

Table S3. Gene Expression For Genes with Top 50% Expression Values during 3 Hours Post Starvation

Name	Number	log2 Fold Change	Standard Deviation	Standard Error	p-value	Category	Definition
PM0001	2	2.23	0.10	0.07	0.00	DNA replication, recombination, and repair	DNA polymerase III, beta chain
PM0008	2	2.39	0.48	0.34	0.01	Conserved hypothetical protein	conserved hypothetical protein
PM0013	2	0.16	0.31	0.22	1.00	Fatty acid, phospholipid and sterol metabolism	RNA-binding region RNP-1 (RNA recognition motif)
PM0015	2	-1.69	0.59	0.41	0.27	Conserved hypothetical protein	Domain of unknown function DUF25
PM0016	2	2.00	0.00	0.00	0.02	Chaperones	Heat shock protein GrpE
PM0017	2	0.57	0.10	0.07	0.85	Chaperones	DnaJ protein
PM0020	2	5.88	2.68	1.89	0.00	Conserved hypothetical protein	conserved hypothetical protein
PM0023	2	-0.73	1.62	1.15	1.00	CO2 fixation	Glyceraldehyde 3-phosphate dehydrogenase(NADP+)[phosphorylating]
PM0025	2	2.18	0.56	0.40	0.01	Protein modification and translation factors	Cyclophilin-type peptidyl-prolyl cis-trans isomerase
PM0026	2	0.09	0.27	0.19	1.00	Protein modification and translation factors	Elongation factor P (EF-P)
PM0027	2	2.07	0.61	0.43	0.02	Fatty acid, phospholipid and sterol metabolism	Biotin / Lipoyl attachment:Acetyl-CoA biotin carrier...
PM0030	2	0.36	0.04	0.03	0.90	Protein modification and translation factors	possible Transcription factor TFIIID (or TATA-b
PM0031	2	-0.81	1.12	0.79	1.00	DNA replication, recombination, and repair	HNH endonuclease:HNH nuclease
PM0032	2	-0.46	0.00	0.00	1.00	Protein and peptide secretion	possible Bacterial type II secretion system pr
PM0033	2	-1.70	0.77	0.55	0.25	Conserved hypothetical protein	conserved hypothetical protein
PM0034	2	2.41	0.04	0.03	0.01	Conserved hypothetical protein	conserved hypothetical protein
PM0035	2	0.87	0.60	0.43	1.00	Hydrogenase	soluble hydrogenase small subunit
PM0037	2	-2.08	0.64	0.45	0.01	Purine ribonucleotide biosynthesis	Glutamine amidotransferase class-i:GMP synthase
PM0043	2	0.25	0.71	0.51	1.00	Other	Flavoprotein
PM0046	2	1.69	0.41	0.29	0.08	Interconversions and salvage of nucleosides and nucle	Nucleoside diphosphate kinase
PM0048	2	0.40	0.21	0.15	1.00	Aminoacyl tRNA synthetases and tRNA modification	Glutamyl-tRNA (Gln) amidotransferase subunit B
PM0051	2	4.52	0.18	0.13	0.00	Conserved hypothetical protein	conserved hypothetical protein
PM0055	2	2.43	0.72	0.51	0.00	Conserved hypothetical protein	conserved hypothetical protein
PM0056	2	3.76	0.03	0.02	0.00	Conserved hypothetical protein	conserved hypothetical protein
PM0058	2	0.12	1.33	0.94	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0059	2	-1.66	0.48	0.34	0.29	Conserved hypothetical protein	conserved hypothetical protein
PM0060	2	0.06	0.68	0.48	1.00	Fatty acid, phospholipid and sterol metabolism	acetyl-CoA carboxylase, biotin carboxylase subunit
PM0061	2	0.70	0.84	0.59	0.65	Other	YGGT family, conserved hypothetical integral membrane protein
PM0062	2	3.87	1.92	1.36	0.00	Photosystem II	photosystem II PsbX protein
PM0063	2	-0.85	0.32	0.22	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0064	2	-1.05	0.38	0.27	0.71	Adaptations and atypical conditions	possible high light inducible protein
PM0068	2	0.83	0.70	0.49	0.71	Regulatory functions	putative formylmethionine deformylase
PM0073	2	0.54	1.12	0.79	1.00	Transport and binding proteins	ABC transporter, membrane component
PM0075	2	-1.42	2.31	1.63	0.00	Conserved hypothetical protein	conserved hypothetical protein
PM0078	2	-1.43	1.79	1.26	0.69	Other	possible 4'-phosphopantetheinyl transferase family protein
PM0079	2	-0.42	1.15	0.81	1.00	Transport and binding proteins	putative bacterioferritin comigratory (BCP) protein
PM0081	2	0.98	0.83	0.59	0.74	Serine family / Sulfur assimilation	Phosphoadenosine phosphosulfate reductase
PM0082	2	-1.91	0.22	0.16	0.08	Regulatory functions	putative NADH dehydrogenase, transport associated
PM0083	2	-0.39	0.37	0.26	1.00	Regulatory functions	putative sodium/sulfate transporter, DASS family
PM0085	2	1.10	0.49	0.35	0.61	Regulatory functions	putative potassium channel, VIC family
PM0086	2	1.46	1.73	1.22	0.39	Conserved hypothetical protein	Conserved hypothetical protein
PM0087	2	-1.03	1.08	0.77	0.48	Conserved hypothetical protein	conserved hypothetical protein
PM0088	2	-1.00	0.18	0.12	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0091	2	1.21	0.29	0.21	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0092	2	0.91	1.17	0.83	0.47	Conserved hypothetical protein	conserved hypothetical protein
PM0093	2	-1.87	0.41	0.29	1.00	Adaptations and atypical conditions	possible high light inducible protein
PM0095	2	-0.20	0.78	0.55	1.00	Other	similar to serum resistance locus BrkB
PM0099	2	-0.50	0.31	0.22	0.95	Conserved hypothetical protein	conserved hypothetical protein
PM0101	2	0.25	0.16	0.11	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0103	2	1.18	0.68	0.48	0.49	Conserved hypothetical protein	conserved hypothetical protein
PM0105	2	-3.02	1.74	1.23	0.03	Riboflavin	RibD/RibC C-terminal domain
PM0106	2	-2.05	0.35	0.25	0.57	Other	6-pyruvoyl tetrahydropterin synthase
PM0111	2	-2.27	0.03	0.02	0.01	Conserved hypothetical protein	conserved hypothetical protein
PM0114	2	-0.86	0.06	0.04	0.80	Conserved hypothetical protein	conserved hypothetical protein
PM0115	2	-0.72	0.27	0.19	1.00	Carotenoid	zeta-carotene desaturase
PM0116	2	-0.92	0.17	0.12	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0117	2	-1.82	1.76	1.25	0.61	Conserved hypothetical protein	conserved hypothetical protein
PM0120	2	-1.58	0.50	0.35	0.08	Cell division	putative cell division inhibitor
PM0121	2	-0.54	0.23	0.16	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0123	2	0.63	2.65	1.87	1.00	Serine family / Sulfur assimilation	O-acetylsulfate (thiol)-lyase A
PM0124	2	-1.88	1.47	1.04	0.10	Conserved hypothetical protein	conserved hypothetical protein in cyanobacteria
PM0125	2	-1.21	2.22	1.57	0.81	Transport and binding proteins	possible ABC transporter, ATP-binding component
PM0126	2	1.23	0.57	0.40	0.61	Other	possible Herpesvirus UL6 like
PM0128	2	2.03	0.02	0.01	0.05	Regulatory functions	two-component response regulator
PM0132	2	-0.47	0.59	0.42	1.00	Other	cyanobacterial conserved hypothetical
PM0133	2	-0.37	0.31	0.22	0.86	Radiation sensitivity	putative DNA repair protein Rada
PM0134	2	2.57	0.76	0.54	0.00	Regulatory functions	two-component response regulator
PM0136	2	-0.40	0.11	0.08	1.00	Fatty acid, phospholipid and sterol metabolism	3-oxoacyl-[acyl-carrier-protein] synthase III
PM0137	2	-0.81	1.58	1.11	1.00	Fatty acid, phospholipid and sterol metabolism	Malonyl coenzyme A-acyl carrier protein transacylase
PM0138	2	-0.27	0.65	0.46	0.89	Fatty acid, phospholipid and sterol metabolism	putative 1-acyl-sn-glycerol-3-phosphate acyltransferase
PM0139	2	-0.10	0.41	0.29	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0140	2	2.86	1.93	1.36	0.00	Regulatory functions	putative Ycf34
PM0142	2	2.14	0.31	0.22	0.00	Fatty acid, phospholipid and sterol metabolism	RNA-binding region RNP-1 (RNA recognition motif)
PM0143	2	0.18	0.12	0.09	1.00	Carotenoid	Squalene and phytoene synthases
PM0144	2	-1.60	1.09	0.77	0.46	Carotenoid	phytoene desaturase
PM0145	2	-0.85	0.47	0.33	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0146	2	-0.09	0.82	0.58	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0147	2	0.05	0.91	0.64	1.00	Regulatory functions	putative Rubisco transcriptional regulator
PM0149	2	-1.45	0.33	0.23	0.49	NADH dehydrogenase	putative NADH Dehydrogenase (complex I) subunit (chain 5)
PM0150	2	-1.59	0.30	0.22	0.45	NADH dehydrogenase	putative NADH dehydrogenase subunit (chain 4)
PM0153	2	-0.43	0.09	0.07	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0154	2	-0.19	0.02	0.01	1.00	Regulatory functions	Bacterial regulatory protein, LuxR family
PM0159	2	-1.62	0.23	0.16	0.65	NADH dehydrogenase	putative NADH Dehydrogenase subunit
PM0160	2	-1.25	0.22	0.16	0.47	NADH dehydrogenase	putative respiratory-chain NADH dehydrogenase subunit
PM0163	2	0.02	0.41	0.29	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM0164	2	-0.65	0.01	0.01	1.00	Aromatic amino acid family	Tryptophan synthase, beta chain:Pyridoxal-5'-phosphate-depend...
PM0166	2	#NAME?	NA	NA	0.01	Serine family / Sulfur assimilation	Adenylylsulfate kinase
PM0172	2	2.48	0.76	0.54	0.00	NADH dehydrogenase	putative NADH dehydrogenase subunit
PM0179	2	1.18	0.18	0.13	0.47	Other	Glutaredoxin
PM0180	2	1.70	0.67	0.48	0.09	Protein modification and translation factors	peptide chain release factor RF-2
PM0184	2	-1.82	0.14	0.10	0.29	Aromatic amino acid family	para-aminobenzoate synthase component II
PM0195	2	-0.50	0.20	0.14	1.00	Other	Phosphoglycerate kinase
PM0200	2	1.64	0.32	0.23	0.05	Degradation of RNA	possible ribonuclease HI
PM0201	2	1.25	0.05	0.04	1.00	Ribosomal proteins	S05 ribosomal protein L7/L12
PM0202	2	0.89	0.33	0.24	0.89	Ribosomal proteins	S05 ribosomal protein L10
PM0203	2	-1.30	0.18	0.12	1.00	Ribosomal proteins	S05 ribosomal protein L1
PM0204	2	-1.51	0.40	0.28	1.00	Ribosomal proteins	S05 ribosomal protein L11
PM0205	2	0.38	1.24	0.87	1.00	RNA synthesis, modification, and DNA transcription	transcription antitermination protein, NusG
PM0206	2	-0.24	0.45	0.32	1.00	Protein and peptide secretion	putative prepeptidyl transferase, SecE subunit
PM0208	2	0.60	0.13	0.09	1.00	Other	Enolase
PM0209	2	0.25	0.45	0.31	1.00	Other	possible kinase
PM0211	2	-1.78	0.82	0.58	0.23	Other	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
PM0212	2	-2.06	1.57	1.11	0.30	Conserved hypothetical protein	conserved hypothetical protein
PM0213	2	-1.30	3.11	2.20	0.85	Transport and binding proteins	putative sodium-dependent bicarbonate transporter
PM0214	2	-0.99	0.88	0.63	1.00	Regulatory functions	putative sulfate transporter
PM0216	2	1.05	1.52	1.08	0.67	Adaptations and atypical conditions	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
PM0218	2	-1.34	0.17	0.12	0.48	Other	GTP1/OBG family
PM0219	2	-2.30	1.80	1.27	0.01	Conserved hypothetical protein	conserved hypothetical
PM0220	2	-1.62	0.29	0.20	1.00	Other	No Cyanobase Name
PM0223	2	-1.77	0.01	0.00	1.00	Photosystem II	Photosystem II PsbA protein (D1)
PM0224	2	2.00	0.70	0.49	0.04	Aromatic amino acid family	Chorismate synthase
PM0226	2	0.95	0.62	0.44	1.00	Cell division	cell division protein FtsH2
PM0228	2	1.07	1.23	0.87	1.00	Photosystem II	Photosystem II manganese-stabilizing protein

PM00231	2	0.75	0.46	0.32	0.90 Conserved hypothetical protein	conserved hypothetical protein
PM00235	2	0.59	0.69	0.49	1.00 Aminoacyl tRNA synthetases and tRNA modification	Glutamyl-tRNA(Gln) amidotransferase subunit C
PM00237	2	-0.51	0.22	0.15	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00239	2	-0.60	0.49	0.35	0.83 Conserved hypothetical protein	conserved hypothetical protein
PM00242	2	-1.94	1.35	0.96	0.10 Thiamine	thioredoxin-like protein TxIA
PM00243	2	-1.24	0.01	0.01	0.50 Pyrimidine ribonucleotide biosynthesis	possible Thy1 protein homolog
PM00244	2	-1.11	0.25	0.18	1.00 Purine ribonucleotide biosynthesis	dCTP Deaminase
PM00245	2	1.28	0.25	0.28	0.39 Cobalamin, heme, phycobilin and porphyrin	colijilalamin adenosyltransferase
PM00246	2	0.57	0.11	0.08	1.00 Transport and binding proteins	Global nitrogen regulatory protein, CRP family of transcriptional regulators
PM00251	2	-0.83	0.59	0.42	1.00 Photosystem II	Photosystem II PsbH protein
PM00252	2	-1.67	0.38	0.27	0.90 Photosystem II	Photosystem II reaction centre N protein (psbN)
PM00253	2	-0.18	0.30	0.21	1.00 Photosystem II	photosystem II reaction center PsbI protein
PM00254	2	-0.65	1.23	0.87	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00258	2	2.05	0.97	0.69	0.03 Other	Serine hydroxymethyltransferase (SHMT)
PM00259	2	-1.60	0.25	0.17	0.13 Conserved hypothetical protein	conserved hypothetical protein
PM00260	2	#NAME? NA	NA	0.00	Conserved hypothetical protein	conserved hypothetical protein
PM00263	2	3.67	0.39	0.28	0.02 Transport and binding proteins	Ammonium transporter family
PM00264	2	-0.26	0.45	0.32	1.00 Murein sacculus and peptidoglycan	LytB protein homolog
PM00265	2	1.04	0.43	0.30	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00267	2	#NAME? NA	NA	0.60	Other	probable esterase
PM00268	2	-0.05	0.19	0.14	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00272	2	-0.80	0.55	0.39	1.00 Photosystem II	Photosystem II protein PskK
PM00273	2	-0.72	0.45	0.32	0.68 Other	probable oxidoreductase
PM00275	2	0.58	1.18	0.83	1.00 Pyrimidine ribonucleotide biosynthesis	Orotate phosphoribosyltransferase
PM00278	2	-1.13	0.70	0.50	0.63 Other	Phosphotransferase superclass
PM00279	2	-1.49	0.54	0.38	0.40 Conserved hypothetical protein	conserved hypothetical protein
PM00282	2	1.73	0.27	0.19	0.15 Fatty acid, phospholipid and sterol metabolism	enoyl-[acyl-carrier-protein] reductase
PM00284	2	-1.94	0.31	0.22	0.02 Regulatory functions	putative pleiotropic regulatory protein
PM00286	2	-1.32	1.49	1.06	0.47 Other	NUDIX hydrolase
PM00289	2	-0.56	0.20	0.14	1.00 Transport and binding proteins	possible ABC transporter
PM00290	2	-1.00	0.13	0.09	0.61 Transport and binding proteins	possible ABC transporter, ATP binding component
PM00293	2	0.51	0.47	0.33	1.00 NADH dehydrogenase	putative respiratory-chain NADH dehydrogenase subunit
PM00294	2	-0.84	0.02	0.01	1.00 NADH dehydrogenase	putative NADH Dehydrogenase (complex I) subunit (chain 3)
PM00295	2	-2.22	0.46	0.33	0.10 Other	probable rubredoxin
PM00296	2	-0.22	0.30	0.21	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00297	2	0.55	0.32	0.22	1.00 Photosystem II	Cytochrome b559 alpha-subunit
PM00298	2	0.42	0.23	0.16	1.00 Photosystem II	Cytochrome b559 beta-subunit
PM00299	2	0.79	0.06	0.04	1.00 Photosystem II	photosystem II PskI protein
PM00300	2	0.57	0.07	0.05	1.00 Photosystem II	photosystem II PskJ protein
PM00301	2	-0.91	0.24	0.17	1.00 Other	5'-methylthioadenosine phosphorylase
PM00305	2	-0.95	0.03	0.02	1.00 Phycobilisome	Phycobilisome protein
PM00306	2	-1.43	0.03	0.02	0.60 Phycobilisome	phycocerythrin linker protein CpeS homolog
PM00307	2	-1.41	0.45	0.32	1.00 Conserved hypothetical protein	hypothetical
PM00308	2	-0.52	0.74	0.52	0.92 Conserved hypothetical protein	conserved hypothetical protein
PM00309	2	-2.76	0.32	0.22	0.00 Other	possible Pollen allergen
PM00311	2	-2.01	0.81	0.57	0.36 Aspartate family	S-adenosylmethionine synthetase
PM00312	2	-0.02	0.15	0.11	1.00 Ribosomal proteins	30S ribosomal protein S1, homolog A
PM00313	2	3.35	0.49	0.35	0.00 Conserved hypothetical protein	conserved hypothetical protein
PM00314	2	-0.31	0.20	0.14	1.00 Photosystem II	Photosystem II PskT protein
PM00315	2	-0.64	0.54	0.38	1.00 Photosystem II	Photosystem II PskB protein (CP47)
PM00316	2	-0.61	0.46	0.33	1.00 Soluble electron carriers	possible ferredoxin
PM00317	2	-1.62	1.22	0.86	0.85 Photosystem II	possible Photosystem II reaction center M protein (PsbM)
PM00318	2	-1.26	1.16	0.82	1.00 Cobalamin, heme, phycobilin and porphyrin	putative protein methyltransferase
PM00321	2	2.31	1.56	1.10	0.00 Cell division	putative septum site-determining protein MinD
PM00324	2	-1.47	1.13	0.80	0.95 Detoxification	PDZ domain [also known as DHR or GLGF]:Tail specific protease...
PM00325	2	-0.74	0.65	0.46	1.00 Cytochrome b6/f complex	Cytochrome b6
PM00326	2	1.50	0.37	0.26	1.00 Cytochrome b6/f complex	PetD protein (subunit IV of the Cytochrome b6f complex)
PM00327	2	0.76	0.54	0.38	1.00 Other	putative neutral invertase-like protein
PM00328	2	0.75	1.02	0.72	1.00 DNA replication, recombination, and repair	Formamidopyrimidine-DNA glycolase (FAPY-DNA glycolase)
PM00329	2	0.92	0.24	0.17	1.00 Photosystem I	Photosystem I PsaE protein (subunit IV)
PM00333	2	-0.56	0.60	0.43	0.95 Other	GCNS-related N-acetyltransferase
PM00334	2	-0.06	0.08	0.06	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00336	2	3.71	0.71	0.50	0.00 Conserved hypothetical protein	conserved hypothetical
PM00337	2	-2.39	0.16	0.11	0.00 Conserved hypothetical protein	conserved hypothetical protein
PM00338	2	3.26	0.82	0.58	0.00 Conserved hypothetical protein	conserved hypothetical
PM00339	2	-0.21	0.25	0.18	1.00 Carotenoid	Bacterial-type phytoene dehydrogenase
PM00341	2	-1.91	1.84	1.30	0.00 Conserved hypothetical protein	conserved hypothetical
PM00342	2	-1.87	0.60	0.43	0.02 Other	possible Helixer component proteinase
PM00343	2	2.52	0.00	0.00	0.00 Other	mttA/Hcf106 family
PM00345	2	-2.67	0.35	0.25	0.00 Transport and binding proteins	putative bacterioferritin comigratory protein
PM00346	2	-0.80	1.17	0.83	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00347	2	-0.74	0.17	0.12	1.00 Conserved hypothetical protein	conserved hypothetical
PM00348	2	-0.95	0.29	0.20	1.00 Other	possible Spectrin repeat
PM00350	2	-2.12	0.86	0.61	0.14 Regulatory functions	possible TIR domain
PM00351	2	#NAME? NA	NA	0.00	Cobalamin, heme, phycobilin and porphyrin	possible Small, acid-soluble spore proteins, a
PM00356	2	-1.01	0.58	0.41	0.57 Fatty acid, phospholipid and sterol metabolism	Alpha/beta hydrolase fold:Esterase/lipase/thioesterase family...
PM00363	2	#NAME? NA	NA	0.38	Regulatory functions	possible MarR family
PM00364	2	-1.04	0.05	0.03	1.00 Other	possible Malic enzyme
PM00365	2	-1.07	0.73	0.52	0.56 Other	possible DsrE-like protein
PM00366	2	0.03	0.87	0.61	1.00 Transport and binding proteins	Type-1 copper (blue) domain
PM00367	2	-2.39	1.72	1.22	0.07 Conserved hypothetical protein	conserved hypothetical protein
PM00368	2	-0.19	0.27	0.19	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00370	2	-1.98	0.91	0.65	0.09 Transport and binding proteins	putative cyanate ABC transporter, substrate binding protein
PM00371	2	0.08	1.47	1.04	1.00 Transport and binding proteins	putative cyanate ABC transporter
PM00373	2	3.49	2.50	1.77	0.00 Other	Cyanate lyase
PM00374	2	-0.04	0.34	0.24	1.00 Other	mttA/Hcf106 family
PM00377	2	1.11	0.18	0.13	0.52 Conserved hypothetical protein	hypothetical
PM00378	2	-1.14	0.80	0.56	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00379	2	3.57	2.46	1.74	0.00 Conserved hypothetical protein	hypothetical
PM00383	2	-1.74	0.44	0.31	0.18 Transport and binding proteins	probable periplasmic protein
PM00388	2	-0.87	2.00	1.41	1.00 Chemotaxis	putative similar to tRNA-[MS2]O[6A]-hydroxylase
PM00395	2	0.83	0.60	0.43	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00400	2	-1.26	1.93	1.36	0.23 Adaptations and atypical conditions	light repressed protein A homolog
PM00403	2	-0.53	0.58	0.41	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00405	2	1.84	1.00	0.71	0.38 Transport and binding proteins	Dihydroalloamide acetyltransferase component (E2) of pyruvate de
PM00407	2	0.23	0.40	0.28	1.00 Serine family / Sulfur assimilation	O-acetylserine (thiol)-lyase A
PM00410	2	-0.72	0.82	0.58	1.00 Ribosomal proteins	30S ribosomal protein S4
PM00411	2	-2.21	0.98	0.70	0.06 Conserved hypothetical protein	conserved hypothetical protein
PM00412	2	-0.32	1.64	1.16	0.78 Conserved hypothetical protein	conserved hypothetical protein
PM00416	2	0.52	0.97	0.69	1.00 RNA synthesis, modification, and DNA transcription	SAM (and some other nucleotide) binding motif:Generic methyl-...
PM00417	2	-1.01	1.24	0.88	0.84 Conserved hypothetical protein	hypothetical
PM00418	2	3.01	1.65	1.17	0.00 Other	NifU-like protein
PM00428	2	-0.49	0.96	0.68	1.00 Cobalamin, heme, phycobilin and porphyrin	chlorophyll synthase 33 kD subunit
PM00429	2	-0.87	0.02	0.01	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00435	2	-0.59	0.46	0.32	1.00 NADH dehydrogenase	putative NADH dehydrogenase (complex I) subunit (chain 2)
PM00436	2	-1.33	0.86	0.61	0.68 DNA replication, recombination, and repair	Prokaryotic DNA topoisomerase
PM00441	2	-0.62	0.52	0.37	1.00 Other	Aldo/keto reductase family
PM00443	2	1.64	0.55	0.39	0.14 Conserved hypothetical protein	conserved hypothetical protein
PM00445	2	0.54	1.75	1.24	1.00 Respiratory terminal oxidases	Cytochrome c oxidase, subunit I
PM00446	2	-0.08	0.20	0.14	1.00 Respiratory terminal oxidases	putative cytochrome c oxidase, subunit 2
PM00447	2	0.23	0.54	0.38	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00448	2	0.64	2.41	1.70	0.58 Cobalamin, heme, phycobilin and porphyrin	putative protoheme IX farnesyltransferase
PM00451	2	-0.70	0.61	0.43	0.79 Other	possible Arenavirus glycoprotein
PM00452	2	-0.74	0.33	0.23	1.00 Chaperones	GroEL2 protein (Chaperonin cpn60 2)
PM00453	2	-1.84	1.33	0.94	0.14 Fatty acid, phospholipid and sterol metabolism	3-oxoacyl-[acyl-carrier-protein] reductase

PM00461	2	2.90	0.62	0.44	0.00 Cytochrome b6/f complex	Cytochrome f
PM00462	2	1.91	0.27	0.19	0.56 Cytochrome b6/f complex	Rieske iron-sulfur protein
PM00465	2	3.42	0.45	0.32	0.00 Conserved hypothetical protein	hypothetical
PM00468	2	0.95	0.52	0.37	1.00 Photosystem I	Photosystem I Psaj protein (subunit IX)
PM00469	2	-0.05	0.66	0.47	1.00 Photosystem I	Photosystem I Psaf protein (subunit III)
PM00470	2	-1.11	0.81	0.57	0.68 Other	probable o-sialoglycoprotein endopeptidase
PM00471	2	-2.38	0.68	0.48	0.00 Adaptations and atypical conditions	possible high light inducible protein
PM00472	2	-0.93	0.15	0.11	0.64 Transport and binding proteins	putative Na ⁺ /H ⁺ antiporter, CPA1 family
PM00473	2	-0.30	0.90	0.64	1.00 Aminoacyl tRNA synthetases and tRNA modification	Glutamyl-tRNA synthetase
PM00474	2	-0.93	0.42	0.30	1.00 Conserved hypothetical protein	Conserved hypothetical protein
PM00475	2	-1.23	0.37	0.26	1.00 Ribosomal proteins	Ribosomal protein L19
PM00476	2	-0.48	0.57	0.40	0.88 Conserved hypothetical protein	conserved hypothetical protein
PM00477	2	-0.23	0.23	0.16	1.00 Protein modification and translation factors	putative methionine aminopeptidase
PM00478	2	-1.44	0.43	0.31	0.35 Conserved hypothetical protein	conserved hypothetical protein
PM00479	2	-1.66	0.87	0.62	0.25 Conserved hypothetical protein	conserved hypothetical protein
PM00480	2	2.26	0.57	0.40	0.01 Conserved hypothetical protein	conserved hypothetical protein
PM00481	2	-1.34	1.62	1.15	0.29 Conserved hypothetical protein	conserved hypothetical protein
PM00482	2	1.25	0.87	0.62	1.00 Other	Band 7 protein
PM00483	2	-0.30	0.24	0.17	1.00 Cobalamin, heme, phycobilin and porphyrin	glutamate-1-semialdehyde 2,1-aminomutase
PM00485	2	3.03	0.54	0.38	0.00 Conserved hypothetical protein	conserved hypothetical protein
PM00491	2	-0.27	1.79	1.27	0.96 Other	4a-hydroxytetrahydrobiopterin dehydratase (PCD)
PM00492	2	-0.85	1.18	0.84	0.87 Conserved hypothetical protein	conserved hypothetical protein
PM00493	2	-0.45	0.94	0.67	1.00 Other	Carboxypeptidase Tag (M32) metallopeptidase
PM00494	2	0.99	0.37	0.26	0.81 Phosphorus compounds	putative inorganic pyrophosphatase
PM00495	2	1.31	0.14	0.10	0.38 Cobalamin, heme, phycobilin and porphyrin	Porphobilinogen deaminase
PM00496	2	-0.46	0.03	0.02	1.00 RNA synthesis, modification, and DNA transcription	Putative principal RNA polymerase sigma factor
PM00500	2	-0.98	0.72	0.51	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00501	2	#NAME? NA	NA		0.57 Conserved hypothetical protein	conserved hypothetical protein
PM00502	2	0.06	0.10	0.07	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00503	2	-0.81	0.69	0.49	0.72 Cobalamin, heme, phycobilin and porphyrin	possible precorrin-6X reductase
PM00506	2	-1.08	1.09	0.77	0.61 Purine ribonucleotide biosynthesis	Adenylosuccinate synthetase
PM00507	2	-1.62	0.79	0.56	0.38 Photosystem II	possible Photosystem II reaction center Psb27 protein
PM00508	2	0.85	0.91	0.64	1.00 Aminoacyl tRNA synthetases and tRNA modification	Prolyl-tRNA synthetase
PM00510	2	-1.33	0.14	0.10	1.00 Transposon-related functions	possible Reverse transcriptase (RNA-dependent
PM00511	2	-1.40	0.70	0.50	1.00 Other	Inorganic pyrophosphatase
PM00515	2	-1.31	0.14	0.10	0.36 Cobalamin, heme, phycobilin and porphyrin	possible alpha-ribazole-5'-P phosphatase
PM00519	2	-0.24	0.97	0.69	1.00 Other	Transaldolase
PM00520	2	-1.48	0.58	0.41	0.44 Other	NAD binding site
PM00522	2	-0.30	1.54	1.09	1.00 Pyrimidine ribonucleotide biosynthesis	uridylyate kinase
PM00525	2	-1.18	0.32	0.23	0.45 Other	Ferrocyclase
PM00526	2	1.97	0.20	0.14	0.16 Branched chain family	Acetolactate synthase large subunit
PM00530	2	-1.68	0.83	0.59	0.41 Ribosomal proteins	30S ribosomal protein S1 homolog B, putative Nbp1
PM00532	2	1.07	0.83	0.59	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00533	2	-1.32	0.14	0.10	0.48 Conserved hypothetical protein	conserved hypothetical protein
PM00534	2	-0.72	0.77	0.55	0.81 Fatty acid, phospholipid and sterol metabolism	acetyl-CoA carboxylase, alpha subunit
PM00536	2	0.20	0.33	0.23	1.00 Folic acid	putative GTP cyclohydrolase I
PM00537	2	-2.19	0.43	0.30	0.01 Aromatic amino acid family	phosphoribosylanthranilate isomerase
PM00540	2	3.64	0.82	0.58	0.00 Photosystem I	possible photosystem I reaction center subunit XII (PsaM)
PM00541	2	2.72	0.46	0.33	0.00 Conserved hypothetical protein	conserved hypothetical protein
PM00543	2	-1.63	0.95	0.67	1.00 Cobalamin, heme, phycobilin and porphyrin	Protochlorophyllide reductase iron-sulfur ATP-binding protein
PM00544	2	0.88	0.41	0.29	1.00 Cobalamin, heme, phycobilin and porphyrin	Light-independent protochlorophyllide reductase subunit B
PM00545	2	1.79	0.06	0.04	1.00 Cobalamin, heme, phycobilin and porphyrin	Light-independent protochlorophyllide reductase subunit N
PM00546	2	3.19	0.60	0.43	0.00 Conserved hypothetical protein	conserved hypothetical
PM00548	2	0.06	1.55	1.10	1.00 Other	HAM1 family protein
PM00549	2	4.96	0.45	0.32	0.00 CO2 fixation	carboxysome shell protein CsoS1
PM00550	2	2.93	0.71	0.50	0.00 CO2 fixation	Ribulose biphosphate carboxylase, large chain
PM00551	2	1.86	1.72	1.22	0.00 CO2 fixation	Ribulose biphosphate carboxylase, small chain
PM00552	2	-1.05	2.29	1.62	1.00 CO2 fixation	carboxysome shell protein CsoS2
PM00554	2	-0.64	0.36	0.26	1.00 CO2 fixation	putative carboxysome peptide A
PM00555	2	-0.32	0.20	0.14	1.00 CO2 fixation	putative carboxysome peptide B
PM00556	2	-1.59	1.24	0.88	0.48 Conserved hypothetical protein	conserved hypothetical protein
PM00557	2	0.88	0.05	0.04	1.00 Conserved hypothetical protein	conserved hypothetical
PM00558	2	-0.80	0.80	0.57	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00560	2	-1.12	0.36	0.26	1.00 Other	possible ATP phosphoribosyltransferase
PM00561	2	-0.21	1.15	0.81	1.00 Transport and binding proteins	putative multidrug efflux ABC transporter
PM00564	2	-1.09	0.33	0.24	0.58 Conserved hypothetical protein	conserved hypothetical protein
PM00565	2	0.16	0.32	0.23	1.00 DNA replication, recombination, and repair	chromosomal replication initiator protein DnaA
PM00570	2	-1.18	0.46	0.32	0.50 NADH dehydrogenase	NADH dehydrogenase subunit NdhI (ndhI)
PM00571	2	#NAME? NA	NA		1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00573	2	2.99	0.41	0.29	0.00 Conserved hypothetical protein	conserved hypothetical protein
PM00574	2	#NAME? NA	NA		0.29 Conserved hypothetical protein	conserved hypothetical protein
PM00577	2	-1.40	0.87	0.61	1.00 RNA synthesis, modification, and DNA transcription	Putative type II alternative sigma factor, sigma70 family
PM00579	2	-1.89	0.88	0.62	0.12 Conserved hypothetical protein	conserved hypothetical protein
PM00580	2	-0.33	0.11	0.08	1.00 Degradation of proteins, peptides, and glycopeptides	ATP-dependent Clp protease, Hsp 100, ATP-binding subunit ClpB
PM00581	2	-0.43	0.95	0.67	1.00 Soluble electron carriers	plastocyanin
PM00583	2	-1.02	1.16	0.82	1.00 Cobalamin, heme, phycobilin and porphyrin	Uroporphyrinogen decarboxylase (URO-D)
PM00586	2	-0.20	0.13	0.09	1.00 Conserved hypothetical protein	conserved hypothetical
PM00593	2	-1.49	0.36	0.26	1.00 Other	Peptidase family M3
PM00594	2	-1.20	0.37	0.26	0.57 NADH dehydrogenase	putative NADH Dehydrogenase (complex I) subunit (chain 4)
PM00595	2	-0.06	0.60	0.42	1.00 Aspartate family	Homoserine kinase:GHMP kinases putative ATP-binding domain
PM00599	2	-1.12	1.39	0.98	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00601	2	-0.09	0.45	0.29	1.00 Transport and binding proteins	ABC transporter, substrate binding protein, possibly Mn
PM00603	2	-1.31	0.65	0.46	0.37 Transport and binding proteins	ABC transporter component, possibly Mn transport
PM00605	2	-0.24	0.47	0.33	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00609	2	-0.43	0.29	0.21	1.00 Polysaccharides and glycoproteins	Putative ADPglucose-glucosyltransferase (GlgA)
PM00613	2	-0.38	0.07	0.05	1.00 Aromatic amino acid family	EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
PM00614	2	1.24	1.07	0.76	0.48 Conserved hypothetical protein	conserved hypothetical protein
PM00615	2	-0.46	0.25	0.18	1.00 Other	Possible nitrilase
PM00618	2	-0.15	1.43	1.01	1.00 Carotenoid	polyprenyl synthetase; solanesyl diphosphate synthase (sds)
PM00619	2	0.75	0.01	0.01	1.00 Pyruvate and acetyl-CoA metabolism	acetyl-coenzyme A synthetase
PM00622	2	0.05	0.29	0.21	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00626	2	-0.75	0.59	0.42	0.81 Conserved hypothetical protein	hypothetical
PM00627	2	-1.44	0.28	0.20	1.00 Photosystem II	light-harvesting complex protein
PM00628	2	-1.07	1.77	1.25	0.52 Transport and binding proteins	possible sodium:solute symporter, ESS family
PM00629	2	-0.74	0.14	0.10	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00633	2	-0.88	0.40	0.28	1.00 Carotenoid	putativeycopene epsilon cyclase
PM00637	2	1.08	0.57	0.40	0.64 Regulatory functions	Ferric uptake regulator family
PM00638	2	0.40	0.14	0.10	0.90 Conserved hypothetical protein	conserved hypothetical protein
PM00641	2	-1.81	0.05	0.04	0.36 Conserved hypothetical protein	conserved hypothetical protein
PM00642	2	3.31	0.02	0.01	0.00 Serine family / Sulfur assimilation	putative O-Acetyl homoserine sulfhydrylase
PM00647	2	-0.64	0.86	0.61	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00649	2	1.82	0.82	0.58	0.10 Other	Pentapeptide repeats
PM00651	2	-1.09	1.17	0.82	0.51 Regulatory functions	possible VHS domain
PM00652	2	-1.08	0.03	0.02	0.57 RNA synthesis, modification, and DNA transcription	possible 5'-3' exonuclease, C-terminal SAM fol
PM00658	2	-0.70	0.46	0.33	0.84 Aminoacyl tRNA synthetases and tRNA modification	putative pseudouridylyate synthase specific to ribosomal small subunit
PM00659	2	-0.45	0.25	0.18	1.00 DNA replication, recombination, and repair	NAD-dependent DNA ligase N-terminus
PM00660	2	2.39	0.22	0.15	0.00 Degradation of RNA	possible RNA recognition motif. (a.k.a. RRM, R
PM00661	2	0.72	0.26	0.18	1.00 Purine ribonucleotide biosynthesis	ribonucleotide reductase (Class II)
PM00664	2	-0.84	1.52	1.08	1.00 Conserved hypothetical protein	conserved hypothetical protein
PM00665	2	-1.87	0.53	0.38	0.08 Other	Hsp33 protein
PM00667	2	-2.07	1.49	1.06	0.00 Conserved hypothetical protein	conserved hypothetical protein
PM00674	2	-1.06	1.17	0.83	1.00 Aspartate family	Aminotransferases class I
PM00681	2	-1.28	1.88	1.33	0.11 Conserved hypothetical protein	conserved hypothetical protein
PM00683	2	-1.47	0.85	0.60	0.17 Purine ribonucleotide biosynthesis	phosphoribosylaminoimidazole carboxylase
PM00684	2	-1.08	0.29	0.20	1.00 Regulatory functions	possible Zinc finger, C2H2 type

PM00685	2	-0.90	0.32	0.22	1.00	Conserved hypothetical protein	hypothetical protein
PM00687	2	-2.33	0.94	0.66	0.00	Conserved hypothetical protein	conserved hypothetical
PM00688	2	0.97	1.18	0.83	1.00	Protein modification and translation factors	possible Elongation factor Tu domain 2
PM00689	2	-1.52	0.92	0.65	0.52	Adaptations and atypical conditions	possible high light inducible protein
PM00690	2	-0.89	0.16	0.11	1.00	Adaptations and atypical conditions	possible high light inducible protein
PM00691	2	0.68	0.96	0.68	0.79	Conserved hypothetical protein	conserved hypothetical protein
PM00692	2	0.70	0.32	0.23	0.70	Regulatory functions	possible BDT domain
PM00693	2	-1.44	1.61	1.14	0.50	Other	possible Hepatitis C virus envelope glycoprotein
PM00697	2	1.36	0.11	0.08	0.43	DNA replication, recombination, and repair	possible D12 class N6 adenine-specific DNA met
PM00698	2	-1.21	1.52	1.07	0.27	Chaperones	possible DnaJ central domain (4 repeats)
PM00699	2	-1.51	1.63	1.15	0.76	Conserved hypothetical protein	conserved hypothetical
PM00700	2	#NAME? NA	NA		1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00703	2	-0.56	0.52	0.37	0.88	Conserved hypothetical protein	conserved hypothetical protein
PM00704	2	-1.42	0.46	0.32	0.26	Regulatory functions	putative potassium channel, VIC family
PM00705	2	-2.06	0.68	0.48	0.01	Regulatory functions	two-component response regulator, phosphate
PM00707	2	-0.48	0.10	0.07	0.94	Other	possible Lipoprotein
PM00708	2	-0.37	0.03	0.02	1.00	Regulatory functions	putative secreted protein
PM00709	2	-0.96	0.41	0.29	1.00	Membranes, lipoproteins and porins	possible porin
PM00710	2	-1.32	0.11	0.08	1.00	Transport and binding proteins	ABC transporter, substrate binding protein, phosphate
PM00714	2	0.35	1.34	0.95	0.97	Regulatory functions	Bacterial regulatory proteins, ArsR family
PM00717	2	-1.66	0.04	0.03	0.19	Conserved hypothetical protein	conserved hypothetical protein
PM00719	2	#NAME? NA	NA		1.00	Conserved hypothetical protein	hypothetical
PM00722	2	4.32	2.69	1.90	0.00	Conserved hypothetical protein	hypothetical
PM00725	2	0.47	0.40	0.28	1.00	Transport and binding proteins	putative phosphate ABC transporter, ATP binding subunit
PM00726	2	2.81	0.94	0.67	0.00	Conserved hypothetical protein	hypothetical
PM00732	2	-0.99	1.75	1.24	0.34	Other	possible Major surface glycoprotein
PM00736	2	0.51	1.20	0.85	0.99	Other	possible Alpha-2-macroglobulin family N-termin
PM00739	2	-2.15	0.56	0.40	0.00	Conserved hypothetical protein	conserved hypothetical protein
PM00740	2	-1.80	0.21	0.15	0.23	Cytochrome b6/f complex	Cytochrome b6-f complex subunit VIII
PM00741	2	-0.99	0.66	0.47	0.72	Conserved hypothetical protein	conserved hypothetical protein
PM00742	2	0.85	1.12	0.79	1.00	Degradation of proteins, peptides, and glycopeptides	Cip protease subunit
PM00743	2	0.40	0.20	0.14	1.00	Cell division	FtsH ATP-dependent protease homolog
PM00744	2	-0.87	0.76	0.53	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00747	2	-0.93	1.32	0.93	0.44	Cobalamin, heme, phycobilin and porphyrin	ferredoxin-dependent biliverdin reductase
PM00751	2	-1.17	0.04	0.03	0.61	Conserved hypothetical protein	conserved hypothetical protein
PM00753	2	1.85	0.76	0.54	1.00	Ribosomal proteins	30S ribosomal protein S2
PM00754	2	0.70	1.58	1.11	1.00	Protein modification and translation factors	putative Elongation factor Ts
PM00758	2	1.80	1.11	0.79	0.32	Serine family / Sulfur assimilation	Ferredoxin-sulfite reductase
PM00760	2	1.81	0.38	0.27	0.24	Cobalamin, heme, phycobilin and porphyrin	Aromatic-ring hydroxylase (flavoprotein monooxygenase)
PM00762	2	-1.43	1.01	0.71	0.44	Aromatic amino acid family	tyrosine binding protein
PM00766	2	-0.55	1.21	0.86	1.00	Other	Ribulose-phosphate 3-epimerase
PM00767	2	-0.11	0.71	0.50	1.00	Surface polysaccharides, lipopolysaccharides and anti	Fructose-1,6-bisphosphatase/sedoheptulose-1,7-bis phosphatase
PM00769	2	-0.65	0.27	0.19	1.00	Other	ADP-glucose pyrophosphorylase
PM00770	2	-0.84	0.54	0.38	0.61	Pentose phosphate pathway	6-phosphogluconate dehydrogenase
PM00772	2	-2.57	1.67	1.18	0.27	Conserved hypothetical protein	conserved hypothetical protein
PM00774	2	-0.81	0.17	0.12	1.00	Branched chain family	Dihydroxy-acid dehydratase
PM00775	2	2.18	1.15	0.82	0.01	Conserved hypothetical protein	conserved hypothetical
PM00777	2	-0.38	0.11	0.08	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00779	2	4.48	0.76	0.54	0.00	Conserved hypothetical protein	conserved hypothetical protein
PM00781	2	1.48	1.14	0.81	1.00	Fatty acid, phospholipid and sterol metabolism	Fructose-bisphosphate/sedoheptulose-1,7-bisphosph ate aldolase
PM00784	2	1.28	0.83	0.58	0.50	Fatty acid, phospholipid and sterol metabolism	acetyl-CoA carboxylase, beta subunit
PM00785	2	0.36	1.07	0.76	1.00	CO2 fixation	phosphoribulokinase
PM00790	2	0.28	0.19	0.13	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00794	2	-0.66	0.49	0.35	0.78	Conserved hypothetical protein	conserved hypothetical protein
PM00797	2	-2.00	1.07	0.76	0.19	Nucleoproteins	possible mRNA binding protein
PM00799	2	-0.15	0.25	0.17	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00800	2	-0.81	0.55	0.39	0.76	Conserved hypothetical protein	conserved hypothetical protein
PM00801	2	-1.32	0.67	0.47	0.48	Conserved hypothetical protein	conserved hypothetical protein
PM00802	2	-1.54	0.60	0.42	0.16	DNA replication, recombination, and repair	putative endonuclease
PM00804	2	-1.16	0.79	0.56	1.00	Other	ferritin
PM00806	2	-0.53	0.27	0.19	0.90	Regulatory functions	Bacterial regulatory proteins, Crp family
PM00810	2	0.40	0.93	0.66	1.00	Conserved hypothetical protein	hypothetical
PM00812	2	#NAME? NA	NA		1.00	Conserved hypothetical protein	hypothetical
PM00814	2	-1.29	0.10	0.07	0.49	Other	possible Cytochrome oxidase c subunit Vlb
PM00815	2	-1.14	0.95	0.67	0.17	Adaptations and atypical conditions	possible high light inducible protein
PM00816	2	-0.16	0.29	0.20	1.00	Adaptations and atypical conditions	possible high light inducible protein
PM00817	2	-0.02	0.04	0.03	0.75	Adaptations and atypical conditions	possible high light inducible protein
PM00818	2	-0.96	0.22	0.16	0.51	Adaptations and atypical conditions	possible high light inducible protein
PM00819	2	0.45	0.69	0.49	1.00	Conserved hypothetical protein	hypothetical
PM00820	2	-0.46	0.81	0.57	0.93	Aromatic amino acid family	possible EPSP synthase (3-phosphoshikimate 1-c
PM00821	2	-0.97	0.52	0.37	0.67	Conserved hypothetical protein	conserved hypothetical protein
PM00824	2	0.49	0.23	0.16	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00828	2	-1.48	1.04	0.73	0.17	Other	S4 domain
PM00829	2	-0.94	1.64	1.16	1.00	Other	Triosephosphate isomerase
PM00835	2	-0.15	1.30	0.92	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00844	2	0.83	0.03	0.02	1.00	Adaptations and atypical conditions	phytochrome-regulated gene
PM00845	2	-0.04	0.21	0.15	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00846	2	-0.61	0.39	0.28	0.84	Other	possible Uncharacterized secreted proteins, Ya
PM00847	2	-0.02	0.11	0.08	1.00	Drug and analog sensitivity	putative acetazolamide conferring resistance protein Zam
PM00851	2	-0.48	1.08	0.76	1.00	Other	Putative CbbY homolog
PM00852	2	-2.78	1.24	0.88	0.01	Conserved hypothetical protein	conserved hypothetical protein
PM00853	2	-2.38	0.79	0.56	0.13	Ribosomal proteins	50S ribosomal protein L32
PM00856	2	-1.93	0.74	0.52	1.00	Detoxification	thioredoxin peroxidase
PM00857	2	-1.58	0.99	0.70	0.48	Other	possible Influenza RNA-dependent RNA polymeras
PM00858	2	-1.20	1.13	0.80	0.44	Conserved hypothetical protein	hypothetical
PM00861	2	-1.70	0.53	0.38	1.00	Transport and binding proteins	possible Virion host shutoff protein
PM00863	2	-1.68	1.79	1.27	0.10	Cobalamin, heme, phycobilin and porphyrin	putative cobinamide kinase
PM00864	2	-0.94	0.56	0.39	1.00	Other	possible Fusion glycoprotein F0.
PM00867	2	-1.25	0.23	0.16	0.47	Aminoacyl tRNA synthetases and tRNA modification	Methionyl-tRNA synthetase
PM00869	2	-1.63	0.92	0.65	0.33	Ribosomal proteins	30S Ribosomal protein S18
PM00870	2	-1.44	0.87	0.61	1.00	Ribosomal proteins	50S Ribosomal protein L33
PM00872	2	-1.69	0.23	0.17	1.00	Other	possible Carboxylesterase
PM00876	2	0.00	0.48	0.34	1.00	Conserved hypothetical protein	conserved hypothetical
PM00878	2	-0.02	1.05	0.74	1.00	Branched-chain family	putative Branched-chain amino acid aminotransferase
PM00881	2	-0.54	0.85	0.60	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00883	2	-2.42	0.58	0.41	0.18	Conserved hypothetical protein	conserved hypothetical protein
PM00889	2	-1.60	1.27	0.90	0.56	Riboflavin	possible GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase
PM00894	2	-0.34	0.56	0.40	1.00	Protein modification and translation factors	Cyclophilin-type peptidyl-prolyl cis-trans isomerase
PM00895	2	0.52	1.38	0.98	0.89	Conserved hypothetical protein	conserved hypothetical protein
PM00896	2	-0.59	0.34	0.24	0.85	Chaperones	DnaJ2 protein
PM00897	2	-0.04	0.08	0.06	1.00	Chaperones	Molecular chaperone DnaK, heat shock protein hsp70
PM00898	2	-1.32	0.45	0.32	0.29	Soluble electron carriers	ferredoxin, petF-like protein
PM00899	2	0.42	0.79	0.56	1.00	Regulatory functions	Possible myo-inositol-1(or 4)-monophosphatase
PM00901	2	-1.45	0.51	0.36	1.00	Chaperones	heat shock protein Htpg
PM00902	2	0.09	0.02	0.01	1.00	Ribosomal proteins	50S ribosomal protein L28
PM00906	2	2.51	0.96	0.68	0.10	Photosystem I	Photosystem I PsaK protein (subunit X)
PM00907	2	0.74	0.35	0.25	1.00	Sugars	1-deoxy-D-xylulose 5-phosphate synthase
PM00910	2	1.33	0.27	0.19	0.31	Conserved hypothetical protein	conserved hypothetical membrane protein
PM00912	2	-1.41	0.60	0.43	0.48	Other	Pyruvate kinase
PM00913	2	-1.46	0.22	0.16	0.27	Transport and binding proteins	possible ABC transporter
PM00919	2	-0.31	0.54	0.38	1.00	Branched chain family	serine-pyruvate/alanine:glyoxylate aminotransferase
PM00920	2	1.50	0.39	0.28	1.00	Glutamate family / Nitrogen assimilation	Glutamine synthetase, glutamate- α -ammonia ligase
PM00922	2	-1.96	1.86	1.31	0.01	Conserved hypothetical protein	conserved hypothetical protein
PM00923	2	-0.66	0.31	0.22	1.00	Conserved hypothetical protein	conserved hypothetical protein
PM00926	2	0.01	0.12	0.09	1.00	Photosystem II	possible Photosystem II reaction center Psb28 protein

PMM0930	2	0.01	0.82	0.58	1.00	Other	Pyruvate dehydrogenase E1 beta subunit
PMM0934	2	-0.53	0.48	0.34	0.90	Conserved hypothetical protein	conserved hypothetical protein
PMM0936	2	-0.20	0.55	0.39	1.00	DNA replication, recombination, and repair	putative SOS mutagenesis protein UmuD
PMM0941	2	1.43	0.99	0.70	1.00	Other	possible cAMP phosphodiesterases class-II
PMM0942	2	1.31	0.56	0.40	1.00	DNA replication, recombination, and repair	putative Holliday junction DNA helicase RuvA
PMM0943	2	0.68	0.34	0.24	1.00	Ribosomal proteins	30S Ribosomal protein S15
PMM0946	2	0.33	0.91	0.64	1.00	Aminoacyl tRNA synthetases and tRNA modification	Glutamyl-tRNA(Gln) amidotransferase A subunit
PMM0947	2	-3.26	2.74	1.94	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0949	2	-0.80	1.19	0.84	0.63	Conserved hypothetical protein	conserved hypothetical protein
PMM0950	2	-1.92	1.29	0.91	0.02	Other	No Cyanobase Name
PMM0953	2	2.16	0.81	0.57	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0954	2	-0.14	0.12	0.09	1.00	Transport and binding proteins	ABC transporter, multidrug efflux family
PMM0955	2	-1.66	0.64	0.45	0.19	Protein modification and translation factors	Peptide methionine sulfoxide reductase
PMM0957	2	-1.72	1.71	1.21	0.21	Regulatory functions	possible GRAM domain
PMM0958	2	-0.39	0.37	0.26	1.00	Conserved hypothetical protein	conserved hypothetical
PMM0963	2	-0.08	0.18	0.13	1.00	Nitrogen metabolism	Urease alpha subunit
PMM0964	2	-1.82	0.09	0.06	0.10	Nitrogen metabolism	Urease beta subunit
PMM0965	2	-1.57	1.25	0.89	0.14	Nitrogen metabolism	Urease gamma subunit
PMM0966	2	-1.96	0.95	0.68	0.14	Nitrogen metabolism	urease accessory protein UreD
PMM0969	2	-1.85	1.01	0.72	0.10	Nitrogen metabolism	urease accessory protein UreG
PMM0970	2	0.22	0.01	0.00	1.00	Transport and binding proteins	putative urea ABC transporter, substrate binding protein
PMM0971	2	-0.57	0.72	0.51	1.00	Transport and binding proteins	Putative urea ABC transporter
PMM0974	2	-0.89	1.31	0.92	0.72	Transport and binding proteins	Putative ATP-binding subunit of urea ABC transport system
PMM0975	2	1.01	0.45	0.32	0.48	Conserved hypothetical protein	conserved hypothetical protein
PMM0982	2	-0.72	0.32	0.23	1.00	DNA replication, recombination, and repair	HNH endonuclease:HNH nuclease
PMM0983	2	0.84	0.32	0.23	0.86	Fatty acid, phospholipid and sterol metabolism	possible ATP synthase protein 8
PMM0987	2	-2.06	0.58	0.41	0.16	Ribosomal proteins	30S Ribosomal protein S21
PMM0988	2	0.99	1.31	0.93	1.00	Regulatory functions	Helix-hairpin-helix DNA-binding motif class 1
PMM0993	2	-1.63	1.71	1.21	0.55	Conserved hypothetical protein	conserved hypothetical protein
PMM0996	2	0.20	1.00	0.71	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0997	2	-1.83	0.39	0.28	0.25	Conserved hypothetical protein	possible Protein of unknown function DUF67
PMM0998	2	-1.29	0.11	0.07	0.38	Conserved hypothetical protein	conserved hypothetical protein
PMM0999	2	2.47	1.32	0.93	0.00	Conserved hypothetical protein	hypothetical
PMM1003	2	-1.18	0.39	0.27	0.47	Photosystem II	possible Photosystem II reaction centre N prot
PMM1005	2	-0.71	0.59	0.42	1.00	Regulatory functions	possible Legume lectins alpha domain
PMM1008	2	-0.79	0.53	0.38	0.77	Conserved hypothetical protein	hypothetical
PMM1011	2	-1.53	0.55	0.39	0.21	Conserved hypothetical protein	hypothetical
PMM1011	2	-1.53	0.55	0.39	0.21	Conserved hypothetical protein	hypothetical
PMM1011	2	-1.53	0.55	0.39	0.21	Conserved hypothetical protein	hypothetical
PMM1015	2	-0.55	0.26	0.19	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1026	2	-2.15	0.89	0.63	0.05	Conserved hypothetical protein	conserved hypothetical protein
PMM1028	2	0.76	0.49	0.35	0.99	Conserved hypothetical protein	conserved hypothetical
PMM102a	2	0.15	0.50	0.35	1.00	Other	No Cyanobase Name
PMM1030	2	0.71	0.37	0.26	1.00	Regulatory functions	Ferric uptake regulator family
PMM1031	2	-1.30	1.10	0.78	0.64	Transport and binding proteins	ABC transporter, ATP binding domain, possibly Mn transport
PMM1032	2	0.36	0.41	0.29	0.92	Transport and binding proteins	ABC transporter, substrate binding protein, possibly Mn.
PMM1033	2	-0.62	0.51	0.36	1.00	Protein modification and translation factors	Cobalamin synthesis protein/P47K
PMM1037	1	#NAME? NA	NA	0.00	Conserved hypothetical protein	conserved hypothetical	
PMM1039	2	-0.78	1.67	1.18	0.61	Conserved hypothetical protein	conserved hypothetical protein
PMM1042	2	-1.18	0.32	0.23	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1045	2	-0.53	0.46	0.32	0.96	Conserved hypothetical protein	conserved hypothetical
PMM1054	2	-1.98	1.21	0.86	0.13	DNA replication, recombination, and repair	Crossover junction endodeoxyribonuclease RuvC
PMM1055	2	0.06	0.72	0.51	1.00	Cobalamin, heme, phycobilin and porphyrin	Protoporphyrin IX Magnesium chelatase, Chl subunit
PMM1058	2	2.37	1.14	0.81	0.03	Cytochrome b6/f complex	Cytochrome b6/f complex, subunit V
PMM1060	2	-0.88	0.37	0.26	1.00	Other	Glutamine amidotransferase class-I
PMM1061	2	-1.73	0.74	0.52	1.00	Thiamine	Thioredoxin
PMM1063	2	1.60	2.09	1.48	1.00	DNA replication, recombination, and repair	DNA gyrase/topoisomerase IV, subunit A
PMM1066	2	0.54	0.46	0.33	1.00	Branched chain family	2-isopropylmalate synthase
PMM1067	2	0.17	0.46	0.32	1.00	WD repeat proteins	possible Adenoviral fiber protein (repeat/shaf
PMM1069	2	-0.80	0.88	0.62	0.87	Folic acid	putative bifunctional Methylenetetrahydrofolate dehydrogenase Methenyltetrahydrofolate/cyclohydrolyase
PMM1074	2	-1.23	0.36	0.25	0.52	Other	Glucose-6-phosphate dehydrogenase
PMM1075	2	0.59	0.03	0.02	1.00	Cytochrome b6/f complex	ferredoxin-NADP oxidoreductase (FNR)
PMM1077	2	-1.64	0.68	0.48	1.00	Regulatory functions	two-component sensor histidine kinase
PMM1078	2	-0.03	0.17	0.12	1.00	Conserved hypothetical protein	conserved hypothetical
PMM1079	2	-2.09	1.38	0.98	0.08	Regulatory functions	possible Villin headpiece domain
PMM1080	2	2.63	1.15	0.82	0.00	Other	Ribose-phosphate pyrophosphokinase
PMM1086	2	-1.47	0.11	0.08	0.25	Fatty acid, phospholipid and sterol metabolism	Alpha/beta hydrolase fold:Esterase/lipase/thioesterase family...
PMM1088	2	1.49	0.30	0.21	1.00	Degradation of proteins, peptides, and glycopeptides	CipC
PMM1090	2	-1.38	0.59	0.42	0.54	Branched chain family	Diaminopimelate decarboxylase
PMM1091	2	-1.20	1.13	0.80	0.47	Conserved hypothetical protein	conserved hypothetical protein
PMM1092	2	-0.89	0.63	0.44	0.88	Other	Undecaprenyl pyrophosphate synthetase (UPPS)
PMM1098	2	-1.97	1.56	1.10	0.38	Photosystem II	photosystem II oxygen evolving complex protein PsbP
PMM1107	2	-1.11	0.38	0.27	0.78	Pyridoxine	Pyridoxal phosphate biosynthetic protein PdxJ
PMM1109	2	0.96	0.74	0.52	0.41	Conserved hypothetical protein	conserved hypothetical protein
PMM1111	2	2.26	1.84	1.30	0.01	Other	Glutaredoxin-related protein
PMM1113	2	1.89	0.17	0.12	0.28	Regulatory functions	two-component response regulator
PMM1116	2	2.02	0.47	0.33	1.00	Cell division	NAD binding site:Glucose inhibited division protein A family
PMM1117	2	2.03	0.48	0.34	0.13	Photosystem II	possible Photosystem II reaction centre Y protein (PsbY)
PMM1118	2	-1.83	0.61	0.43	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1119	2	-1.73	0.31	0.22	1.00	Membranes, lipoproteins and porins	possible porin
PMM1121	2	-1.65	0.18	0.12	1.00	Membranes, lipoproteins and porins	possible porin
PMM1123	2	1.20	0.73	0.51	1.00	Hydrogenase	putative Hydrogenase accessory protein
PMM1124	2	0.11	1.04	0.74	1.00	Other	possible Natural resistance-associated macroph
PMM1125	2	#NAME? NA	NA	0.05	Regulatory functions	possible Bacterial regulatory proteins, deoR f	
PMM1128	2	0.57	0.62	0.44	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1129	2	-1.75	0.25	0.18	0.19	Regulatory functions	possible Notch (DSL) domain
PMM1131	2	0.28	0.52	0.37	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1132	2	-1.65	1.07	0.76	0.40	Conserved hypothetical protein	conserved hypothetical protein
PMM1133	2	-0.81	0.84	0.59	0.74	Conserved hypothetical protein	conserved hypothetical protein
PMM1134	2	2.16	0.42	0.29	0.01	Other	possible Phosphatidylinositol-specific phospho
PMM1135	2	-2.08	0.37	0.27	0.15	Adaptations and atypical conditions	possible high light inducible protein
PMM1138	2	-0.54	0.70	0.49	0.80	Regulatory functions	probable GTP-binding protein
PMM1139	2	#NAME? NA	NA	0.40	Drug and analog sensitivity	possible membrane fusion protein	
PMM1145	2	0.65	1.25	0.88	0.86	Respiration	putative nicotinamide nucleotide transhydrogenase, subunit beta
PMM1146	2	3.88	0.96	0.68	0.00	Nicotinate and nicotinamide	putative nicotinamide nucleotide transhydrogenase, subunit alpha 2 (A2)
PMM1147	2	-1.57	0.78	0.55	0.39	DNA replication, recombination, and repair	putative nicotinamide nucleotide transhydrogenase, subunit alpha 1 (A1)
PMM1148	2	2.18	0.31	0.22	0.38	Protein modification and translation factors	possible EF-1 guanine nucleotide exchange doma
PMM1149	2	-1.25	0.59	0.42	1.00	Conserved hypothetical protein	conserved hypothetical
PMM1150	2	0.89	0.56	0.39	1.00	Regulatory functions	putative thioredoxin reductase
PMM1151	2	3.00	1.09	0.77	0.00	Protein modification and translation factors	translation initiation factor IF-1
PMM1152	2	-1.20	0.29	0.20	1.00	Photosystem II	putative chaperon-like protein for quinone binding in photosystem II
PMM1152a	2	-1.48	0.06	0.04	1.00	Other	No Cyanobase Name
PMM1154	2	1.04	0.80	0.57	1.00	Branched chain family	Acetolactate synthase small subunit
PMM1156	2	-2.19	0.17	0.12	0.01	Photosystem I	photosystem I assembly related protein Ycf4
PMM1157	2	-0.87	0.58	0.41	1.00	Photosystem II	Photosystem II PsbD protein (D2)
PMM1158	2	-0.43	0.58	0.41	1.00	Photosystem II	Photosystem II PsbC protein (CP43)
PMM1165	2	-0.92	0.14	0.10	0.65	Aminoacyl tRNA synthetases and tRNA modification	Glycyl-tRNA synthetase alpha subunit
PMM1167	2	-0.87	2.69	1.90	0.85	Other	Macrophage migration inhibitory factor family
PMM1168	2	-1.90	0.87	0.62	0.25	Conserved hypothetical protein	conserved hypothetical protein
PMM1169	2	-1.33	0.50	0.35	0.53	Conserved hypothetical protein	hypothetical
PMM1170	2	-1.13	0.99	0.70	0.61	Conserved hypothetical protein	conserved hypothetical protein
PMM1171	2	-0.30	0.90	0.64	1.00	Soluble electron carriers	Flavodoxin
PMM1174	2	0.84	0.25	0.17	0.65	Conserved hypothetical protein	hypothetical
PMM1176	2	-0.32	0.11	0.08	1.00	Regulatory functions	possible Helix-turn-helix protein, copG family
PMM1179	2	-2.05	2.94	2.08	0.80	Regulatory functions	putative SMR family transporter, possible pecM homologue
PMM1180	2	-0.06	0.48	0.34	1.00	Degradation of proteins, peptides, and glycopeptides	signal peptide peptidase SppA (protease IV)
PMM1183	2	-0.72	1.00	0.71	1.00	Ribosomal proteins	50S ribosomal protein L34

PMM1184	2	0.40	0.62	0.44	0.98	Degradation of RNA	Bacterial ribonuclease P protein component
PMM1185	2	-0.85	0.48	0.34	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1186	2	-0.79	0.38	0.27	1.00	Regulatory functions	Putative inner membrane protein; similar to 60 kDa inner membrane protein family
PMM1188	2	-0.55	0.17	0.12	0.92	Aminoacyl tRNA synthetases and tRNA modification	Seryl-tRNA synthetase
PMM1190	2	-0.98	0.13	0.09	1.00	Ribosomal proteins	30S Ribosomal protein S14
PMM1191	2	-0.24	1.07	0.76	1.00	RNA synthesis, modification, and DNA transcription	polyribonucleotide nucleotidyltransferase
PMM1192	2	-1.49	0.14	0.10	0.47	Other	CysQ protein homolog
PMM1204	2	0.52	0.42	0.30	1.00	Surface polysaccharides, lipopolysaccharides and anti	glucose-1-phosphate cytidyltransferase
PMM1205	2	-2.72	0.57	0.40	0.00	Sugars	NDP-hexose 3,4-dehydratase
PMM1229	2	-0.52	1.38	0.98	1.00	Respiration	Dehydrogenase, E1 component
PMM1234	2	0.03	0.33	0.24	1.00	Hydrogenase	Zinc-containing alcohol dehydrogenase superfamily
PMM1235	2	-0.44	0.21	0.15	0.90	Transport and binding proteins	possible N-terminal fragment of transketolase
PMM1240	2	-1.47	1.27	0.90	0.84	Other	methyltransferase
PMM1241	2	-1.46	1.07	0.76	0.25	Conserved hypothetical protein	hypothetical protein
PMM1244	2	#NAME? NA	NA		1.00	Conserved hypothetical protein	hypothetical protein
PMM1245	2	-0.31	1.51	1.07	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1250	2	-1.01	0.74	0.52	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM1251	2	-0.65	0.29	0.21	1.00	Other	Carbamoyltransferase
PMM1252	2	-0.91	0.57	0.40	0.58	Other	possible acetyltransferase
PMM1257	2	-1.57	0.47	0.33	0.23	Surface polysaccharides, lipopolysaccharides and anti	possible dTDP-glucose 4,6-dehydratase
PMM1258	2	-0.75	0.72	0.51	1.00	Pyridoxine	pyridoxal-phosphate-dependent aminotransferase
PMM1259	2	0.62	0.14	0.10	1.00	Pyridoxine	pyridoxal-phosphate-dependent aminotransferase
PMM1260	2	-0.86	0.43	0.30	1.00	Transport and binding proteins	Nucleoside-diphosphate-sugar epimerase
PMM1261	2	-0.77	0.35	0.25	0.72	Sugars	UDP-glucose 6-dehydrogenase
PMM1262	2	2.37	0.51	0.36	0.02	Regulatory functions	SOS function regulatory protein, LexA repressor
PMM1264	2	0.75	0.05	0.04	1.00	Cell division	cell division protein FtsH3
PMM1267	2	-2.15	1.04	0.74	0.03	Conserved hypothetical protein	conserved hypothetical
PMM1269	2	-0.27	0.27	0.19	1.00	Transport and binding proteins	predicted sugar kinase
PMM1270	2	-0.40	0.22	0.16	1.00	Aminoacyl tRNA synthetases and tRNA modification	Phenylalanyl-tRNA synthetase alpha chain
PMM1272	2	2.09	0.65	0.46	0.01	Conserved hypothetical protein	conserved hypothetical protein
PMM1273	2	-0.81	0.50	0.36	0.80	Riboflavin	putative riboflavin kinase/FAD synthase
PMM1275	2	-0.16	1.01	0.72	1.00	Conserved hypothetical protein	DUF170
PMM1276	2	-1.18	0.90	0.64	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1277	2	-1.70	0.96	0.68	0.10	Conserved hypothetical protein	conserved hypothetical protein
PMM1283	2	0.33	0.55	0.39	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1284	2	-0.72	0.85	0.60	0.89	Adaptations and atypical conditions	PhoH-like phosphate starvation-inducible protein
PMM1285	2	-0.28	0.05	0.03	1.00	Ribosomal proteins	30S Ribosomal protein S16
PMM1286	2	-0.28	0.38	0.28	1.00	Protein and peptide secretion	signal recognition particle protein (SRP54)
PMM1287	2	0.36	0.22	0.15	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1288	2	-0.84	0.39	0.28	1.00	Other	Pyruvate dehydrogenase E1 alpha subunit
PMM1289	2	-1.67	0.63	0.45	1.00	Transport and binding proteins	Type II alternative RNA polymerase sigma factor, sigma-70 family
PMM1293	2	1.90	0.23	0.16	0.28	Other	FKBP-type peptidyl-prolyl cis-trans isomerase (PPIase)
PMM1294	2	2.39	0.25	0.17	0.14	Hydrogenase	putative nickel-containing superoxide dismutase precursor (NISOD)
PMM1296	2	-0.71	1.04	0.73	1.00	Other	marine cyanobacterial conserved hypothetical
PMM1298	2	-1.96	0.88	0.62	0.59	Regulatory functions	putative dihydroliipoamide dehydrogenase
PMM1299	2	-0.23	0.36	0.25	1.00	RNA synthesis, modification, and DNA transcription	tRNA/rRNA methyltransferase (SpoU)
PMM1300	2	-1.39	0.78	0.55	0.37	Degradation of RNA	UDP-N-glucosamine 1-carboxyvinyltransferase
PMM1301	2	-1.02	0.91	0.64	1.00	Glutamate family / Nitrogen assimilation	Aminotransferase class-III pyridoxal-phosphate:Acetylornithin...
PMM1304	2	0.10	0.45	0.32	1.00	Other	possible cytosine deaminase
PMM1305	2	-1.03	0.55	0.39	0.66	Conserved hypothetical protein	conserved hypothetical protein
PMM1307	2	-0.28	0.02	0.02	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1309	2	1.24	0.48	0.34	1.00	Cell division	Cell division protein FtsZ;Tubulin/FtsZ family
PMM1310	2	-0.54	0.83	0.59	1.00	Regulatory functions	putative Ketopantoate hydroxymethyltransferase
PMM1312	2	-1.35	0.32	0.23	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1313	2	0.85	0.49	0.34	1.00	Degradation of proteins, peptides, and glycopeptides	Cip protease proteolytic subunit
PMM1314	2	1.82	0.67	0.47	0.39	Degradation of proteins, peptides, and glycopeptides	Cip protease proteolytic subunit
PMM1315	2	-0.74	0.31	0.22	1.00	Branched chain family	Ketol-acid reductoisomerase
PMM1317	2	2.15	0.35	0.25	0.02	Adaptations and atypical conditions	possible high light inducible protein
PMM1318	2	-1.54	1.65	1.16	0.70	Conserved hypothetical protein	conserved hypothetical
PMM1319	2	-1.40	0.76	0.54	0.41	Drug and analog sensitivity	possible Beta-lactamase
PMM1321	2	-0.69	0.44	0.31	1.00	Nucleoproteins	Bacterial histone-like DNA-binding protein
PMM1322	2	-0.15	0.15	0.11	1.00	Other	Putative isoamylase
PMM1323	2	-0.90	1.03	0.73	1.00	Regulatory functions	putative GPH family sugar transporter
PMM1324	2	-0.80	0.06	0.04	1.00	Transport and binding proteins	possible transporter, membrane component
PMM1325	2	-0.42	0.88	0.63	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1327	2	-0.88	0.61	0.43	0.78	Conserved hypothetical protein	conserved hypothetical protein
PMM1330	2	3.55	1.56	1.10	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1331	2	0.01	0.68	0.48	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1333	2	-1.95	1.29	0.91	0.00	Protein modification and translation factors	Peptide methionine sulfoxide reductase
PMM1336	2	-3.15	3.93	2.78	1.00	Fatty acid, phospholipid and sterol metabolism	Putative (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase
PMM1339	2	-1.02	0.16	0.11	1.00	Purine ribonucleotide biosynthesis	SAICAR synthetase
PMM1340	2	-1.35	0.25	0.18	1.00	Purine ribonucleotide biosynthesis	phosphoribosylglycinamide synthetase
PMM1342	2	-0.57	0.28	0.20	1.00	Other	possible circadian clock protein KaiC
PMM1343	2	-0.03	0.28	0.20	1.00	Other	possible circadian oscillation regulator KaiB
PMM1344	2	0.45	0.44	0.31	1.00	Ribosomal proteins	50S ribosomal protein L21
PMM1345	2	-0.08	0.80	0.57	1.00	Ribosomal proteins	50S ribosomal protein L27
PMM1346	2	0.32	0.73	0.52	0.88	Conserved hypothetical protein	conserved hypothetical protein
PMM1349	2	-0.55	0.66	0.47	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1350	2	-0.59	0.99	0.70	1.00	Other	Pentapeptide repeats
PMM1351	2	0.99	0.68	0.48	0.67	Conserved hypothetical protein	conserved hypothetical protein
PMM1352	2	-1.94	0.54	0.38	1.00	Soluble electron carriers	Ferredoxin
PMM1354	2	-1.18	1.16	0.89	0.82	Regulatory functions	putative D-3-phosphoglycerate dehydrogenase (PGDH)
PMM1355	2	-1.62	0.50	0.36	0.18	Conserved hypothetical protein	conserved hypothetical protein
PMM1363	2	0.33	0.05	0.03	0.90	Conserved hypothetical protein	hypothetical
PMM1365	2	2.65	0.69	0.49	0.00	Regulatory functions	possible MATH domain
PMM1368	2	-0.63	0.09	0.06	0.95	Conserved hypothetical protein	conserved hypothetical protein
PMM1369	2	-0.79	0.15	0.11	1.00	Regulatory functions	GAF domain
PMM1372	2	-1.45	0.97	0.68	0.50	Conserved hypothetical protein	conserved hypothetical protein
PMM1375	2	-1.84	0.52	0.37	0.33	Conserved hypothetical protein	possible M protein repeat
PMM1376	2	-0.61	1.11	0.79	0.64	Nucleoproteins	RNA-binding protein RbpD
PMM1377	2	4.12	2.01	1.42	0.00	Other	possible dihydroflavonol-4-reductase (maize, petunia, tomato)...
PMM1382	2	-0.92	0.06	0.04	0.68	Fatty acid, phospholipid and sterol metabolism	fatty acid desaturase, type 2
PMM1383	2	1.26	1.35	0.95	0.67	Conserved hypothetical protein	conserved hypothetical protein
PMM1384	2	-0.80	0.09	0.06	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1385	2	-0.74	0.08	0.06	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1387	2	-3.21	1.01	0.72	0.00	Conserved hypothetical protein	hypothetical
PMM1388	2	-2.52	0.57	0.40	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1390	2	-1.39	0.56	0.39	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1391	2	3.45	0.43	0.30	0.00	Regulatory functions	possible Helix-turn-helix protein, copG family
PMM1392	2	-2.53	1.15	0.81	0.00	Branched chain family	possible Heat-labile enterotoxin alpha chain
PMM1394	2	-2.31	0.28	0.20	0.00	Conserved hypothetical protein	hypothetical
PMM1395	2	-3.47	1.42	1.01	0.00	Conserved hypothetical protein	hypothetical
PMM1396	2	-2.02	0.68	0.48	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1397	2	-0.84	0.68	0.48	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1398	2	-0.82	0.37	0.26	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1399	2	-1.90	0.64	0.45	0.16	Adaptations and atypical conditions	possible high light inducible protein
PMM1400	2	-1.46	0.37	0.26	1.00	Other	possible Hemagglutinin-neuraminidase
PMM1401	2	-0.18	0.23	0.17	1.00	Conserved hypothetical protein	conserved hypothetical
PMM1402	2	-1.00	0.42	0.29	0.98	Conserved hypothetical protein	unnamed protein product
PMM1404	2	-2.03	1.38	0.98	0.41	Adaptations and atypical conditions	possible high light inducible protein
PMM1405	2	-0.82	0.04	0.03	0.88	Conserved hypothetical protein	hypothetical
PMM1407	2	-1.31	0.22	0.16	0.40	Other	possible SRP19 protein
PMM1408	2	-1.97	0.93	0.66	0.00	Conserved hypothetical protein	hypothetical
PMM1409	2	-1.46	0.02	0.02	0.38	Other	possible Rubredoxin
PMM1412	2	3.01	1.15	0.81	0.00	Conserved hypothetical protein	conserved hypothetical protein

PMM1413	2	0.73	0.78	0.55	0.85	Conserved hypothetical protein	conserved hypothetical
PMM1416	2	-0.37	0.23	0.16	1.00	Conserved hypothetical protein	conserved hypothetical
PMM1419	2	-0.67	0.62	0.44	1.00	Transport and binding proteins	possible ATP synthase B/B' CF(0)
PMM1422	2	-1.44	0.39	0.27	0.21	Conserved hypothetical protein	conserved hypothetical protein
PMM1423	2	-0.87	0.72	0.51	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM1424	2	-0.14	0.39	0.28	1.00	Other	possible Uncharacterized protein family UPF003
PMM1427	2	0.21	0.97	0.68	1.00	Conserved hypothetical protein	conserved hypothetical
PMM1428	2	-1.19	0.63	0.45	0.45	Conserved hypothetical protein	conserved hypothetical protein
PMM1429	2	-2.61	1.78	1.26	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1430	2	-0.22	0.31	0.22	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1431	2	-0.32	0.15	0.11	1.00	RNA synthesis, modification, and DNA transcription	putative DNA-directed RNA polymerase (omega chain)
PMM1434	2	-1.01	0.61	0.43	1.00	Glycolysis	Phosphoglycerate mutase, co-factor-independent (iPGM)
PMM1435	2	-1.79	1.02	0.72	0.02	Conserved hypothetical protein	conserved hypothetical protein
PMM1436	2	1.77	0.10	0.07	1.00	Chaperones	GroEL protein (Chaperonin cpn60)
PMM1437	2	1.71	0.45	0.32	1.00	Chaperones	GroES protein (Chaperonin cpn10)
PMM1438	2	-0.57	0.51	0.36	1.00	ATP synthase	ATP synthase beta subunit, central region:ATP synth...
PMM1440	2	0.01	0.58	0.41	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1441	2	0.07	0.14	0.10	1.00	Conserved hypothetical protein	hypothetical
PMM1442	2	-1.81	0.44	0.31	0.06	Regulatory functions	putative aminopeptidase P
PMM1443	2	-0.96	0.40	0.29	0.66	Conserved hypothetical protein	Domain of unknown function DUF21
PMM1449	2	-1.65	1.70	1.20	0.46	Soluble electron carriers	Ferredoxin
PMM1451	2	0.40	0.28	0.20	1.00	ATP synthase	ATP synthase alpha subunit, central region:ATP synth...
PMM1452	2	0.00	1.00	0.71	1.00	ATP synthase	ATP synthase delta (OSCP) subunit
PMM1453	2	-0.68	0.46	0.33	1.00	ATP synthase	ATP synthase B/B' CF(0)
PMM1454	2	-0.92	0.17	0.12	1.00	ATP synthase	ATP synthase B/B' CF(0)
PMM1455	2	-0.61	0.72	0.51	1.00	Membranes, lipoproteins and porins	Eubacterial and plasma membrane ATP synthase subunit C:ATP sy...
PMM1456	2	-0.47	1.69	1.19	1.00	ATP synthase	ATP synthase A subunit
PMM1457	2	-0.64	0.02	0.02	1.00	Conserved hypothetical protein	possible ATP synthase subunit 1
PMM1459	2	-0.09	1.22	0.86	1.00	Regulatory functions	putative c-type cytochrome biogenesis protein CcdA
PMM1462	2	-1.78	1.06	0.75	0.23	Conserved hypothetical protein	conserved hypothetical protein
PMM1463	2	-1.74	0.99	0.70	0.23	Other	Nitrogen regulatory protein P-II
PMM1477	2	0.79	0.81	0.57	0.81	Conserved hypothetical protein	conserved hypothetical
PMM1478	2	-0.22	0.27	0.19	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1479	2	-0.37	0.18	0.13	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1480	2	0.22	0.73	0.52	0.98	Conserved hypothetical protein	conserved hypothetical protein
PMM1482	2	#NAME? NA	NA	0.09	0.09	Adaptations and atypical conditions	possible high light inducible protein
PMM1483	2	-0.03	0.20	0.14	1.00	RNA synthesis, modification, and DNA transcription	RNA polymerase beta prime subunit
PMM1484	2	-0.19	0.32	0.22	1.00	RNA synthesis, modification, and DNA transcription	RNA polymerase gamma subunit
PMM1485	2	-0.61	0.18	0.12	1.00	RNA synthesis, modification, and DNA transcription	RNA polymerase beta subunit
PMM1487	2	-0.31	0.81	0.58	1.00	Ribosomal proteins	30S Ribosomal protein S20
PMM1489	2	1.85	0.33	0.23	0.04	Other	Ribose 5-phosphate isomerase
PMM1490	2	-1.38	0.54	0.38	0.30	Degradation of proteins, peptides, and glycopeptides	Serine proteases, trypsin family:Chymotrypsin serine protease...
PMM1492	2	0.42	0.06	0.04	1.00	RNA synthesis, modification, and DNA transcription	N utilization substance protein A
PMM1494	2	-0.31	0.61	0.43	1.00	Protein modification and translation factors	Translation initiation factor IF-2
PMM1495	2	-1.49	0.89	0.63	0.48	Conserved hypothetical protein	hypothetical
PMM1498	2	-1.22	0.60	0.42	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1499	2	1.26	0.94	0.66	0.31	Conserved hypothetical protein	conserved hypothetical protein
PMM1500	2	-0.73	0.02	0.02	1.00	Regulatory functions	putative aminotransferase
PMM1501	2	-0.72	0.06	0.04	1.00	Other	S1 RNA binding domain:Ribonuclease E and G
PMM1504	2	-1.60	1.02	0.72	0.23	Aromatic amino acid family	Chorismate mutase-Prephenate dehydratase
PMM1506	2	2.35	1.08	0.76	0.00	Regulatory functions	ATP-dependent protease La (LON) domain
PMM1507	2	0.91	0.73	0.51	1.00	Ribosomal proteins	30S ribosomal protein S10
PMM1508	2	0.03	1.65	1.17	1.00	Protein modification and translation factors	Elongation factor Tu
PMM1509	2	0.54	0.69	0.49	1.00	Protein modification and translation factors	Elongation factor G
PMM1510	2	-0.05	0.42	0.30	1.00	Ribosomal proteins	30S ribosomal protein S7
PMM1511	2	-0.34	0.07	0.05	1.00	Ribosomal proteins	30S ribosomal protein S12
PMM1512	2	-0.12	0.30	0.21	1.00	Glutamate family / Nitrogen assimilation	Ferredoxin-dependent glutamate synthase, Fd-GOGAT
PMM1514	2	2.02	1.62	1.14	0.10	Other	lipoic acid synthetase
PMM1515	2	-0.25	1.96	1.39	0.85	Other	Site-specific recombinase
PMM1519	2	0.80	0.71	0.50	1.00	Photosystem I	Photosystem I PsaI protein (subunit XI)
PMM1520	2	-0.12	0.54	0.38	1.00	Photosystem I	photosystem I subunit VIII (PsaI)
PMM1523	2	1.99	0.07	0.05	1.00	Photosystem I	Photosystem I PsaB protein
PMM1524	2	0.91	0.28	0.20	1.00	Photosystem I	Photosystem I PsaA protein
PMM1528	2	1.08	1.19	0.84	0.46	DNA replication, recombination, and repair	HNH endonuclease family protein
PMM1530	2	-1.54	0.28	0.20	0.37	Ribosomal proteins	50S ribosomal protein L31
PMM1531	2	-1.59	0.25	0.17	1.00	Ribosomal proteins	30S ribosomal protein S9
PMM1532	2	0.58	0.45	0.32	1.00	Ribosomal proteins	50S ribosomal protein L13
PMM1534	2	-0.15	0.84	0.59	1.00	Ribosomal proteins	50S ribosomal protein L17
PMM1535	2	0.65	1.11	0.79	1.00	RNA synthesis, modification, and DNA transcription	Bacterial RNA polymerase, alpha chain
PMM1536	2	0.51	0.09	0.06	1.00	Ribosomal proteins	30S ribosomal protein S11
PMM1537	2	-0.34	0.40	0.28	1.00	Ribosomal proteins	30S ribosomal protein S13
PMM1538	2	-0.55	0.15	0.10	1.00	Ribosomal proteins	50S Ribosomal protein L36
PMM1540	2	-1.06	0.64	0.45	0.75	Protein and peptide secretion	preprotein translocase SecY subunit
PMM1541	2	0.41	0.89	0.63	0.68	Ribosomal proteins	50S ribosomal protein L15
PMM1542	2	0.94	0.22	0.16	0.56	Ribosomal proteins	30S ribosomal protein S5
PMM1543	2	2.03	1.21	0.85	0.00	Ribosomal proteins	50S ribosomal protein L18
PMM1544	2	0.59	1.00	0.71	1.00	Ribosomal proteins	50S ribosomal protein L6
PMM1545	2	-0.48	0.64	0.45	0.82	Ribosomal proteins	30S ribosomal protein S8
PMM1546	2	0.14	1.41	1.00	1.00	Ribosomal proteins	50S ribosomal protein L5
PMM1548	2	0.48	0.10	0.07	0.85	Ribosomal proteins	50S Ribosomal protein L14
PMM1549	2	0.94	1.99	1.40	1.00	Ribosomal proteins	30S Ribosomal protein S17
PMM1550	2	-1.74	1.62	1.30	0.06	Conserved hypothetical protein	50S ribosomal protein L29
PMM1551	2	0.75	0.22	0.15	1.00	Ribosomal proteins	50S ribosomal protein L16
PMM1552	2	-0.45	0.44	0.31	1.00	Ribosomal proteins	30S ribosomal protein S3
PMM1553	2	-0.32	0.23	0.16	1.00	Ribosomal proteins	50S ribosomal protein L22
PMM1554	2	0.52	0.32	0.22	0.91	Ribosomal proteins	30S Ribosomal protein S19
PMM1555	2	-0.72	0.29	0.21	1.00	Ribosomal proteins	50S ribosomal protein L2
PMM1556	2	-0.73	0.18	0.13	1.00	Ribosomal proteins	50S ribosomal protein L23
PMM1557	2	-0.74	2.31	1.64	0.89	Ribosomal proteins	50S ribosomal protein L4
PMM1558	2	-0.82	0.94	0.66	1.00	Ribosomal proteins	50S ribosomal protein L3
PMM1559	2	0.05	1.31	0.92	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1562	2	-1.32	0.89	0.63	1.00	DNA replication, recombination, and repair	RecA bacterial DNA recombination protein
PMM1563	2	0.15	1.32	0.93	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1566	2	-1.14	1.29	0.91	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1568	2	0.23	0.03	0.02	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1570	2	-1.74	0.30	0.21	0.48	Cobalamin, heme, phycobillin and porphyrin	ATP:corrinoid adenosyltransferase BtuR/CobO/CobP
PMM1571	2	-0.23	0.90	0.64	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1575	2	-0.35	0.59	0.42	1.00	Pyruvate and acetyl-CoA metabolism	Phosphoenolpyruvate carboxylase
PMM1578	2	4.02	0.37	0.26	0.00	Photosystem I	Photosystem I protein PsaD
PMM1581	2	-0.70	0.60	0.42	1.00	Regulatory functions	MRP protein homolog
PMM1583	2	-0.69	0.11	0.08	0.75	Conserved hypothetical protein	conserved hypothetical protein
PMM1585	2	#NAME? NA	NA	1.00	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1588	2	-0.55	0.68	0.48	1.00	Regulatory functions	possible Conserved carboxylase domain
PMM1594	2	-0.68	0.24	0.17	1.00	Cobalamin, heme, phycobillin and porphyrin	Heme oxygenase
PMM1596	2	0.42	0.41	0.29	1.00	Other	Isocitrate dehydrogenase
PMM1599	2	-0.57	0.31	0.22	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1600	2	1.05	1.40	0.99	0.67	Transport and binding proteins	putative Na ⁺ /H ⁺ antiporter, CPA2 family
PMM1601	2	-0.61	0.01	0.01	1.00	Other	phosphorylase
PMM1602	2	1.01	0.82	0.58	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1603	2	0.55	2.08	1.47	1.00	Regulatory functions	putative ribonuclease III
PMM1604	2	0.09	0.34	0.24	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1605	2	0.95	0.35	0.03	1.00	Protein modification and translation factors	possible 16S rRNA processing protein RimM
PMM1606	2	-0.52	0.71	0.50	1.00	Other	Glutamine-fructose-6-phosphate transaminase (isomerizing)
PMM1607	2	0.71	0.31	0.22	1.00	Photosystem I	Photosystem I subunit PsaC
PMM1608	2	2.09	0.51	0.36	0.46	Fatty acid, phospholipid and sterol metabolism	acyl carrier protein (ACP)

PMM1609	2	1.53	0.32	0.22	1.00 Fatty acid, phospholipid and sterol metabolism	3-oxoacyl-[acyl-carrier-protein] synthase II
PMM1610	2	0.04	1.00	0.70	1.00 Other	Transekolase
PMM1611	2	-0.47	0.01	1.00 Thiamine	ThiC family	
PMM1613	2	0.10	1.31	0.93	1.00 Other	Zinc metallopeptidase M20/M25/M40 family
PMM1615	2	-2.79	0.10	0.07	0.00 DNA replication, recombination, and repair	Holliday junction DNA helicase RuvB
PMM1616	2	0.34	1.60	1.13	0.78 Other	tmRNA binding protein SmpB
PMM1617	2	-0.87	0.44	0.31	1.00 Conserved hypothetical protein	conserved hypothetical protein
PMM1619	2	-0.70	0.20	0.14	1.00 Regulatory functions	two-component response regulator
PMM1622	2	1.09	0.03	0.02	0.86 Murein sacculus and peptidoglycan	Rod shape determining protein
PMM1623	2	0.70	0.11	0.08	1.00 DNA replication, recombination, and repair	single-stranded DNA-binding protein
PMM1625	2	1.17	0.60	0.43	1.00 Amino acids and amines	putative adenosylhomocysteinase
PMM1626	2	-1.42	0.13	0.09	0.43 Conserved hypothetical protein	conserved hypothetical protein
PMM1629	2	0.40	0.04	0.03	1.00 Transport and binding proteins	Type II alternative RNA polymerase sigma factor, sigma-70 family
PMM1630	2	-0.92	0.51	0.36	1.00 Transport and binding proteins	MgtE family, putative magnesium transport protein
PMM1634	2	1.28	0.85	0.60	0.64 DNA replication, recombination, and repair	DNA gyrase, subunit B
PMM1635	2	-1.24	0.49	0.35	0.53 Aminoacyl tRNA synthetases and tRNA modification	tRNA delta-2-isopentenylpyrophosphate (IPP) transferase
PMM1636	2	-1.24	0.20	0.14	1.00 Protein modification and translation factors	Translation initiation factor 3
PMM1639	2	-0.09	0.25	0.18	1.00 Protein and peptide secretion	Preprotein translocase SecA subunit
PMM1640	2	-1.80	0.13	0.09	0.20 Regulatory functions	putative acetyltransferase, GNAT family
PMM1642	2	-1.00	0.59	0.42	1.00 Regulatory functions	possible transcription regulator
PMM1643	2	-0.59	0.70	0.50	1.00 Riboflavin	Putative 6,7-dimethyl-8-ribitylumazine synthase or riboflavin synthase beta chain
PMM1644	2	-0.24	0.72	0.51	1.00 Photosystem II	possible Photosystem II reaction center Z protein (PsbZ)
PMM1648	2	-0.37	0.41	0.29	1.00 Branched chain family	Aspartate kinase
PMM1649	2	1.60	0.81	0.57	0.23 DNA replication, recombination, and repair	Excinuclease ABC subunit B (UvrB)
PMM1650	2	1.55	0.53	0.37	0.44 Conserved hypothetical protein	conserved hypothetical protein
PMM1652	2	-0.42	0.83	0.58	1.00 Conserved hypothetical protein	conserved hypothetical protein
PMM1653	2	0.51	0.45	0.31	1.00 Aspartate family	Dihydrodipicolinate synthetase
PMM1655	2	-1.35	0.99	0.70	0.57 Other	FKBP-type peptidyl-prolyl cis-trans isomerase (PPIase)
PMM1656	2	1.19	1.49	1.06	0.64 Degradation of proteins, peptides, and glycopeptides	Clp protease proteolytic subunit
PMM1657	2	-0.41	0.38	0.27	1.00 Degradation of proteins, peptides, and glycopeptides	Clp protease ATP-binding subunit, ClpX
PMM1661	2	-1.53	0.33	0.23	0.78 Ribosomal proteins	50S ribosomal protein L35
PMM1662	2	-1.39	0.64	0.46	1.00 Ribosomal proteins	50S ribosomal protein L20
PMM1665	2	-0.22	0.05	0.04	1.00 Fatty acid, phospholipid and sterol metabolism	sulfolipid (UDP-sulfoquinovose) biosynthesis protein
PMM1667	2	-0.28	0.63	0.45	1.00 Conserved hypothetical protein	conserved hypothetical protein
PMM1669	2	-1.58	0.58	0.41	0.12 Regulatory functions	putative Glycine cleavage H-protein
PMM1671	2	-1.53	0.00	0.00	0.57 Conserved hypothetical protein	conserved hypothetical protein
PMM1672	2	0.09	0.09	0.07	1.00 Fatty acid, phospholipid and sterol metabolism	Fatty acid desaturase, type 1
PMM1673	2	-0.40	0.95	0.67	1.00 Ribosomal proteins	50S ribosomal protein L9
PMM1676	2	2.17	0.06	0.04	0.01 Conserved hypothetical protein	conserved hypothetical protein
PMM1678	2	-0.05	0.50	0.36	1.00 Conserved hypothetical protein	conserved hypothetical protein
PMM1680	2	-1.50	0.25	0.18	0.57 Conserved hypothetical protein	conserved hypothetical protein
PMM1683	2	0.14	0.08	0.05	1.00 Conserved hypothetical protein	conserved hypothetical protein
PMM1685	2	-0.35	0.13	0.09	1.00 Regulatory functions	putative spermidine synthase
PMM1688	2	-1.71	0.01	0.01	0.11 Aminoacyl tRNA synthetases and tRNA modification	Aspartyl-tRNA synthetase
PMM1689	2	0.68	0.07	0.05	1.00 Pyrimidine ribonucleotide biosynthesis	Glutamine amidotransferase class-I:CTP synthase
PMM1694	2	-0.57	0.26	0.19	0.84 Cobalamin, heme, phycobilin and porphyrin	putative uroporphyrin-III C-methyltransferase
PMM1697	2	0.36	0.12	0.09	1.00 Transport and binding proteins	Type II alternative RNA polymerase sigma factor, sigma-70 family
PMM1700	2	-0.78	0.14	0.10	1.00 Other	Aconitate hydratase B
PMM1702	2	-1.43	0.54	0.38	0.33 Purine ribonucleotide biosynthesis	formyltetrahydrofolate deformylase
PMM1703	2	-0.12	0.77	0.55	1.00 Transport and binding proteins	NAD binding site:D-amino acid oxidase
PMM1704	2	-0.62	0.02	0.01	1.00 Chaperones	Molecular chaperone DnaK2, heat shock protein hsp70-2
PMM1706	2	2.06	2.45	1.73	1.00 Ribosomal proteins	30S ribosomal protein S6
PMM1707	2	-0.38	0.43	0.30	1.00 Glutamate family / Nitrogen assimilation	Argininosuccinate synthase
PMM1708	2	1.33	1.42	1.00	1.00 Conserved hypothetical protein	conserved hypothetical protein
PMM1716	2	0.12	0.77	0.54	1.00 Aspartate family	No Cyanobase Name
PMM1717	2	-0.80	0.36	0.26	1.00 Other	No Cyanobase Name
PMM1718	2	-2.32	1.19	0.84	1.00 Other	No Cyanobase Name