domain protein						-1.3
23630.peg.1043	Conserved domain protein	-1.4			-1.0	-1.2	
23630.peg.2288	Conserved domain protein	-0.8	-1.0			-0.7	
23630.peg.880	Conserved domain protein	1.8	1.6	0.6	1.2	1.9	
23630.peg.1805	Conserved domain protein				1.4		
23630.peg.3466	Conserved domain protein			0.8	1.8		
23630.peg.3302	Conserved domain protein			-0.7			
23630.peg.148	Conserved domain protein			-0.6			
23630.peg.3124	conserved hypothetical protein					0.6	
23630.peg.4260	conserved hypothetical protein	-1.6					
23630.peg.4508	CopG domain-containing protein						-1.6
23630.peg.3248	CopG domain-containing protein	0.3	0.9				
23630.peg.4243	Cyanate MFS transporter			0.8			
23630.peg.2473	Cyanide insensitive terminal oxidase, putative subunit III						-1.2
23630.peg.4863	Cyclohexanone monooxygenase (EC 1.14.13.22)					-0.8	
23630.peg.4554	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)	-1.0					
23630.peg.4403	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79), plant type					0.8	
23630.peg.41	Cysteine desulfurase CsdA-CsdE, sulfur acceptor protein CsdE	-1.0	-0.7	-0.6			
23630.peg.2826	cystine ABC transporter, periplasmic cystine binding protein	0.8				0.7	
23630.peg.701	Cytochrome b	1.1	1.3	2.6	0.7	2.0	
23630.peg.3731	Cytochrome B561		-1.0		-1.5		-0.6

23630.peg.1036	Cytochrome c family protein	-1.0		-0.5		-1.2	-1.5
23630.peg.1973	Cytochrome c family protein		-0.7		1.1	-0.7	
23630.peg.4278	D-2-hydroxyglutarate dehydrogenase		-0.4				
23630.peg.1259	D-2-hydroxyglutarate dehydrogenase	0.7					
23630.peg.2098	Decarboxylase family protein		0.9				
23630.peg.1979	DedA family protein	0.9	1.0	0.8	0.9	0.9	
23630.peg.4300	deoxyribodipyrimidine photolyase-related protein	-1.3					
23630.peg.1645	diguanylate cyclase	-0.9	-1.0	-0.5			
23630.peg.140	diguanylate cyclase	-1.1					
23630.peg.732	diguanylate cyclase (GGDEF domain) with PAS/PAC sensor			-0.8			
23630.peg.1067	diguanylate cyclase (GGDEF domain) with PAS/PAC sensor		-0.9				
23630.peg.2167	diguanylate cyclase with PAS/PAC sensor		0.5	0.7		-1.3	
23630.peg.225	diguanylate cyclase/phosphodiesterase	-0.8	-1.3	-0.6	-1.2	-0.9	
23630.peg.809	diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	0.9					
23630.peg.987	dimethyladenosine transferase(EC:2.1.1.48)	1.1	0.9	1.4	1.2	1.0	
23630.peg.2516	DNA polymerase, beta domain protein region					-0.8	
23630.peg.3102	DNA polymerase-like protein PA0670		-1.0			-0.8	
23630.peg.2749	DNA-binding response regulator, LuxR family		-0.7				0.6
23630.peg.4968	DNA-binding response regulator, LuxR family		-0.7				0.6
23630.peg.2456	DNA-damage-inducible protein F	0.9	0.9	0.8		0.7	
23630.peg.3013	DNA-directed RNA polymerase specialized sigma subunit, sigma24-like		-0.7			-1.0	
23630.peg.4307	DnaK suppressor protein	-0.9	-0.8		-0.9		-0.4
23630.peg.1701	Dodecin (COG3360) Flavin-binding			-0.8			
23630.peg.3619	Dolichol-phosphate mannosyltransferase (EC 2.4.1.83) in lipid-linked oligosaccharide synthesis cluster	-1.6			1.1		-1.0
23630.peg.4711	efflux transporter, RND family, MFP subunit		0.7				
23630.peg.1954	endo alpha-1,4 polygalactosaminidase precursor		-0.9				
23630.peg.4136	Endonuclease I precursor (EC 3.1.21.1)		0.6	0.7		-1.6	
23630.peg.3077	Endonuclease/Exonuclease/phosphatase family protein	-2.1			-1.1		
23630.peg.1789	Endonuclease/exonuclease/phosphatase family protein				1.0		
23630.peg.742	endonuclease/exonuclease/phosphatase family protein			0.4			
23630.peg.1921	Endoribonuclease L-PSP			1.8		0.9	
23630.peg.2865	Endoribonuclease L-PSP				-1.3		
23630.peg.4110	Enoyl-CoA hydratase [valine degradation] (EC 4.2.1.17)	1.6	0.8	0.8			
23630.peg.860	Epoxide hydrolase (EC 3.3.2.9)	-0.9	-1.0	0.7	-1.4		
23630.peg.3008	Esterase/lipase/thioesterase family protein				0.6		
23630.peg.3506	Ethanolamine ammonia-lyase heavy chain (EC 4.3.1.7)			1.1			
23630.peg.2728	Ethanolamine utilization protein eutQ	-1.1			-1.3		
23630.peg.1550	Excinuclease ATPase subunit					-0.9	
23630.peg.1392	Fatty acid desaturase			-0.7			
23630.peg.765	Ferrichrome transport system permease protein FhuB (TC 3.A.1.14.3)			-0.3			
23630.peg.416	Ferrichrome-iron receptor	-1.0	-1.2	0.6		-1.9	
23630.peg.4729	Ferrichrome-iron receptor	-0.6	-1.0	-1.0		-1.6	

23630.peg.2550	Ferrichrome-iron receptor	-0.9				-0.8	
23630.peg.2477	Ferrichrome-iron receptor					0.5	
23630.peg.1117	Ferrichrome-iron receptor		0.6	-0.5	0.9		
23630.peg.2632	Ferrichrome-iron receptor		-0.7	1.2	1.0		
23630.peg.411	Ferrichrome-iron receptor				1.0		
23630.peg.2354	Fe-S OXIDOREDUCTASE (1.8.-.-)	1.7	0.7		1.3		
23630.peg.169	FHA domain containing protein				-1.0		
23630.peg.3339	FIG001454: Transglutaminase-like enzymes, putative cysteine proteases	-1.3			-0.7		
23630.peg.4337	FIG002188: hypothetical protein				1.1		
23630.peg.646	FIG002188: hypothetical protein	0.5					
23630.peg.3483	FIG002283: Isochorismatase family protein	1.1	0.9	0.9		0.7	
23630.peg.3340	FIG002343: hypothetical protein			-0.6			
23630.peg.85	FIG002577: Putative lipoprotein precursor					1.0	
23630.peg.3295	FIG002776: hypothetical protein			0.8		0.7	
23630.peg.4399	FIG002994: Putative transcriptional regulator	1.3				1.2	1.6
23630.peg.886	FIG003461: hypothetical protein	0.9				0.9	
23630.peg.1169	FIG003551: hypothetical protein		0.7			0.6	
23630.peg.2349	FIG003573: hypothetical protein				1.0		
23630.peg.605	FIG004454: RNA binding protein			0.7			
23630.peg.3286	FIG00456413: hypothetical protein	-1.1	-0.9				
23630.peg.3236	FIG00457034: hypothetical protein	0.4	0.9				1.9
23630.peg.2161	FIG004891: hypothetical protein in carnitine cluster	-1.1		-0.5			
23630.peg.2606	FIG005080: Possible exported protein			-0.6			
23630.peg.3915	FIG005107: hypothetical protein	-2.0	-1.8		-0.8	-1.1	-0.4
23630.peg.3221	FIG00582580: hypothetical protein					0.6	
23630.peg.1532	FIG006045: Sigma factor, ECF subfamily	0.8			0.8		
23630.peg.2474	FIG006045: Sigma factor, ECF subfamily		1.8				
23630.peg.814	FIG00784312: hypothetical protein	1.9			1.2		
23630.peg.2266	FIG00784450: hypothetical protein	-1.2	-1.5			-1.4	
23630.peg.2977	FIG00809136: hypothetical protein		0.7				
23630.peg.2807	FIG00857858: hypothetical protein	1.0	0.9				
23630.peg.971	FIG00883731: hypothetical protein		-0.6	-0.7			
23630.peg.2156	FIG00953113: hypothetical protein		0.9			0.7	1.1
23630.peg.4764	FIG00953167: hypothetical protein		-0.7				
23630.peg.4898	FIG00953170: hypothetical protein					-0.9	
23630.peg.952	FIG00953184: hypothetical protein						1.4
23630.peg.4063	FIG00953202: hypothetical protein		-0.9				
23630.peg.4651	FIG00953208: hypothetical protein				-1.0		
23630.peg.3436	FIG00953282: hypothetical protein		-0.7				
23630.peg.3387	FIG00953296: hypothetical protein		0.6				
23630.peg.2745	FIG00953323: hypothetical protein				-1.1	-0.6	
23630.peg.4972	FIG00953323: hypothetical protein				-1.1	-0.6	
23630.peg.3737	FIG00953335: hypothetical protein	1.8				0.7	
23630.peg.175	FIG00953341: hypothetical protein			0.7			
23630.peg.3080	FIG00953356: hypothetical protein					-0.9	
23630.peg.2000	FIG00953390: hypothetical protein		-0.8				
23630.peg.1368	FIG00953394: hypothetical protein	2.0	1.5		0.4	1.5	

23630.peg.1316	FIG00953395: hypothetical protein			1.4	0.6	0.9	
23630.peg.1908	FIG00953403: hypothetical protein		-0.8	-0.8			
23630.peg.353	FIG00953405: hypothetical protein						1.9
23630.peg.4342	FIG00953409: hypothetical protein		-0.7		-0.5		
23630.peg.3897	FIG00953423: hypothetical protein			-0.6			
23630.peg.1460	FIG00953482: hypothetical protein		0.4				
23630.peg.1938	FIG00953808: hypothetical protein		-1.1	-0.9	1.0	-1.2	
23630.peg.2980	FIG00953861: hypothetical protein	0.8		0.7			
23630.peg.2504	FIG00953980: hypothetical protein			0.7			
23630.peg.3894	FIG00954079: hypothetical protein		-0.8				-1.4
23630.peg.3752	FIG00954136: hypothetical protein	0.9	0.8	1.0		0.8	
23630.peg.1456	FIG00954150: hypothetical protein			1.7		0.6	
23630.peg.259	FIG00954264: hypothetical protein	-0.9					
23630.peg.2925	FIG00954367: hypothetical protein			-0.6			
23630.peg.781	FIG00954429: hypothetical protein			-0.6			
23630.peg.2806	FIG00954456: hypothetical protein	0.9					
23630.peg.3869	FIG00954461: hypothetical protein			0.6	1.0		
23630.peg.1166	FIG00954467: hypothetical protein			-0.6			
23630.peg.3990	FIG00954516: hypothetical protein	-1.0	-1.3	-0.6	-1.0	-1.8	-2.1
23630.peg.2353	FIG00954617: hypothetical protein			-0.7		-0.7	
23630.peg.4671	FIG00954674: hypothetical protein		0.8	0.6			
23630.peg.541	FIG00954796: hypothetical protein					0.6	
23630.peg.3676	FIG00954807: hypothetical protein						1.6
23630.peg.2737	FIG00955015: hypothetical protein			-0.6	-0.8		
23630.peg.4980	FIG00955015: hypothetical protein			-0.6	-0.8		
23630.peg.3058	FIG00955186: hypothetical protein		0.8				
23630.peg.404	FIG00955190: hypothetical protein				1.4		
23630.peg.1040	FIG00955197: hypothetical protein	-1.8			-0.9	-1.3	-1.5
23630.peg.3223	FIG00955278: hypothetical protein		-1.0			-1.4	
23630.peg.3399	FIG00955285: hypothetical protein			0.7			
23630.peg.774	FIG00955339: hypothetical protein	1.4		1.0			
23630.peg.4594	FIG00955360: hypothetical protein						1.3
23630.peg.1648	FIG00955422: hypothetical protein					-1.0	
23630.peg.4005	FIG00955424: hypothetical protein	-1.2	-1.6	-0.7		-1.1	
23630.peg.297	FIG00955586: hypothetical protein			-0.9			
23630.peg.4740	FIG00955605: hypothetical protein		-0.7			-0.8	
23630.peg.2164	FIG00955680: hypothetical protein	1.7			1.0		
23630.peg.3640	FIG00955751: hypothetical protein	1.0					0.9
23630.peg.1425	FIG00955818: hypothetical protein	-1.1					
23630.peg.324	FIG00955883: hypothetical protein				-0.8		
23630.peg.661	FIG00955916: hypothetical protein	0.8					
23630.peg.2165	FIG00955932: hypothetical protein			-0.6			
23630.peg.662	FIG00955938: hypothetical protein	-1.0			1.0	-0.7	
23630.peg.1369	FIG00956018: hypothetical protein	2.1	1.3		0.9	1.6	
23630.peg.3338	FIG00956090: hypothetical protein	-0.7		-0.7			
23630.peg.4586	FIG00956101: hypothetical protein					0.6	
23630.peg.3259	FIG00956188: hypothetical protein				1.0		-1.4
23630.peg.4886	FIG00956241: hypothetical protein	0.8				0.7	

23630.peg.2124	FIG00956403: hypothetical protein					0.6	
23630.peg.3167	FIG00956413: hypothetical protein				-0.8		
23630.peg.232	FIG00956494: hypothetical protein		-0.7			-0.7	
23630.peg.1153	FIG00956533: hypothetical protein	0.7					
23630.peg.943	FIG00956751: hypothetical protein				-1.0		
23630.peg.540	FIG00956780: hypothetical protein		-0.9				
23630.peg.472	FIG00957284: hypothetical protein			0.8			
23630.peg.323	FIG00957314: hypothetical protein			1.1	1.7		
23630.peg.4200	FIG00957354: hypothetical protein				-1.5		
23630.peg.785	FIG00957593: hypothetical protein			1.2	-1.1	0.7	
23630.peg.1033	FIG00958355: hypothetical protein	-2.6		-0.3		-1.9	-1.3
23630.peg.2273	FIG00958582: hypothetical protein			-0.6			
23630.peg.4602	FIG00958722: hypothetical protein						1.5
23630.peg.2986	FIG00958794: hypothetical protein	-1.1	-1.0	-0.7		-0.7	
23630.peg.352	FIG00958830: hypothetical protein			-0.6			
23630.peg.4327	FIG00958979: hypothetical protein		-0.9		-0.6		
23630.peg.3189	FIG00959020: hypothetical protein	-0.9	-0.6	-0.9		-1.6	-2.1
23630.peg.153	FIG00959330: hypothetical protein		-1.3			-0.9	-0.6
23630.peg.4238	FIG00960458: hypothetical protein	-1.2					
23630.peg.4580	FIG00960787: hypothetical protein					-0.7	
23630.peg.2121	FIG00960943: hypothetical protein						2.3
23630.peg.2747	FIG00963224: hypothetical protein						1.4
23630.peg.4970	FIG00963224: hypothetical protein						1.4
23630.peg.2454	FIG00964132: hypothetical protein		-0.6				
23630.peg.168	FIG00964654: hypothetical protein	-1.1		0.7	-1.1		-1.1
23630.peg.2720	FIG00964765: hypothetical protein						-1.2
23630.peg.4510	FIG01066055: hypothetical protein	-1.1	-0.8				
23630.peg.256	FIG01200150: hypothetical protein			1.1		0.9	
23630.peg.1190	FIG015287: Zinc protease		0.8			0.8	
23630.peg.1189	FIG015547: peptidase, M16 family			0.7			
23630.peg.433	FIG021952: putative membrane protein			-0.6			
23630.peg.467	FIG023103: Predicted transmembrane protein	0.9					
23630.peg.3916	FIG023677: hypothetical protein					-0.7	
23630.peg.4404	FIG024285: Hypothetical protein				0.8		
23630.peg.1380	FIG028593: membrane protein			-0.6			
23630.peg.1201	FIG028932: hypothetical protein		-0.7	-0.6			
23630.peg.166	FIG033889: YebC paralog in Betaproteobacteria		0.6				
23630.peg.647	FIG067310: hypothetical protein		-0.6	-0.7	-0.9		
23630.peg.4338	FIG067310: hypothetical protein	0.7	0.5				
23630.peg.1272	FIG136845: Rhodanese-related sulfurtransferase	1.1		1.1	1.2		
23630.peg.38	FIG138056: a glutathione-dependent thiol reductase			0.7			
23630.peg.4412	FIG140336: TPR domain protein		0.7				
23630.peg.1116	FIG152265: Sodium:solute symporter associated protein			0.8		0.7	
23630.peg.3633	FIGfam010717			-0.6			
23630.peg.2816	FMN-dependent NADH-azoreductase		0.7	0.6		0.9	-1.2
23630.peg.4187	FMN-dependent NADH-azoreductase		0.6	0.6	1.0		
23630.peg.3069	FOG: CBS domain						-1.1
23630.peg.97	FOG: EAL domain protein				-1.3		

23630.peg.1362	fosmidomycin resistance protein	0.6				
23630.peg.3432	FUPA27 P-type ATPase		0.9	0.7		
23630.peg.318	GCN5-related N-acetyltransferase	1.1				1.6
23630.peg.2015	GENE II AND X PROTEINS	-1.1				
23630.peg.3810	Gfa-like protein					1.7
23630.peg.3598	GGDEF domain protein			-0.7		
23630.peg.1091	GGDEF domain protein	1.1				
23630.peg.4823	GlcG protein	-0.6		-0.9		
23630.peg.50	gliding motility protein GldG	0.6				
23630.peg.3095	Gll3326 protein	0.7	0.8	0.8		
23630.peg.3059	glutamate--cysteine ligase, GCS2	0.8				
23630.peg.3646	glutamine ABC transporter ATP-binding component	-1.3	1.1	-0.5		
23630.peg.4388	Glutamine amidotransferase, class I			-0.8		
23630.peg.3409	Glutamine amidotransferase, class I	-0.7				
23630.peg.1451	Glutaryl-CoA dehydrogenase (EC 1.3.99.7)		-0.7			
23630.peg.3237	Glycosidases	0.9	0.6		0.6	
23630.peg.3569	glycosyl transferase, group 1	-0.9			-0.9	
23630.peg.554	Glycosyltransferase					-1.3
23630.peg.4459	Glycosyltransferase	-1.2		1.1		
23630.peg.3373	Helicase subunit of the DNA excision repair complex			1.4		
23630.peg.3057	HemK family modification methylase PA2179	-1.0				
23630.peg.1230	Hemolysin activation/secretion protein	-1.0	-0.9	-1.0	-0.9	
23630.peg.3664	Hemolysin-type calcium-binding region		0.7	0.6	-1.5	
23630.peg.2283	Heptose kinase WapQ, eukaryotic type	-0.8	-0.7	-0.7		-1.2
23630.peg.1604	Histone acetyltransferase HPA2 and related acetyltransferases			-0.6	-0.8	
23630.peg.753	Histone acetyltransferase HPA2 and related acetyltransferases		0.6		0.6	
23630.peg.1761	Histone acetyltransferase HPA2 and related acetyltransferases		0.8	0.7	0.8	
23630.peg.1997	HlyD family secretion protein	-1.2		-1.0		-1.8
23630.peg.2446	HlyD family secretion protein				-0.6	
23630.peg.4716	hydrolase, alpha/beta fold family			-1.5		
23630.peg.1080	Hydrolases of the alpha/beta superfamily					-0.2
23630.peg.3070	Hydrolases of the alpha/beta superfamily	-1.1		-0.7		
23630.peg.4031	hypothetical membrane protein	-1.2		-0.9		
23630.peg.1044	hypothetical protein	-2.0	-0.6	-0.7	-1.7	-2.7
23630.peg.4432	hypothetical protein			-1.2		-2.3
23630.peg.371	hypothetical protein			0.7	0.7	-2.0
23630.peg.1512	hypothetical protein			0.6		-1.9
23630.peg.410	hypothetical protein	-1.6	-1.7		-1.0	-1.7
23630.peg.712	hypothetical protein				-0.7	-1.7
23630.peg.2701	hypothetical protein			-1.3	-0.8	-1.6
23630.peg.3384	hypothetical protein				-1.0	-1.5
23630.peg.412	hypothetical protein	-1.3			-1.0	-1.5
23630.peg.3410	hypothetical protein					-1.4
23630.peg.2903	hypothetical protein	-0.7	-1.2	-1.4	-1.1	-1.4
23630.peg.2225	hypothetical protein			1.0		-1.3

23630.peg.1061	hypothetical protein						-1.3
23630.peg.4523	hypothetical protein	-1.1	-0.8		-1.7		-1.2
23630.peg.2141	hypothetical protein	-1.5					-1.2
23630.peg.1041	hypothetical protein					-0.9	-1.2
23630.peg.4438	hypothetical protein	-2.0	-1.5		-2.3		-0.9
23630.peg.1118	hypothetical protein	-1.1		-0.4		-1.9	-0.7
23630.peg.4240	hypothetical protein						-0.7
23630.peg.4981	hypothetical protein	-1.1	-1.5	-0.7	-1.0	-0.9	-0.5
23630.peg.4914	hypothetical protein	-0.9					-0.2
23630.peg.2882	hypothetical protein	-0.6		-0.6	-1.5		0.2
23630.peg.3074	hypothetical protein		0.8	0.8			0.8
23630.peg.1575	hypothetical protein						0.9
23630.peg.3367	hypothetical protein	0.8	2.0	0.6	0.5		1.0
23630.peg.1062	hypothetical protein						1.1
23630.peg.3348	hypothetical protein	0.8				0.7	1.3
23630.peg.4283	hypothetical protein						1.4
23630.peg.3808	hypothetical protein	-1.0			-0.6		1.5
23630.peg.116	hypothetical protein		0.9	0.8			1.5
23630.peg.458	hypothetical protein						1.7
23630.peg.3814	hypothetical protein						1.7
23630.peg.767	hypothetical protein	2.8	2.8	1.0	2.4	2.0	1.9
23630.peg.2563	hypothetical protein						1.9
23630.peg.1748	hypothetical protein	2.2	2.1	3.5	1.0	2.6	1.9
23630.peg.3523	hypothetical protein						1.9
23630.peg.1359	hypothetical protein						2.2
23630.peg.1707	hypothetical protein	-1.1	-1.1			-0.8	2.3
23630.peg.3580	hypothetical protein	-1.0	-1.2			-1.7	
23630.peg.4131	hypothetical protein	-1.3	-1.8	-0.9	-0.7	-1.7	
23630.peg.3981	hypothetical protein	-1.5	-1.6		-0.7	-1.7	
23630.peg.2759	hypothetical protein					-1.6	
23630.peg.4958	hypothetical protein					-1.6	
23630.peg.190	hypothetical protein	-0.8	-1.1	-0.8	-1.4	-1.4	
23630.peg.3022	hypothetical protein		-1.0	0.6		-1.4	
23630.peg.4421	hypothetical protein	-1.1			-0.8	-1.4	
23630.peg.3019	hypothetical protein	-3.0	-2.6		-2.3	-1.3	
23630.peg.2148	hypothetical protein	-1.0	-0.8			-1.3	
23630.peg.319	hypothetical protein					-1.2	
23630.peg.1052	hypothetical protein	-1.6				-1.1	
23630.peg.2821	hypothetical protein	-1.8	-1.0	-0.5	-1.6	-1.0	
23630.peg.3036	hypothetical protein					-1.0	
23630.peg.3222	hypothetical protein	-1.8		-0.3	-2.0	-1.0	
23630.peg.312	hypothetical protein	-1.1	-1.3			-1.0	
23630.peg.3576	hypothetical protein	-1.1	-1.3	-1.2	-1.4	-1.0	
23630.peg.576	hypothetical protein					-0.9	
23630.peg.2900	hypothetical protein		-1.1			-0.9	
23630.peg.42	hypothetical protein		-0.7			-0.9	
23630.peg.3287	hypothetical protein			-0.6		-0.9	
23630.peg.1607	hypothetical protein	-0.9	-1.2	-0.7		-0.9	

23630.peg.1028	hypothetical protein	-1.9			-0.7	-0.9
23630.peg.3600	hypothetical protein					-0.9
23630.peg.3197	hypothetical protein					-0.9
23630.peg.4284	hypothetical protein	-0.6		-0.8		-0.9
23630.peg.2901	hypothetical protein	-1.0	-1.0	-0.8	-1.1	-0.9
23630.peg.3931	hypothetical protein		-1.6			-0.9
23630.peg.2693	hypothetical protein		-1.0	-0.8	-0.8	-0.8
23630.peg.1031	hypothetical protein		-0.9	-0.9	-0.9	-0.8
23630.peg.413	hypothetical protein		-0.7	-0.6		-0.8
23630.peg.1047	hypothetical protein		-0.9	-0.7	-0.8	-0.8
23630.peg.2830	hypothetical protein					-0.8
23630.peg.2722	hypothetical protein		-0.7			-0.8
23630.peg.493	hypothetical protein	-1.0	-0.8	-0.7		-0.8
23630.peg.1491	hypothetical protein					-0.8
23630.peg.1534	hypothetical protein					-0.8
23630.peg.1733	hypothetical protein					-0.8
23630.peg.2938	hypothetical protein					-0.7
23630.peg.4377	hypothetical protein	-1.1		-0.2	-0.7	-0.7
23630.peg.4550	hypothetical protein	-0.9	-1.0	-0.7	-0.9	-0.7
23630.peg.1801	hypothetical protein			-0.6		-0.7
23630.peg.3900	hypothetical protein	-1.0				-0.7
23630.peg.1816	hypothetical protein					-0.7
23630.peg.2561	hypothetical protein					-0.7
23630.peg.204	hypothetical protein					-0.7
23630.peg.1795	hypothetical protein			-0.9		-0.7
23630.peg.3198	hypothetical protein			-0.7	-1.0	-0.7
23630.peg.1434	hypothetical protein					-0.7
23630.peg.1108	hypothetical protein	-1.0				-0.7
23630.peg.2939	hypothetical protein		-0.8			-0.7
23630.peg.1606	hypothetical protein					-0.7
23630.peg.4608	hypothetical protein					-0.7
23630.peg.2711	hypothetical protein					-0.7
23630.peg.1071	hypothetical protein					-0.5
23630.peg.4920	hypothetical protein					0.5
23630.peg.2393	hypothetical protein	0.9				0.6
23630.peg.1723	hypothetical protein					0.6
23630.peg.279	hypothetical protein			0.8		0.6
23630.peg.149	hypothetical protein	1.0	0.6	0.8		0.7
23630.peg.3040	hypothetical protein					0.7
23630.peg.176	hypothetical protein	0.8		1.0		0.7
23630.peg.2395	hypothetical protein	0.9	0.9	0.5		0.7
23630.peg.2394	hypothetical protein	1.3			0.7	0.7
23630.peg.3023	hypothetical protein	0.9		1.0		0.8
23630.peg.3232	hypothetical protein		1.0			0.8
23630.peg.2758	hypothetical protein	0.9	0.6	0.9		0.8
23630.peg.4959	hypothetical protein	0.9	0.6	0.9		0.8
23630.peg.3024	hypothetical protein	0.7		1.0	0.9	0.8
23630.peg.2067	hypothetical protein	0.8	0.7	1.0	1.0	0.9

23630.peg.3029	hypothetical protein	1.5	1.3			1.0
23630.peg.3922	hypothetical protein	0.9			1.0	1.0
23630.peg.4924	hypothetical protein			0.7		1.1
23630.peg.760	hypothetical protein	0.7	1.0	0.9		1.2
23630.peg.702	hypothetical protein		1.2	2.1		1.5
23630.peg.1746	hypothetical protein	1.2	1.3	1.8		1.5
23630.peg.4582	hypothetical protein				-1.5	
23630.peg.160	hypothetical protein			0.9	-1.4	
23630.peg.2838	hypothetical protein	-1.1		-0.5	-1.2	
23630.peg.3031	hypothetical protein	-0.9	-0.7	0.8	-1.2	
23630.peg.1301	hypothetical protein	-0.9			-1.1	
23630.peg.3099	hypothetical protein				-1.1	
23630.peg.2837	hypothetical protein				-1.0	
23630.peg.1298	hypothetical protein	-1.5			-1.0	
23630.peg.4826	hypothetical protein				-0.9	
23630.peg.2492	hypothetical protein		-1.0		-0.9	
23630.peg.3196	hypothetical protein				-0.9	
23630.peg.3187	hypothetical protein				-0.9	
23630.peg.1299	hypothetical protein	-1.0	-1.7		-0.8	
23630.peg.1895	hypothetical protein		-0.7		-0.8	
23630.peg.1046	hypothetical protein				-0.8	
23630.peg.1898	hypothetical protein		-0.8	0.7	-0.8	
23630.peg.4532	hypothetical protein				-0.8	
23630.peg.150	hypothetical protein				-0.8	
23630.peg.1016	hypothetical protein				-0.7	
23630.peg.3205	hypothetical protein				-0.6	
23630.peg.1353	hypothetical protein	0.8		-0.5	0.0	
23630.peg.1822	hypothetical protein				0.8	
23630.peg.3381	hypothetical protein		0.7		0.9	
23630.peg.800	hypothetical protein	1.2			0.9	
23630.peg.2055	hypothetical protein			-0.8	0.9	
23630.peg.2190	hypothetical protein				1.0	
23630.peg.1121	hypothetical protein		0.6		1.0	
23630.peg.145	hypothetical protein		0.6		1.0	
23630.peg.2383	hypothetical protein		0.6		1.0	
23630.peg.2945	hypothetical protein				1.0	
23630.peg.2220	hypothetical protein				1.1	
23630.peg.2434	hypothetical protein	1.0			1.1	
23630.peg.381	hypothetical protein			0.8	1.1	
23630.peg.772	hypothetical protein		0.6		1.1	
23630.peg.2009	hypothetical protein		1.5		1.1	
23630.peg.1974	hypothetical protein			0.9	1.2	
23630.peg.2338	hypothetical protein				1.2	
23630.peg.720	hypothetical protein		0.7		1.2	
23630.peg.3407	hypothetical protein				1.2	
23630.peg.664	hypothetical protein				1.2	
23630.peg.1743	hypothetical protein	0.8			1.3	
23630.peg.1847	hypothetical protein			0.7	1.3	

23630.peg.3389	hypothetical protein			1.3
23630.peg.4709	hypothetical protein			1.3
23630.peg.1599	hypothetical protein			1.4
23630.peg.2643	hypothetical protein		0.3	-1.0
23630.peg.3206	hypothetical protein		0.6	-0.8
23630.peg.3144	hypothetical protein			-0.8
23630.peg.1338	hypothetical protein	-0.4	-1.2	-0.8
23630.peg.1569	hypothetical protein	-1.0		-0.8
23630.peg.3713	hypothetical protein			-0.7
23630.peg.3109	hypothetical protein			-0.7
23630.peg.3142	hypothetical protein			-0.6
23630.peg.3301	hypothetical protein	-1.0	-1.2	-0.6
23630.peg.3160	hypothetical protein	-0.9		-0.6
23630.peg.3839	hypothetical protein	-1.2		-0.6
23630.peg.4285	hypothetical protein	-1.0	-0.7	-0.6
23630.peg.1581	hypothetical protein			-0.6
23630.peg.3662	hypothetical protein		-0.8	-0.6
23630.peg.2223	hypothetical protein			-0.6
23630.peg.2534	hypothetical protein			-0.6
23630.peg.833	hypothetical protein			-0.6
23630.peg.4713	hypothetical protein	-1.4	-1.0	-0.5
23630.peg.1194	hypothetical protein			0.5
23630.peg.1519	hypothetical protein			0.6
23630.peg.1066	hypothetical protein			0.6
23630.peg.2849	hypothetical protein			0.6
23630.peg.4597	hypothetical protein	-1.1	-0.6	0.7
23630.peg.3868	hypothetical protein	1.0		0.7
23630.peg.1914	hypothetical protein			0.7
23630.peg.139	hypothetical protein			0.7
23630.peg.4426	hypothetical protein			0.8
23630.peg.3467	hypothetical protein			0.8
23630.peg.188	hypothetical protein		0.7	0.9
23630.peg.294	hypothetical protein	0.8		0.9
23630.peg.3597	hypothetical protein		0.7	0.9
23630.peg.1011	hypothetical protein			0.9
23630.peg.678	hypothetical protein	0.9	0.6	1.0
23630.peg.756	hypothetical protein			1.0
23630.peg.1388	hypothetical protein			1.3
23630.peg.2507	hypothetical protein	-0.7		1.5
23630.peg.3956	hypothetical protein	-1.5	-1.4	
23630.peg.221	hypothetical protein		-1.4	
23630.peg.4357	hypothetical protein		-1.4	
23630.peg.3033	hypothetical protein	-1.4	-1.2	
23630.peg.1300	hypothetical protein	-0.8	-1.0	
23630.peg.3685	hypothetical protein		-1.0	
23630.peg.861	hypothetical protein		-0.9	
23630.peg.1055	hypothetical protein		-0.9	
23630.peg.4122	hypothetical protein		-0.9	

23630.peg.4261	hypothetical protein	-0.9
23630.peg.1896	hypothetical protein	-0.9
23630.peg.2795	hypothetical protein	-1.3
23630.peg.3090	hypothetical protein	-0.8
23630.peg.49	hypothetical protein	-0.8
23630.peg.1894	hypothetical protein	-0.8
23630.peg.1148	hypothetical protein	-0.8
23630.peg.310	hypothetical protein	-0.8
23630.peg.4905	hypothetical protein	-0.7
23630.peg.4631	hypothetical protein	-0.7
23630.peg.2361	hypothetical protein	-0.7
23630.peg.1060	hypothetical protein	-0.6
23630.peg.3155	hypothetical protein	-1.0
23630.peg.523	hypothetical protein	0.4
23630.peg.4075	hypothetical protein	0.5
23630.peg.1291	hypothetical protein	0.6
23630.peg.4902	hypothetical protein	0.7
23630.peg.3705	hypothetical protein	1.4
23630.peg.241	hypothetical protein	0.7
23630.peg.164	hypothetical protein	0.7
23630.peg.1595	hypothetical protein	0.7
23630.peg.3479	hypothetical protein	0.8
23630.peg.1564	hypothetical protein	0.8
23630.peg.266	hypothetical protein	0.8
23630.peg.3043	hypothetical protein	-1.4
23630.peg.2734	hypothetical protein	-1.4
23630.peg.58	hypothetical protein	-1.3
23630.peg.4904	hypothetical protein	-1.2
23630.peg.2703	hypothetical protein	-1.2
23630.peg.3462	hypothetical protein	-1.1
23630.peg.4133	hypothetical protein	-1.0
23630.peg.1188	hypothetical protein	-1.0
23630.peg.697	hypothetical protein	-1.0
23630.peg.3065	hypothetical protein	-1.0
23630.peg.2868	hypothetical protein	-1.0
23630.peg.2917	hypothetical protein	-0.9
23630.peg.2818	hypothetical protein	-0.9
23630.peg.3204	hypothetical protein	-0.8
23630.peg.1846	hypothetical protein	-0.7
23630.peg.1025	hypothetical protein	-0.7
23630.peg.3228	hypothetical protein	-0.7
23630.peg.4678	hypothetical protein	-0.7
23630.peg.4113	hypothetical protein	-0.4
23630.peg.3035	hypothetical protein	0.6
23630.peg.4495	hypothetical protein	0.6
23630.peg.1526	hypothetical protein	0.7
23630.peg.1882	hypothetical protein	0.7
23630.peg.3039	hypothetical protein	0.8

23630.peg.2746	hypothetical protein	0.8					
23630.peg.4971	hypothetical protein	0.8					
23630.peg.1616	hypothetical protein	0.8					
23630.peg.2388	hypothetical protein	0.9					
23630.peg.2118	hypothetical protein	0.9					
23630.peg.3443	hypothetical protein	0.9					
23630.peg.4584	hypothetical protein	0.9					
23630.peg.2402	hypothetical protein	1.0					
23630.peg.4672	hypothetical protein PA3071				-1.0		
23630.peg.2045	hypothetical protein sometimes fused to ribosomal protein S6				1.0		
	glutaminy transferase						
23630.peg.1122	Hypothetical protein, restriction endonuclease-like VRR-NUC domain	0.8					
23630.peg.2405	Hypothetical Zinc-finger containing protein	-0.8		-0.7			
23630.peg.3225	HYPOTHETICAL/UNKNOWN PROTEIN			0.9			
23630.peg.2284	InaA protein	-0.8		-0.6		-0.8	
23630.peg.677	InaA protein					-0.7	
23630.peg.348	Inactive homolog of metal-dependent proteases, putative molecular chaperone	1.1	0.6	0.9		0.8	0.9
23630.peg.2953	Inhibitor of the KinA pathway to sporulation, predicted exonuclease					-0.8	
23630.peg.3563	Inner membrane component of tripartite multidrug resistance system				-0.9		
23630.peg.447	Inositol-1-monophosphatase (EC 3.1.3.25)			0.7		0.7	
23630.peg.3329	Integral membrane protein TerC						1.5
23630.peg.1971	Integral membrane protein TerC	-1.0				-0.8	
23630.peg.526	Integral membrane protein TerC			0.8			
23630.peg.3688	integral membrane sensor hybrid histidine kinase		-0.8			-1.1	
23630.peg.3471	Integrase	-1.9	-1.5	-0.5	-0.7	-1.1	
23630.peg.316	Iron-regulated protein A precursor	2.0	1.6		1.5	1.0	1.1
23630.peg.250	Isopropylmalate/homocitrate/citramalate synthases		0.7			0.8	
23630.peg.4150	Lactoylglutathione lyase and related lyases		0.9			0.6	
23630.peg.1231	Large exoproteins involved in heme utilization or adhesion		-0.7				
23630.peg.1450	L-carnitine dehydratase/bile acid-inducible protein F			-0.7			
23630.peg.104	L-carnitine dehydratase/bile acid-inducible protein F (EC 2.8.3.16)			-0.7			
23630.peg.3482	Lipase					0.7	
23630.peg.2973	Lipase activator protein, Lipase-specific foldase		-0.7		-0.9		
23630.peg.3689	Lipase chaperone (Lipase foldase) (Lipase helper protein) (Lipase activator protein) (Lipase modulator)	-1.3					
23630.peg.2560	lipase family protein					-0.7	
23630.peg.2974	Lipase precursor (EC 3.1.1.3)					0.9	
23630.peg.1944	Lipoprotein LppL-related protein				0.9		
23630.peg.663	lipoprotein, putative	1.2	1.0	1.1	1.0	1.0	
23630.peg.1414	lipoprotein, putative				0.8		
23630.peg.3832	lipoprotein, putative	1.2	0.8	0.9			
23630.peg.4102	lipoprotein, putative		0.8				

23630.peg.879	lipoprotein, putative	1.0				
23630.peg.4262	Long-chain fatty acid transport protein			0.7		
23630.peg.3862	Low molecular weight protein tyrosine phosphatase (EC 3.1.3.48)			0.9		
23630.peg.2658	LppC putative lipoprotein	0.7				
23630.peg.1416	L-rhamnose operon transcriptional activator RhaR				-0.9	
23630.peg.4358	Lysine efflux permease				-1.0	
23630.peg.1842	Lytic transglycosylase, catalytic		0.7			
23630.peg.1966	Macrophage infectivity potentiator			-0.7		
23630.peg.4320	major facilitator family transporter	-0.9	-0.5		-0.9	
23630.peg.1910	Major facilitator family transporter	0.8				
23630.peg.2691	major facilitator superfamily MFS_1	0.9				
23630.peg.2982	Major outer membrane lipoprotein I		0.6	1.1		
23630.peg.665	Malate:quinone oxidoreductase (EC 1.1.5.4)		0.8			
23630.peg.4707	mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase(EC:2.7.7.22)	0.7		2.0		
23630.peg.648	Medium-chain-fatty-acid--CoA ligase (EC 6.2.1.-)		-0.8			1.8
23630.peg.4232	Membrane carboxypeptidase (penicillin-binding protein)		-0.6			
23630.peg.3	membrane protein		0.7		0.7	
23630.peg.3944	membrane protein	-0.8				
23630.peg.3812	membrane protein, putative	-0.9			-0.8	
23630.peg.2397	membrane protein, putative				0.5	
23630.peg.3623	membrane protein, putative		1.0		0.7	
23630.peg.4718	membrane protein, putative	0.9	0.9			
23630.peg.4719	membrane protein, putative		0.7	1.3		
23630.peg.1376	membrane protein, putative	1.0				
23630.peg.1168	Methionine biosynthesis protein MetW	0.9	0.7			
23630.peg.2718	Methyl-accepting chemotaxis protein	-0.9		-0.5	-0.9	-1.8
23630.peg.3335	Methyl-accepting chemotaxis protein		-1.2		-1.6	-1.6
23630.peg.2102	Methyl-accepting chemotaxis protein	-2.2	-1.5	-1.5	-1.8	-1.0
23630.peg.656	Methyl-accepting chemotaxis protein	1.0				1.0
23630.peg.98	Methyl-accepting chemotaxis protein				-0.9	
23630.peg.3211	Methyl-accepting chemotaxis protein		-0.7		-0.8	
23630.peg.2459	Methyl-accepting chemotaxis protein			-1.5		
23630.peg.2814	Methyl-accepting chemotaxis protein		-0.8	-1.1		
23630.peg.2344	Methyl-accepting chemotaxis protein		-0.8	-0.8		
23630.peg.3472	Methyl-accepting chemotaxis protein		-0.7	-0.6		
23630.peg.1173	methyl-accepting chemotaxis sensory transducer	0.8				
23630.peg.4489	methylated-DNA--protein-cysteine methyltransferase-related protein			0.7		
23630.peg.586	Methyltransferase (EC 2.1.1.-)	0.0				
23630.peg.1358	MFS general substrate transporter			0.8	1.5	
23630.peg.3942	MFS transporter	1.0	0.6		0.8	1.0
23630.peg.109	MmgE/PrpD family protein	0.9			0.7	0.9
23630.peg.1302	Mobile element protein				-0.8	-0.8
23630.peg.2790	Mobile element protein				-0.8	-0.8
23630.peg.4982	Mobile element protein	-1.6	-1.5		-2.9	
23630.peg.1891	Mobile element protein				0.9	

23630.peg.826	Mobile element protein			0.8	1.0		
23630.peg.1003	Mobile element protein			-0.6			
23630.peg.2056	monooxygenase, flavin-binding family			-0.8			
23630.peg.3151	Monooxygenase, flavin-binding family		-0.7				
23630.peg.4673	MoxR-like ATPase in aerotolerance operon	0.8		0.9			
23630.peg.3562	Multidrug resistance protein A				1.7		
23630.peg.474	Na ⁺ /H ⁺ antiporter NhaC		0.8				
23630.peg.4032	NAD(FAD)-utilizing dehydrogenase, slt0175 homolog	1.3					
23630.peg.3755	NAD(P)H dehydrogenase, quinone family					0.6	
23630.peg.4352	NADH:flavin oxidoreductases, Old Yellow Enzyme family		0.6				1.1
23630.peg.4144	NADPH-dependent FMN reductase	2.6	1.1	1.3		1.9	
23630.peg.2794	N-ethylmaleimide reductase (EC 1.-.-.)	-1.1					
23630.peg.1156	Nitrogen Metabolism Transcriptional Regulator, NtrC, Fis Family					0.8	
23630.peg.3707	NLP/P60 family protein			0.6			
23630.peg.1673	NLP/P60 family protein	1.0		0.8			
23630.peg.1012	NreA-like protein	0.7					
23630.peg.4551	NTP pyrophosphohydrolases including oxidative damage repair enzymes				-0.9		
23630.peg.973	NtrC family transcriptional regulator			-0.5			
23630.peg.4527	Nucleoside-binding outer membrane protein	-1.9	-1.0		-1.4	-1.5	-1.8
23630.peg.4385	Nucleoside-binding outer membrane protein				-1.1		
23630.peg.1417	Nucleoside-diphosphate-sugar epimerases			-0.7			
23630.peg.3567	nucleotide sugar epimerase/dehydratase WbpM		-0.8			-0.8	
23630.peg.2521	Nucleotidyltransferase (EC 2.7.7.-)					-0.7	
23630.peg.4757	O-antigen biosynthesis protein			-0.6		-0.8	
23630.peg.3529	OmpA family protein				-0.8		
23630.peg.3207	OmpA/MotB domain protein	-1.4	-1.0				
23630.peg.962	OsmC/Ohr family protein			0.7		0.6	
23630.peg.4259	Outer membrane efflux family protein		-0.7				
23630.peg.4414	Outer membrane lipoprotein LolB precursor		0.9				
23630.peg.1255	Outer membrane protein	0.9	1.0			0.8	0.2
23630.peg.2735	Outer membrane protein (porin)	-1.4	-1.0	-0.9	-1.0		-1.5
23630.peg.4616	outer membrane protein H1	-1.0	-1.1	-0.7	0.4	-0.8	1.7
23630.peg.893	Outer membrane protein W precursor				-0.9		
23630.peg.2744	outer membrane protein, putative	1.0	-0.5	-0.6	-0.7	-0.7	
23630.peg.4973	outer membrane protein, putative	1.0	-0.5	-0.6	-0.7	-0.7	
23630.peg.1284	Oxalate/formate antiporter			-0.8			-1.6
23630.peg.3457	Oxidoreductase (EC 1.1.1.-)						-1.8
23630.peg.4229	Oxidoreductase, aldo/keto reductase family				-0.9		
23630.peg.2315	Oxidoreductase, FAD-binding	0.9			0.9		
23630.peg.4244	Oxidoreductase, short chain dehydrogenase/reductase family					0.7	
23630.peg.4452	Oxidoreductase, short chain dehydrogenase/reductase family		0.6			0.8	
23630.peg.261	Oxidoreductase, short chain dehydrogenase/reductase family	1.0	0.9			1.0	

23630.peg.3596	Oxidoreductase, short chain dehydrogenase/reductase family		0.7			
23630.peg.3536	Oxidoreductase, short chain dehydrogenase/reductase family		-0.8			
23630.peg.4373	Oxidoreductase, short chain dehydrogenase/reductase family	0.8	0.6			
23630.peg.3933	oxidoreductase, short-chain alcohol dehydrogenase/reductase family(EC:1.-)					-0.8
23630.peg.3501	Oxidoreductase, short-chain dehydrogenase/reductase family	0.9	0.7		0.9	1.3
23630.peg.255	Oxidoreductase, short-chain dehydrogenase/reductase family			1.8	1.4	
23630.peg.4400	Oxidoreductase, short-chain dehydrogenase/reductase family (EC 1.1.1.-)	1.5			1.1	
23630.peg.2730	oxidoreductase-related protein					0.8
23630.peg.2727	Oxidoreductase-related protein			0.6		
23630.peg.3609	P pilus assembly/Cpx signaling pathway, periplasmic inhibitor/zinc-resistance associated protein		1.0			
23630.peg.1217	PAS sensor protein			0.7		
23630.peg.4251	Patatin			-0.7		
23630.peg.4070	Penicillin acylase (EC 3.5.1.11)	0.8		0.7		
23630.peg.1267	Penicillin acylase II (EC 3.5.1.11)					0.5
23630.peg.2752	pentapeptide repeat family protein				-0.9	
23630.peg.4965	pentapeptide repeat family protein				-0.9	
23630.peg.2365	Peptidase M50					-1.2
23630.peg.2933	Peptidase, U7 family				-1.1	
23630.peg.3627	Peptidoglycan-binding LysM			-0.9		
23630.peg.3511	Periplasmic binding protein		-0.8			
23630.peg.4731	periplasmic binding protein	-1.8	-0.8			
23630.peg.2859	periplasmic binding protein	0.8				
23630.peg.537	Periplasmic protein TonB, links inner and outer membranes		0.8			
23630.peg.3833	Permease of the major facilitator superfamily					-1.2
23630.peg.866	Permeases of the major facilitator superfamily	0.8				
23630.peg.4391	Permeases of the major facilitator superfamily	1.7				
23630.peg.1901	Phage integrase	0.9				
23630.peg.2902	Phage late control D	-0.8	-1.1			
23630.peg.465	phage related integrase		-0.7	-0.6		
23630.peg.3470	phage single-stranded DNA-binding protein, putative	-1.1	0.5		-0.9	
23630.peg.3328	Phosphate-binding protein				1.0	
23630.peg.1233	phosphoesterase, putative			0.6		
23630.peg.129	Phosphogluconate repressor HexR, RpiR family	0.9		0.7		0.7
23630.peg.1110	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily	0.9				
23630.peg.4265	Phosphoheptose isomerase					0.8
23630.peg.4058	Phosphoribosylcarboxyaminoimidazole (NCAIR) mutase		0.6			
23630.peg.2515	Pilin glycosylation enzyme	-0.9	-1.0			-1.2
23630.peg.4250	Pirin		0.6			

23630.peg.3909	Pirin-like protein CC_1473			1.3	0.8
23630.peg.3063	Plasmid stabilization system protein		0.6		
23630.peg.2421	PLP-dependent aminotransferase NCgl2355 (class III)		0.7	0.9	
23630.peg.746	Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)	0.6	0.8	1.2	
23630.peg.1734	Polysaccharide deacetylase		-0.8	-1.0	
23630.peg.3996	POSSIBLE MEMBRANE PROTEIN	1.1	0.6		0.9
23630.peg.2119	PQQ-dependent oxidoreductase, gdhB family	0.8			0.7
23630.peg.2696	Predicted DNA-binding protein, possible transcriptional regulator			0.9	
23630.peg.1085	Predicted histidine uptake transporter				0.2
23630.peg.3091	predicted membrane protein		0.6		
23630.peg.3154	Predicted permease			-0.9	
23630.peg.3777	predicted protein		0.7		
23630.peg.4516	Predicted protein-tyrosine phosphatase		0.8		0.9
23630.peg.3835	Predicted protein-tyrosine phosphatase		0.6		
23630.peg.4104	predicted signal transduction protein			-0.7	-0.7
23630.peg.883	Predicted zinc-binding protein	-1.5			
23630.peg.907	Preprotein translocase secY subunit (TC 3.A.5.1.1)			0.9	
23630.peg.4856	Probable 3-phenylpropionic acid transporter		1.0		0.5
23630.peg.1107	probable acetyltransferase		-0.8	-0.9	-0.9
23630.peg.2299	Probable acyl-CoA dehydrogenase (EC 1.3.99.3)		0.7		0.6
23630.peg.110	Probable acyl-CoA dehydrogenase (EC 1.3.99.3)	1.2	0.6		0.7
23630.peg.1759	Probable AGCS sodium/alanine/glycine symporter		0.6	0.9	1.0
23630.peg.489	probable amino acid permease	0.9	0.6		0.6
23630.peg.4623	PROBABLE ANTIBIOTIC-RESISTANCE PROTEIN	0.8	0.8	0.6	0.8
23630.peg.3032	Probable bacteriophage integrase	-1.8	-0.6	-0.8	
23630.peg.1537	probable dioxygenase				1.7
23630.peg.448	probable exported protein YPO1624		0.9	0.8	0.8
23630.peg.496	Probable glutathione s-transferase protein (EC 2.5.1.18)			-0.6	
23630.peg.189	probable helicase	-1.3	-0.8	-0.6	-0.8
23630.peg.3558	Probable hydrolase	-1.3			
23630.peg.1238	probable integral membrane protein NMA1899			0.9	
23630.peg.3230	Probable lipoprotein			0.7	
23630.peg.2101	probable membrane protein NMA1176	-1.4		0.6	-1.8
23630.peg.1014	probable membrane protein YPO3302			-0.8	
23630.peg.2587	probable metallopeptidase				-1.5
23630.peg.3940	probable oxidoreductase/Short-chain dehydrogenase			-0.9	
23630.peg.719	probable oxidoreductase/Short-chain dehydrogenase		0.6		
23630.peg.694	probable permease of ABC transporter		-1.3	1.4	
23630.peg.4891	Probable RND efflux membrane fusion protein		1.0		
23630.peg.196	Probable short chain dehydrogenase	-1.0	-1.7	-0.6	
23630.peg.199	probable short-chain dehydrogenase		-1.0		-0.6
23630.peg.3519	Probable short-chain dehydrogenase	1.1			
23630.peg.282	Probable thiol oxidoreductase with 2 cytochrome c heme-binding sites			0.8	
23630.peg.4336	probable transcriptional regulator			-1.5	
23630.peg.2995	Probable transcriptional regulator		0.7	0.6	

23630.peg.1536	probable transcriptional regulator	1.0					
23630.peg.2896	Probable transmembrane protein	1.5		-0.6		0.3	1.1
23630.peg.2014	Probable transmembrane protein	-1.3	-0.8		-0.8		
23630.peg.2166	Probable transmembrane protein			-0.9			
23630.peg.1778	Probable transmembrane protein	1.4					
23630.peg.3503	Probable two-component response regulator	-1.4		1.0			-1.5
23630.peg.3097	Protease subunit of ATP-dependent Clp proteases			0.8			-1.4
23630.peg.2370	Protein containing transglutaminase-like domain, putative cysteine protease	-0.7					
23630.peg.2104	protein of unknown function DUF1090	-0.8	-0.8				-1.4
23630.peg.1912	protein of unknown function DUF1127	-1.3	-0.7		-2.0		-1.6
23630.peg.1457	protein of unknown function DUF1127			0.8			
23630.peg.3129	protein of unknown function DUF1272			0.7	1.0		
23630.peg.1357	protein of unknown function DUF395, YeeE/YedE		-1.0		-0.7		
23630.peg.4430	protein of unknown function DUF6, transmembrane	0.8					-1.0
23630.peg.1243	Protein of unknown function DUF81					-0.7	
23630.peg.1766	protein of unknown function DUF81		-1.1				
23630.peg.146	protein of unknown function DUF861, cupin_3		-2.0		-0.7		
23630.peg.3401	protein of unknown function DUF903	0.9					1.7
23630.peg.4241	Protein of unknown function UPF0060				-0.7		
23630.peg.1105	Protein rarD					0.6	
23630.peg.3622	Protein secretion chaperonin CsaA	0.8	0.6			0.7	
23630.peg.1729	Protein serine/threonine phosphatase PrpC, regulation of stationary phase		-1.1				
23630.peg.1256	Protein ygiW precursor	1.3	1.1	0.6		0.7	
23630.peg.1638	Protein YidD	0.9		0.8	1.1		1.1
23630.peg.1561	Protein YidD	0.1		1.0	2.0	-0.6	
23630.peg.449	Protein-export membrane protein SecF (TC 3.A.5.1.1)						-1.9
23630.peg.1799	Protein-glutamate methyltransferase (EC 3.1.1.61)	0.9	0.6		1.0		
23630.peg.4852	Protein-N(5)-glutamine methyltransferase PrmB, methylates LSU ribosomal protein L3p	0.7		0.8			
23630.peg.3577	Pseudaminic acid cytidyltransferase (EC 2.7.7.43)	-1.1	-1.1	-0.7		-1.3	
23630.peg.3945	putative 2-pyrone-4,6-dicarboxylic acid hydrolase		-0.6			-1.0	
23630.peg.4258	putative ABC transporter		-0.9		-0.8	-1.2	
23630.peg.1319	Putative activity regulator of membrane protease YbbK			-1.0			
23630.peg.2264	putative acyl-CoA dehydrogenase		1.0			0.7	
23630.peg.1090	putative acyl-CoA dehydrogenase	0.7					
23630.peg.1985	Putative amino acid ABC transporter, permease protein		0.7		1.0		
23630.peg.4375	putative amino acid binding protein		1.4	1.4	1.2		
23630.peg.4724	Putative ATP-binding component of a transport system				0.8		
23630.peg.3645	putative bacterial extracellular solute-binding protein, family 3		0.7	1.3		0.7	
23630.peg.48	putative cold-shock DNA-binding domain protein						-1.7
23630.peg.4197	Putative cytoplasmic protein					1.4	
23630.peg.3674	putative cytoplasmic protein		-0.7				
23630.peg.3178	Putative cytoplasmic protein USSDB7A	1.3	0.7			1.0	
23630.peg.2875	Putative diguanylate cyclase (GGDEF domain)				-1.0		

23630.peg.2951	Putative DMT superfamily metabolite efflux protein precursor				0.8	
23630.peg.461	putative DNA-binding protein	-1.5	-1.4	-0.6		
23630.peg.2305	Putative esterase, FIGfam005057					0.7
23630.peg.2783	putative exonuclease	-1.3				-0.8
23630.peg.4934	putative exonuclease	-1.3				-0.8
23630.peg.587	putative exported protein		-0.7		-0.8	
23630.peg.3324	putative exported protein	-0.9		-0.7		
23630.peg.2396	Putative heat shock protein YegD	-0.8				
23630.peg.4346	Putative hemolysin	-0.9			1.1	
23630.peg.3660	Putative inner membrane protein		-0.8			
23630.peg.3217	putative integrase		0.9			0.8
23630.peg.4230	putative lyase			-0.6		
23630.peg.273	putative membrane protein			1.3		0.6
23630.peg.3484	putative membrane protein		0.7			0.7
23630.peg.1543	putative membrane protein		0.7			
23630.peg.3958	Putative membrane protein	-0.9				
23630.peg.2125	Putative membrane-bound ClpP-class protease associated with aq_911			-0.8		
23630.peg.3157	Putative metalloprotease yggG (EC 3.4.24.-)		0.6			0.7
23630.peg.488	Putative methyltransferase		0.9			
23630.peg.618	Putative oligoketide cyclase/dehydratase or lipid transport protein YfjG					1.6
23630.peg.321	putative oxidoreductase		-0.7			
23630.peg.3300	Putative phosphatase	-1.7			-0.7	-0.7
23630.peg.3224	putative plasmid stabilization protein		0.7	0.8		-2.5
23630.peg.4030	putative polyketide synthase	1.0		0.9		
23630.peg.1113	Putative protease			0.7		0.6
23630.peg.4454	putative RecF protein	0.8	0.7			
23630.peg.1024	putative regulatory protein (P-II) for nitrogen assimilation by glutamine synthetase (ATase)					-0.2
23630.peg.2800	putative short-chain dehydrogenase				-1.3	
23630.peg.2885	putative short-chain dehydrogenase		0.7			
23630.peg.1505	putative sodium-dependent bicarbonate transporter			0.7		0.8
23630.peg.2126	Putative stomatin/prohibitin-family membrane protease subunit aq_911	1.1			-1.1	0.7
23630.peg.3973	Putative transport protein			0.6		0.6
23630.peg.897	Putative transport protein	0.8	0.7	0.7		
23630.peg.1862	putative zinc-containing dehydrogenase			-0.6		
23630.peg.3138	Putrescine ABC transporter, periplasmic putrescine-binding protein			-0.7	-1.0	
23630.peg.2760	Quino(hemo)protein alcohol dehydrogenase, PQQ-dependent (EC 1.1.99.8)			-0.8	-0.9	
23630.peg.4957	Quino(hemo)protein alcohol dehydrogenase, PQQ-dependent (EC 1.1.99.8)			-0.8	-0.9	
23630.peg.1158	Radical SAM domain protein	1.5	0.7			0.7
23630.peg.3101	RecA/RadA recombinase			-0.5		
23630.peg.3056	Regulator of cell morphogenesis and NO signaling	-0.6				

23630.peg.1965	Regulator of sigma D			-0.6		-0.8	
23630.peg.718	regulatory protein, TetR						-1.3
23630.peg.4297	Response regulator			0.8			
23630.peg.659	Restriction endonuclease	-0.7		-0.9			
23630.peg.3416	Rhodanese domain protein				-1.0		
23630.peg.4800	Rhodanese domain protein	-0.7					
23630.peg.2741	Rhodanese-related sulfurtransferase	1.3					
23630.peg.4976	Rhodanese-related sulfurtransferase	1.3					
23630.peg.1320	Ribonucleotide reductase, alpha subunit						1.6
23630.peg.1129	Ribosomal protein S6 glutaminyl transferase	0.8		0.8		0.7	
23630.peg.1191	Ribosomal RNA small subunit methyltransferase D (EC 2.1.1.-)				0.9		
23630.peg.11	ribosomal subunit interface protein, putative	-1.0				-0.7	
23630.peg.265	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases	0.8				0.6	
23630.peg.3647	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases					0.7	
23630.peg.3720	RNA methyltransferase, TrmA family			-0.6		-0.7	
23630.peg.3994	RNA polymerase associated protein RapA (EC 3.6.1.-)			-0.6			
23630.peg.3494	RNA polymerase sigma-70 factor, ECF subfamily	2.7	2.0	0.7		1.7	0.9
23630.peg.341	RND efflux membrane fusion protein		-0.7				
23630.peg.1360	SAM-dependent methyltransferases	0.8	0.6		1.1	0.7	
23630.peg.3370	SAM-dependent methyltransferases	0.8	1.6	0.6	1.5		
23630.peg.144	SAM-dependent methyltransferases	-0.6					
23630.peg.1195	Sensor protein DegS				-0.9		
23630.peg.1803	Sensory box histidine kinase				1.1		
23630.peg.2738	Sensory box histidine kinase/response regulator	-1.3	-1.2	-1.3	-1.2	-1.0	
23630.peg.4979	Sensory box histidine kinase/response regulator	-1.3	-1.2	-1.3	-1.2	-1.0	
23630.peg.2768	Sensory box histidine kinase/response regulator			-0.6		-0.8	
23630.peg.4949	Sensory box histidine kinase/response regulator			-0.6		-0.8	
23630.peg.1002	Sensory box/GGDEF family protein				-1.1		
23630.peg.633	Sensory box/GGDEF family protein			-0.7	-1.0		
23630.peg.2499	Sensory box/GGDEF family protein				0.6		
23630.peg.2123	sensory box-containing diguanylate cyclase		0.6				
23630.peg.1649	Ser/Thr and Tyr protein phosphatase (dual specificity)	-2.2					-1.2
23630.peg.3620	Ser/Thr protein phosphatase family protein, UDP-2,3-diacetylglucosamine hydrolase (EC 3.6.1.-) homolog	-0.6			1.5		
23630.peg.2285	Serine/threonine protein kinase		-1.0	-0.5		-1.1	-1.5
23630.peg.823	Serine/threonine protein kinase		-0.6				
23630.peg.1730	Serine/threonine protein kinase (EC 2.7.11.1)		-1.5				
23630.peg.3153	short chain dehydrogenase		-0.8	-0.6			
23630.peg.3948	short-chain dehydrogenase/reductase	-1.6	-1.8	1.0			1.0
23630.peg.740	Short-chain dehydrogenase/reductase SDR			-0.7			
23630.peg.86	short-chain dehydrogenase/reductase SDR		-0.8				
23630.peg.2891	sigma-54 dependent transcriptional regulator	1.2					
23630.peg.1797	Signal transduction histidine kinase			-0.7		-0.8	
23630.peg.4296	Signal transduction histidine kinase			0.6	-1.1		
23630.peg.3504	Signal transduction histidine kinase	-0.9			1.0		

23630.peg.812	Signal transduction histidine kinase			-0.9		
23630.peg.1309	Signal transduction histidine kinase regulating C4-dicarboxylate transport system				0.6	
23630.peg.2733	Similar to pyrroloquinoline quinone biosynthesis protein F			-0.8		-1.0
23630.peg.4848	Smr domain protein			0.7		
23630.peg.4737	sodium:dicarboxylate symporter		0.6			1.1
23630.peg.130	Sodium-dependent transporter	1.4				
23630.peg.3740	Sodium-dependent transporter family protein	0.7	1.1			0.7
23630.peg.619	Sodium-dependent transporter family protein	0.9			1.0	
23630.peg.4135	sodium-solute symporter, putative	1.2				
23630.peg.3923	Spermidine/putrescine-binding periplasmic protein	-1.0	-1.2			1.6
23630.peg.1470	SrfB	-1.0		-0.5		-0.8
23630.peg.928	SSU ribosomal protein S10p (S20e)	0.9		0.8		
23630.peg.905	SSU ribosomal protein S13p (S18e)					1.4
23630.peg.593	SSU ribosomal protein S15p (S13e)				1.0	
23630.peg.918	SSU ribosomal protein S17p (S11e)				0.9	2.0
23630.peg.923	SSU ribosomal protein S19p (S15e)	-0.8				
23630.peg.3584	SSU ribosomal protein S1p				1.0	
23630.peg.4481	SSU ribosomal protein S20p	1.0		0.9	1.0	
23630.peg.34	SSU ribosomal protein S2p (SAe)	1.0		0.8		
23630.peg.921	SSU ribosomal protein S3p (S3e)				0.5	
23630.peg.910	SSU ribosomal protein S5p (S2e)					1.4
23630.peg.2347	SSU ribosomal protein S6p			0.7		0.9
23630.peg.2649	SSU ribosomal protein S9p (S16e)			0.8		
23630.peg.993	Stage V sporulation protein involved in spore cortex synthesis (SpoVR)	0.8				
23630.peg.1978	Sterol desaturase				-1.5	
23630.peg.4457	Sterol desaturase		-0.7	-0.7		
23630.peg.2088	still frameshift probable component of chemotactic signal transduction system			-0.6		-1.0
23630.peg.2751	Succinate dehydrogenase cytochrome b subunit family protein		-0.8			
23630.peg.4966	Succinate dehydrogenase cytochrome b subunit family protein		-0.8			
23630.peg.1675	Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)					-0.7
23630.peg.970	Succinate-semialdehyde dehydrogenase [NADP+] (EC 1.2.1.16)		1.1			-0.3
23630.peg.693	Sugar ABC transporter, ATP-binding protein		-0.9	0.5	-1.0	
23630.peg.1907	Sugar efflux permease, MFS-like		-1.1			
23630.peg.1887	SUGAR TRANSPORTER	1.3	0.7		1.1	1.1
23630.peg.569	Sugar/maltose fermentation stimulation protein homolog			1.0		-1.3
23630.peg.4560	sulfatase	-1.5	-1.9		-1.0	-1.2
23630.peg.366	Sulfate transporter				0.5	-0.5
23630.peg.1422	Superfamily II DNA and RNA helicases	0.9	0.6			
23630.peg.4866	Superfamily II DNA/RNA helicases, SNF2 family	0.9				
23630.peg.4248	Surface lipoprotein		0.6	0.7		

23630.peg.2199	Thermonuclease family protein				-1.0		
23630.peg.252	Thermostable hemolysin delta-VPH	2.3	2.4	4.0	1.6	3.0	
23630.peg.44	ThiF family protein		0.6				
23630.peg.3951	ThiJ/PfpI family protein			0.8		-1.0	
23630.peg.260	ThiJ/PfpI family protein	-0.9		-0.5	-0.9		
23630.peg.2163	thioesterase-like protein		-0.7			-1.2	
23630.peg.3712	Thiol-disulfide isomerase and thioredoxins		-0.7			-0.7	
23630.peg.1265	Thiol-disulfide isomerase and thioredoxins					0.9	
23630.peg.3684	Thiosulfate sulfurtransferase, rhodanese (EC 2.8.1.1)						1.9
23630.peg.1356	Thiosulfate sulfurtransferase, rhodanese (EC 2.8.1.1)	0.9	0.6			0.7	
23630.peg.3356	Threonine efflux protein	-0.9	-0.8	-0.6			
23630.peg.1917	transcription regulator protein			-0.7			
23630.peg.1751	Transcriptional regulator			0.8	1.3		
23630.peg.3170	transcriptional regulator			-0.7			
23630.peg.2150	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain			-0.8			
23630.peg.2159	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	-0.9	-0.8	-0.7			
23630.peg.4494	transcriptional regulator MvaT, P16 subunit, putative		-0.7			-0.8	
23630.peg.2187	Transcriptional regulator PhaD			0.8			
23630.peg.4862	Transcriptional regulator, AraC family	-1.5				-0.8	-0.9
23630.peg.582	Transcriptional regulator, AraC family	-1.4	-2.5	-1.0	-1.3	-1.4	
23630.peg.500	Transcriptional regulator, AraC family	-1.2		0.7		-0.8	
23630.peg.4648	Transcriptional regulator, AraC family	0.7	0.8			0.7	
23630.peg.1600	transcriptional regulator, AraC family	1.0	1.3		0.9	0.8	
23630.peg.3141	Transcriptional regulator, AraC family					0.9	
23630.peg.245	Transcriptional regulator, AraC family	-1.2			-1.2		
23630.peg.4270	Transcriptional regulator, AraC family			0.6	0.8		
23630.peg.2468	Transcriptional regulator, AraC family	0.8			1.1		
23630.peg.583	Transcriptional regulator, AraC family			0.6			
23630.peg.3827	Transcriptional regulator, AraC family		-0.7				
23630.peg.1266	Transcriptional regulator, AraC family	-1.5					
23630.peg.3490	transcriptional regulator, AraC family, putative			0.8		0.7	
23630.peg.516	transcriptional regulator, AraC-family	-1.5					
23630.peg.517	transcriptional regulator, AraC-family	1.1					
23630.peg.2108	Transcriptional regulator, ArsR family / Methyltransferase fusion	-0.7	-1.1		0.0		
23630.peg.2214	transcriptional regulator, Fis family	-1.5				-1.6	
23630.peg.1988	Transcriptional regulator, GntR family						1.6
23630.peg.2428	Transcriptional regulator, GntR family	0.2	0.8				
23630.peg.2740	Transcriptional regulator, LuxR family	1.1					
23630.peg.4977	Transcriptional regulator, LuxR family	1.1					
23630.peg.3934	transcriptional regulator, LysR family						-1.6
23630.peg.197	Transcriptional regulator, LysR family	-1.9	-1.7			-1.0	-1.5
23630.peg.3747	Transcriptional regulator, LysR family	-0.7				-1.1	
23630.peg.4291	Transcriptional regulator, LysR family	-2.6	-1.2	0.8	-1.8	-1.1	
23630.peg.2815	Transcriptional regulator, LysR family					-0.9	
23630.peg.4045	Transcriptional regulator, LysR family			-1.0		-0.8	

23630.peg.3331	Transcriptional regulator, LysR family					0.8	
23630.peg.3165	Transcriptional regulator, LysR family					0.9	
23630.peg.4534	Transcriptional regulator, LysR family	-1.0	-1.6	-0.5	-1.1		
23630.peg.4000	Transcriptional regulator, LysR family			-0.7			
23630.peg.3561	Transcriptional regulator, LysR family			0.6			
23630.peg.2109	Transcriptional regulator, LysR family		-0.9				
23630.peg.2798	Transcriptional regulator, LysR family	-1.5					
23630.peg.207	transcriptional regulator, LysR family	-0.9					
23630.peg.3976	Transcriptional regulator, MarR family	1.3	2.5	0.9	0.8	1.3	
23630.peg.3493	Transcriptional regulator, MarR family		0.3				
23630.peg.4397	Transcriptional regulator, MerR family, associated with photolyase						1.9
23630.peg.1906	Transcriptional regulator, TetR family			-1.2	-1.0	-0.8	
23630.peg.4461	Transcriptional regulator, TetR family		0.8			0.6	
23630.peg.762	Transcriptional regulator, TetR family			0.6		0.6	
23630.peg.4824	Transcriptional regulator, TetR family	1.1		1.2	1.0	0.9	
23630.peg.2789	Transcriptional regulator, TetR family		-0.7		-1.1		
23630.peg.4928	Transcriptional regulator, TetR family		-0.7		-1.1		
23630.peg.2020	Transcriptional regulator, TetR family			0.8			
23630.peg.2380	Transcriptional regulator, TetR family			0.8			
23630.peg.1079	Transcriptional regulator, TetR family			0.9			
23630.peg.1199	Transcriptional regulator, TetR family		1.1	0.9			
23630.peg.342	Transcriptional regulator, TetR family	-0.6	-0.9				
23630.peg.3559	Transcriptional regulator, TetR family	-1.2	-0.8				
23630.peg.1542	Transcriptional regulator, TetR family		-0.7				
23630.peg.2127	Transcriptional regulator, TetR family	0.8					
23630.peg.3028	Transcriptional regulators			0.8			
23630.peg.112	Transcriptional regulators, LysR family			-0.5			
23630.peg.1900	Transcription-repair coupling factor (superfamily II helicase)		-1.9	-0.5	-0.7	-1.1	
23630.peg.4888	Transglutaminase-like enzymes, putative cysteine proteases	-1.0				-0.9	-1.2
23630.peg.3333	Transglycosylase, Slt family			-0.6	-1.1	-1.0	
23630.peg.3495	Transmembrane sensor	1.6	1.2		0.8	1.1	
23630.peg.768	Transport protein	-1.0		0.7			
23630.peg.3977	TRANSPORTER, DME FAMILY	2.4	4.7	2.5	1.6	2.5	
23630.peg.3498	Transporter, LysE family		0.6	1.2		0.9	
23630.peg.1592	transporter, LysE family				0.8		
23630.peg.4739	Transporter, MFS superfamily			-0.8			
23630.peg.124	Transposase and inactivated derivatives		-0.7				
23630.peg.3212	Transthyretin family protein	-1.0					
23630.peg.1015	TraX family protein	-1.3	-0.7				
23630.peg.2260	TrkA domain protein	1.2		0.7		0.7	1.3
23630.peg.4603	Trp repressor-binding protein		0.9	0.7		0.8	1.6
23630.peg.2796	Twin-arginine translocation pathway signal	-1.3	-1.4				
23630.peg.2083	twitching motility protein PilG					-0.9	-1.5
23630.peg.1890	Two-component response regulator			-0.6			
23630.peg.2536	Two-component response regulator	-0.8		0.7			

23630.peg.1196	Two-component response regulator	0.8				
23630.peg.3725	Two-component response regulator PfeR, enterobactin		-0.7			
23630.peg.574	Two-component sensor CbrA: intracellular carbon:nitrogen balance		-0.7		-0.9	
23630.peg.3489	Two-component system regulatory protein	-0.8				
23630.peg.2040	Two-component system response regulator OmpR	0.8				
23630.peg.3369	two-component system sensor protein	-0.9	-0.6			-1.6
23630.peg.3488	two-component system sensor protein			0.7		
23630.peg.3298	Type II and III secretion system family protein		0.7		0.8	
23630.peg.3247	Type IV secretion system protein VirD4					1.5
23630.peg.4509	Type IV secretion system protein VirD4	-1.3	-1.2		-0.6	
23630.peg.2698	Type IV secretory pathway, protease TraF	-1.9	-1.6		-3.0	-0.9
23630.peg.2697	Type IV secretory pathway, VirD2 components (relaxase)				-0.7	
23630.peg.3239	Type IV secretory pathway, VirD2 components (relaxase)	0.8				
23630.peg.3047	UDP-glucose dehydrogenase (EC 1.1.1.22)	-1.0	-1.7	0.6	1.4	
23630.peg.4105	uncharacterized domain 1				0.9	
23630.peg.2548	Uncharacterized iron-regulated membrane protein; Iron-uptake factor PiuB	-0.9			-0.2	-1.3
23630.peg.1042	Uncharacterized protein conserved in bacteria, NMA0228-like	-1.5		-0.9	-1.1	-0.7
23630.peg.327	Uncharacterized protein ynbE; probable lipoprotein STY1424					-1.4
23630.peg.2038	Uncharacterized protein, possibly involved in aromatic compounds catabolism				1.1	
23630.peg.2257	Universal stress protein family		-0.7		-1.2	
23630.peg.2990	Universal stress protein family		-0.8	-0.8		
23630.peg.3902	Universal stress protein family COG0589			-0.7		
23630.peg.992	UPF0229 protein YeaH	0.8				
23630.peg.4437	UPF0246 protein YaaA		0.6			
23630.peg.2538	Urea ABC transporter, urea binding protein			1.1		-1.8
23630.peg.32	Uridylate kinase (EC 2.7.4.-)				0.9	
23630.peg.3053	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	1.0	1.0	0.7	1.1	0.6
23630.peg.214	UvrD/REP helicase family protein		0.4			
23630.peg.3527	von Willebrand factor, type A			-0.6	-1.1	
23630.peg.4838	XdhC protein (assists in molybdopterin insertion into xanthine dehydrogenase)		0.9			
23630.peg.1524	Zinc ABC transporter, inner membrane permease protein ZnuB	1.1	1.7	0.8	2.0	0.8
23630.peg.1521	Zinc ABC transporter, periplasmic-binding protein ZnuA			0.7		
23630.peg.741	Zinc finger, CDGSH-type			-0.8		
23630.peg.817	Zn-dependent hydrolases, including glyoxylases			-0.6		
23630.peg.3034	Zonular occludens toxin	-0.9		0.7		

^a Relative gene expression is presented as the mean ratio of the fluorescence intensity of K₂CrO₄-exposed cells to control cells. Each gene showed significant differential expression ($p < 0.05$).

^b Time in minutes at which cells were harvested for RNA isolation following addition of 1 mM K₂CrO₄ to the experimental culture.

^c Relative gene expression is presented as the mean ratio of the fluorescence intensity of 7-h developing biofilm to planktonic cells. Each gene showed significant differential expression ($p < 0.05$).