Table S4. Gene Expression For Genes with Top 50% Expression Values during 12 Hours Post Starvation

Name	Number	log2 Fold Change	Standard Deviation	Standard Error	p-value	Category	Definition
PMM0001	2	0.89	1.01	0.71	0.54	DNA replication, recombination, and repair	DNA polymerase III, beta chain
PMM0008	2	1.34	0.16	0.11	0.28	Conserved hypothetical protein	conserved hypothetical protein
PMM0013	2	-1.48	0.60	0.42	0.88	Fatty acid, phospholipid and sterol metabolism	RNA-binding region RNP-1 (RNA recognition motif)
PMM0015	2	0.25	0.37	0.26	0.93	Conserved hypothetical protein	Domain of unknown function DUF25
PMM0016	2	-1.51	1.08	0.76	0.27	Chaperones	Heat shock protein GrpE
PMM0017	2	1.71	0.02	0.01	0.10	Chaperones	DnaJ protein
PMM0020	2	-0.90	2.70	1.91	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0023	2	-0.58	0.75	0.53	0.46	CO2 fixation	Glyceraldehyde 3-phosphate dehydrogenase(NADP+)(phosphorylating)
PMM0025	2	0.18	0.31	0.22	0.83	Protein modification and translation factors	Cyclophilin-type peptidyl-prolyl cis-trans isomerase
PMM0026	2	-1.42	1.65	1.16	0.08	Protein modification and translation factors	Elongation factor P (EF-P)
PMM0027	2	0.53	0.68	0.48	1.00	Fatty acid, phospholipid and sterol metabolism	Biotin / Lipoyl attachment:Acetyl-CoA biotin carboxyl carrier...
PMM0030	2	5.12	1.40	0.99	0.00	Protein modification and translation factors	possible Transcription factor TFIID (or TATA-b
PMM0031	2	1.08	0.16	0.11	0.87	DNA replication, recombination, and repair	HNH endonuclease:HNH nuclease
PMM0032	2	0.40	0.91	0.65	0.82	Protein and peptide secretion	possible Bacterial type II secretion system pr
PMM0033	2	0.93	0.78	0.55	0.96	Conserved hypothetical protein	conserved hypothetical protein
PMM0034	2	-0.09	0.89	0.63	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM0035	2	2.04	1.39	0.99	0.22	Hydrogenase	soluble hydrogenase small subunit
PMM0037	2	1.19	0.33	0.24	0.55	Purine ribonucleotide biosynthesis	Glutamine amidotransferase class-I:GMP synthase
PMM0043	2	-0.98	1.23	0.87	0.14	Other	flavoprotein
PMM0046	2	-1.93	0.52	0.37	0.01	Interconversions and salvage of nucleosides and nucleotides	Nucleoside diphosphate kinase
PMM0048	2	0.54	0.01	0.00	0.87	Aminoacyl tRNA synthetases and tRNA modification	Glutamyl-tRNA (Gln) amidotransferase subunit B
PMM0051	2	0.83	0.16	0.11	0.72	Conserved hypothetical protein	conserved hypothetical protein
PMM0055	2	0.88	1.12	0.79	0.68	Conserved hypothetical protein	conserved hypothetical protein
PMM0056	2	-1.09	2.52	1.78	0.86	Conserved hypothetical protein	conserved hypothetical protein
PMM0058	2	3.06	0.22	0.15	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0059	2	0.52	0.37	0.26	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0060	2	-0.41	0.32	0.23	0.57	Fatty acid, phospholipid and sterol metabolism	acetyl-CoA carboxylase, biotin carboxylase subunit
PMM0061	2	-0.44	1.00	0.71	0.46	Other	YGGT family, conserved hypothetical integral membrane protein
PMM0062	2	-2.04	0.53	0.37	0.00	Photosystem II	photosystem II PsbX protein
PMM0063	2	1.82	0.14	0.10	0.89	Conserved hypothetical protein	conserved hypothetical protein
PMM0064	2	1.71	1.19	0.84	0.46	Adaptations and atypical conditions	possible high light inducible protein
PMM0068	2	0.43	0.25	0.17	0.95	Regulatory functions	putative formylmethionine deformylase
PMM0073	2	-0.26	0.45	0.31	0.68	Transport and binding proteins	ABC transporter, membrane component
PMM0075	2	1.95	1.06	0.75	0.05	Conserved hypothetical protein	conserved hypothetical protein
PMM0078	2	-0.92	0.11	0.08	0.39	Other	possible 4'-phosphopantetheinyl transferase family protein
PMM0079	2	-1.86	0.23	0.16	0.00	Transport and binding proteins	putative bacterioferritin comigratory (BCP) protein
PMM0081	2	1.48	1.51	1.06	0.49	Serine family / Sulfur assimilation	Phosphoadenosine phosphosulfate reductase
PMM0082	2	3.47	2.30	1.63	0.00	Regulatory functions	putative NADH dehydrogenase, transport associated
PMM0083	2	-0.80	1.01	0.71	0.23	Regulatory functions	putative sodium/sulfate transporter, DASS family
PMM0085	2	0.55	0.54	0.38	1.00	Regulatory functions	putative potassium channel, VIC family
PMM0086	2	-0.01	2.04	1.45	0.71	Conserved hypothetical protein	Conserved hypothetical protein
PMM0087	2	2.87	1.77	1.25	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0088	2	1.77	0.94	0.67	0.19	Conserved hypothetical protein	conserved hypothetical protein
PMM0091	2	1.28	1.46	1.03	0.36	Conserved hypothetical protein	conserved hypothetical protein
PMM0092	2	2.26	1.76	1.24	0.19	Conserved hypothetical protein	conserved hypothetical protein
PMM0093	2	-0.68	0.13	0.09	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM0095	2	-0.61	1.40	0.99	0.35	Other	similar to serum resistance locus BrkB
PMM0099	2	1.68	1.07	0.76	0.22	Conserved hypothetical protein	conserved hypothetical protein
PMM0101	2	0.93	0.34	0.24	0.56	Conserved hypothetical protein	conserved hypothetical protein
PMM0103	2	1.79	0.56	0.40	0.19	Conserved hypothetical protein	conserved hypothetical protein
PMM0105	2	1.05	0.53	0.37	0.37	Riboflavin	RibD/ribG C-terminal domain
PMM0106	2	0.76	0.27	0.19	0.97	Other	6-pyruvoyl tetrahydropterin synthase
PMM0111	2	-0.06	0.64	0.45	0.73	Conserved hypothetical protein	conserved hypothetical protein
PMM0114	2	-0.79	2.06	1.46	0.19	Conserved hypothetical protein	conserved hypothetical protein
PMM0115	2	0.28	0.75	0.53	0.85	Carotenoid	zeta-carotene desaturase
PMM0116	2	0.46	0.60	0.43	0.80	Conserved hypothetical protein	conserved hypothetical protein
PMM0117	2	2.10	0.18	0.13	0.01	Conserved hypothetical protein	conserved hypothetical protein
PMM0120	2	1.65	1.06	0.75	0.11	Cell division	putative cell division inhibitor
PMM0121	2	0.59	0.43	0.30	0.76	Conserved hypothetical protein	conserved hypothetical protein
PMM0123	2	0.65	0.62	0.44	1.00	Serine family / Sulfur assimilation	O-acetylserine (thiol)-lyase A
PMM0124	2	1.03	1.55	1.10	0.85	Conserved hypothetical protein	conserved hypothetical protein in cyanobacteria
PMM0125	2	-0.12	0.26	0.18	0.72	Transport and binding proteins	possible ABC transporter, ATP-binding component
PMM0126	2	0.52	0.49	0.34	0.85	Other	possible Herpesvirus UL6 like
PMM0128	2	0.16	0.15	0.10	0.81	Regulatory functions	two-component response regulator
PMM0132	2	-1.10	0.03	0.02	0.25	Other	cyanobacterial conserved hypothetical
PMM0133	2	2.05	0.32	0.23	0.02	Radiation sensitivity	putative DNA repair protein RadA
PMM0134	2	-1.66	1.09	0.77	0.11	Regulatory functions	two-component response regulator
PMM0136	2	-1.05	1.72	1.22	0.12	Fatty acid, phospholipid and sterol metabolism	3-oxoacyl-[acyl-carrier-protein] synthase III
PMM0137	2	0.32	0.41	0.29	1.00	Fatty acid, phospholipid and sterol metabolism	Malonyl coenzyme A-acyl carrier protein transacylase
PMM0138	2	0.66	0.03	0.02	0.86	Fatty acid, phospholipid and sterol metabolism	putative 1-acyl-sn-glycerol-3-phosphate acyltransferase
PMM0139	2	-0.17	3.00	2.12	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM0140	2	Inf	NA	NA	1.00	Regulatory functions	putative Ycf34
PMM0142	2	#NAME?	NA	NA	0.27	Fatty acid, phospholipid and sterol metabolism	RNA-binding region RNP-1 (RNA recognition motif)
PMM0143	2	1.41	0.25	0.17	0.25	Carotenoid	Squalene and phytoene synthases
PMM0144	2	1.68	0.41	0.29	0.19	Carotenoid	phytoene desaturase
PMM0145	2	2.07	0.33	0.23	0.04	Conserved hypothetical protein	conserved hypothetical protein
PMM0146	2	1.89	0.08	0.05	0.11	Conserved hypothetical protein	conserved hypothetical protein
PMM0147	2	-0.01	0.04	0.03	0.69	Regulatory functions	putative Rubisco transcriptional regulator
PMM0149	2	0.91	0.12	0.08	1.00	NADH dehydrogenase	putative NADH Dehydrogenase (complex I) subunit (chain 5)
PMM0150	2	1.71	0.14	0.10	0.19	NADH dehydrogenase	putative NADH dehydrogenase subunit (chain 4)
PMM0153	2	-1.82	0.65	0.46	0.03	Conserved hypothetical protein	conserved hypothetical protein
PMM0154	2	-0.58	0.29	0.21	0.42	Regulatory functions	Bacterial regulatory protein, LuxR family
PMM0159	2	0.92	0.37	0.26	1.00	NADH dehydrogenase	putative NADH Dehydrogenase subunit
PMM0160	2	2.66	0.59	0.42	0.00	NADH dehydrogenase	putative respiratory-chain NADH dehydrogenase subunit
PMM0163	2	-0.73	0.05	0.04	0.49	Conserved hypothetical protein	conserved hypothetical protein
PMM0164	2	1.56	0.36	0.26	0.28	Aromatic amino acid family	Tryptophan synthase, beta chain:Pyridoxal-5'-phosphate-depend...
PMM0166	2	-0.93	1.19	0.84	0.49	Serine family / Sulfur assimilation	Adenylylsulfate kinase
PMM0172	2	1.24	0.37	0.26	0.34	NADH dehydrogenase	putative NADH dehydrogenase subunit
PMM0179	2	1.26	1.73	1.22	0.95	Other	Glutaredoxin
PMM0180	2	0.54	1.74	1.23	1.00	Protein modification and translation factors	peptide chain release factor RF-2
PMM0184	2	1.60	0.61	0.43	0.28	Aromatic amino acid family	para-aminobenzoate synthase component II
PMM0195	2	-0.11	1.01	0.72	0.66	Other	Phosphoglycerate kinase
PMM0200	2	-0.50	0.01	0.01	0.64	Degradation of RNA	possible ribonuclease HI
PMM0201	2	-2.45	0.00	0.00	0.00	Ribosomal proteins	50S ribosomal protein L7/L12
PMM0202	2	-2.54	0.58	0.41	0.00	Ribosomal proteins	50S ribosomal protein L10
PMM0203	2	-2.46	0.22	0.16	0.00	Ribosomal proteins	50S ribosomal protein L1
PMM0204	2	-1.53	0.79	0.56	0.00	Ribosomal proteins	50S ribosomal protein L11
PMM0205	2	1.15	0.38	0.27	0.71	RNA synthesis, modification, and DNA transcription	transcription antitermination protein, NusG
PMM0206	2	-1.11	0.31	0.22	0.24	Protein and peptide secretion	putative preprotein translocase, SecE subunit
PMM0208	2	-0.04	0.84	0.60	0.78	Other	Enolase
PMM0209	2	-0.83	0.94	0.66	0.34	Other	possible kinase
PMM0211	2	0.33	0.88	0.63	0.76	Other	FAD-dependent pyridine nucleotide-disulphide oxidoreductase
PMM0212	2	3.02	0.23	0.16	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0213	2	2.02	0.33	0.24	0.01	Transport and binding proteins	putative sodium-dependent bicarbonate transporter
PMM0214	2	-2.59	0.49	0.35	0.00	Regulatory functions	putative sulfate transporter
PMM0216	2	#NAME?	NA	NA	0.23	Adaptations and atypical conditions	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
PMM0218	2	-0.12	0.22	0.15	0.65	Other	GTP1/OBG family
PMM0219	2	0.17	0.57	0.40	0.86	Conserved hypothetical protein	conserved hypothetical
PMM0220	2	1.95	0.05	0.03	1.00	Other	No Cyanobase Name
PMM0223	2	2.84	0.21	0.15	0.08	Photosystem II	Photosystem II PsbA protein (D1)
PMM0224	2	1.54	0.84	0.59	0.17	Aromatic amino acid family	Chorismate synthase
PMM0226	2	0.03	0.74	0.53	0.65	Cell division	cell division protein FtsH2
PMM0228	2	-0.40	1.40	0.99	0.42	Photosystem II	Photosystem II manganese-stabilizing protein
PMM0231	2	-1.01	1.50	1.06	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0235	2	0.98	1.50	1.06	0.30	Aminoacyl tRNA synthetases and tRNA modification	Glutamyl-tRNA(Gln) amidotransferase subunit C
PMM0237	2	-0.30	1.41	1.00	0.67	Conserved hypothetical protein	conserved hypothetical protein

PMM0239	2	-1.41	0.03	0.02	0.08	Conserved hypothetical protein	conserved hypothetical protein
PMM0242	2	0.33	0.70	0.50	1.00	Thiamine	thioredoxin-like protein TxlA
PMM0243	2	0.45	0.94	0.67	0.80	Pyrimidine ribonucleotide biosynthesis	possible Thy1 protein homolog
PMM0244	2	0.71	0.11	0.08	1.00	Purine ribonucleotide biosynthesis	dCTP Deaminase
PMM0245	2	1.73	0.81	0.57	0.08	Cobalamin, heme, phycobilin and porphyrin	cob(I)alamin adenosyltransferase
PMM0246	2	1.71	1.56	1.10	0.26	Transport and binding proteins	Global nitrogen regulatory protein, CRP family of transcriptional regulators
PMM0251	2	-2.46	0.06	0.04	0.00	Photosystem II	Photosystem II PsbH protein
PMM0252	2	1.68	0.27	0.19	0.30	Photosystem II	Photosystem II reaction centre N protein (psbN)
PMM0253	2	0.53	0.24	0.17	0.64	Photosystem II	photosystem II reaction center PsbI protein
PMM0254	2	0.59	1.24	0.88	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0258	2	1.89	0.96	0.68	0.03	Other	Serine hydroxymethyltransferase (SHMT)
PMM0259	2	0.56	1.64	1.16	0.64	Conserved hypothetical protein	conserved hypothetical protein
PMM0260	2	1.47	1.58	1.12	0.50	Conserved hypothetical protein	conserved hypothetical protein
PMM0263	2	2.27	0.09	0.07	1.00	Transport and binding proteins	Ammonium transporter family
PMM0264	2	-1.80	0.22	0.16	0.01	Murein sacculus and peptidoglycan	LytB protein homolog
PMM0265	2	-0.66	0.23	0.16	0.49	Conserved hypothetical protein	conserved hypothetical protein
PMM0267	2	-1.81	1.02	0.72	0.11	Other	probable esterase
PMM0268	2	-0.25	0.13	0.09	0.92	Conserved hypothetical protein	conserved hypothetical protein
PMM0272	2	-3.34	0.67	0.47	0.00	Photosystem II	Photosystem II protein PsbK
PMM0273	2	-1.81	1.74	1.23	0.04	Other	probable oxidoreductase
PMM0275	2	0.11	0.33	0.23	0.88	Pyrimidine ribonucleotide biosynthesis	Orotate phosphoribosyltransferase
PMM0278	2	-0.13	0.00	0.00	0.75	Other	Phosphotransferase superclass
PMM0279	2	-1.18	0.45	0.32	0.26	Conserved hypothetical protein	conserved hypothetical protein
PMM0282	2	-0.17	1.35	0.95	0.52	Fatty acid, phospholipid and sterol metabolism	enoyl-[acyl-carrier-protein] reductase
PMM0284	2	-1.60	0.92	0.65	0.00	Regulatory functions	putative pleiotropic regulatory protein
PMM0286	2	0.02	0.87	0.62	0.80	Other	NUDIX hydrolase
PMM0289	2	1.44	0.76	0.54	0.29	Transport and binding proteins	possible ABC transporter
PMM0290	2	0.90	0.81	0.57	0.71	Transport and binding proteins	possible ABC transporter, ATP binding component
PMM0293	2	1.41	0.02	0.01	0.45	NADH dehydrogenase	putative respiratory-chain NADH dehydrogenase subunit
PMM0294	2	1.69	0.23	0.16	0.21	NADH dehydrogenase	putative NADH Dehydrogenase (complex I) subunit (chain 3)
PMM0295	2	-1.27	1.33	0.94	0.45	Other	probable rubredoxin
PMM0296	2	-1.61	0.86	0.61	0.05	Conserved hypothetical protein	conserved hypothetical protein
PMM0297	2	-0.21	0.12	0.08	0.81	Photosystem II	Cytochrome b559 alpha-subunit
PMM0298	2	-0.10	0.05	0.03	0.85	Photosystem II	Cytochrome b559 beta-subunit
PMM0299	2	-0.06	0.22	0.15	0.69	Photosystem II	photosystem II PsbL protein
PMM0300	2	-0.32	0.43	0.30	0.54	Photosystem II	photosytem II PsbJ protein
PMM0301	2	1.36	0.45	0.32	0.41	Other	5'-methylthioadenosine phosphorylase
PMM0305	2	-1.72	1.40	0.99	0.00	Phycobilisome	Phycobilisome protein
PMM0306	2	-3.32	0.23	0.16	0.00	Phycobilisome	phycoerythrin linker protein CpeS homolog
PMM0307	2	-3.12	0.51	0.36	0.00	Conserved hypothetical protein	hypothetical
PMM0308	2	-0.12	0.26	0.19	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM0309	2	1.57	1.52	1.08	0.19	Other	possible Pollen allergen
PMM0311	2	-1.49	0.32	0.23	0.02	Aspartate family	S-adenosylmethionine synthetase
PMM0312	2	-2.38	0.00	0.00	0.00	Ribosomal proteins	30S ribosomal protein S1, homolog A
PMM0313	2	-0.66	0.38	0.27	0.64	Conserved hypothetical protein	conserved hypothetical protein
PMM0314	2	-1.63	0.35	0.25	0.01	Photosystem II	Photosystem II PsbT protein
PMM0315	2	-1.13	0.30	0.21	0.96	Photosystem II	Photosystem II PsbB protein (CP47)
PMM0316	2	0.89	0.80	0.57	0.99	Soluble electron carriers	possible ferredoxin
PMM0317	2	-1.40	2.09	1.48	0.00	Photosystem II	possible Photosystem II reaction center M protein (PsbM)
PMM0318	2	-0.98	1.65	1.17	0.03	Cobalamin, heme, phycobilin and porphyrin	putative protein methyltransferase
PMM0321	2	0.28	0.31	0.22	1.00	Cell division	putative septum site-determining protein MinD
PMM0324	2	-0.14	0.98	0.69	1.00	Detoxification	PDZ domain (also known as DHR or GLGF):Tail specific protease...
PMM0325	2	-0.41	0.72	0.51	0.88	Cytochrome b6/f complex	Cytochrome b6
PMM0326	2	0.62	0.76	0.54	0.97	Cytochrome b6/f complex	PetD protein (subunit IV of the Cytochrome b6f complex)
PMM0327	2	-0.43	0.08	0.06	0.51	Other	putative neutral invertase-like protein
PMM0328	2	-0.86	0.20	0.14	0.42	DNA replication, recombination, and repair	Formamidopyrimidine-DNA glycolase (FAPY-DNA glycolase)
PMM0329	2	-2.52	0.13	0.09	0.00	Photosystem I	Photosystem I PsaE protein (subunit IV)
PMM0333	2	0.16	0.60	0.42	0.79	Other	GCN5-related N-acetyltransferase
PMM0334	2	4.37	0.06	0.04	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0336	2	2.32	0.38	0.27	0.00	Conserved hypothetical protein	conserved hypothetical
PMM0337	2	8.66	0.91	0.64	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0338	2	0.42	2.04	1.44	1.00	Conserved hypothetical protein	conserved hypothetical
PMM0339	2	1.25	0.88	0.62	0.63	Carotenoid	Bacterial-type phytoene dehydrogenase
PMM0341	2	2.10	0.55	0.39	0.01	Conserved hypothetical protein	conserved hypothetical
PMM0342	2	1.61	0.48	0.34	0.12	Other	possible Helper component proteinase
PMM0343	2	1.49	1.27	0.90	0.20	Other	mttA/Hcf106 family
PMM0345	2	-0.84	0.07	0.05	0.29	Transport and binding proteins	putative bacterioferritin comigratory protein
PMM0346	2	-4.87	1.50	1.06	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0347	2	-0.58	0.37	0.26	0.52	Conserved hypothetical protein	conserved hypothetical
PMM0348	2	-2.28	0.25	0.18	0.05	Other	possible Spectrin repeat
PMM0350	2	-0.67	0.53	0.38	1.00	Regulatory functions	possible TIR domain
PMM0351	2	Inf	NA	NA	0.22	Cobalamin, heme, phycobilin and porphyrin	possible Small, acid-soluble spore proteins, a
PMM0356	2	-1.54	0.83	0.59	0.11	Fatty acid, phospholipid and sterol metabolism	Alpha/beta hydrolase fold:Esterase/lipase/thioesterase family...
PMM0363	2	1.46	0.07	0.05	0.22	Regulatory functions	possible MarR family
PMM0364	2	3.43	0.56	0.39	0.00	Other	possible Malic enzyme
PMM0365	2	4.49	0.36	0.26	0.00	Other	possible DsrE-like protein
PMM0366	2	1.17	0.09	0.07	0.39	Transport and binding proteins	Type-1 copper (blue) domain
PMM0367	2	1.30	0.97	0.68	0.74	Conserved hypothetical protein	conserved hypothetical protein
PMM0368	2	2.72	1.12	0.79	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0370	2	3.85	0.60	0.42	0.00	Transport and binding proteins	putative cyanate ABC transporter, substrate binding protein
PMM0371	2	0.52	0.67	0.47	0.69	Transport and binding proteins	putative cyanate ABC transporter
PMM0373	2	1.71	0.48	0.34	0.22	Other	Cyanate lyase
PMM0374	2	1.55	1.44	1.02	0.43	Other	mttA/Hcf106 family
PMM0377	2	1.81	0.00	0.00	0.06	Conserved hypothetical protein	hypothetical
PMM0378	2	2.07	1.02	0.72	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM0379	2	-0.31	1.17	0.83	0.87	Conserved hypothetical protein	hypothetical
PMM0383	2	1.86	0.29	0.20	0.17	Transport and binding proteins	probable periplasmic protein
PMM0388	2	0.32	1.33	0.94	1.00	Chemotaxis	putative similar to tRNA-(MS[2]IO[6]A)-hydroxylase
PMM0395	2	1.05	0.97	0.69	0.90	Conserved hypothetical protein	conserved hypothetical protein
PMM0400	2	-0.86	0.67	0.47	0.48	Adaptations and atypical conditions	light repressed protein A homolog
PMM0403	2	-0.02	0.70	0.50	0.70	Conserved hypothetical protein	conserved hypothetical protein
PMM0405	2	-0.15	0.36	0.26	0.66	Transport and binding proteins	Dihydrolipoamide acetyltransferase component (E2) of pyruvate de
PMM0407	2	0.01	0.49	0.35	0.87	Serine family / Sulfur assimilation	O-acetylserine (thiol)-lyase A
PMM0410	2	-2.04	0.69	0.49	0.00	Ribosomal proteins	30S ribosomal protein S4
PMM0411	2	0.75	0.21	0.15	0.75	Conserved hypothetical protein	conserved hypothetical protein
PMM0412	2	1.30	0.07	0.05	0.28	Conserved hypothetical protein	conserved hypothetical protein
PMM0416	2	-1.60	0.14	0.10	0.02	RNA synthesis, modification, and DNA transcription	SAM (and some other nucleotide) binding motif:Generic methyl-...
PMM0417	2	-0.42	0.59	0.42	0.71	Conserved hypothetical protein	hypothetical
PMM0418	2	0.70	1.72	1.22	0.33	Other	NifU-like protein
PMM0428	2	-1.92	0.78	0.56	0.00	Cobalamin, heme, phycobilin and porphyrin	chlorophyll synthase 33 kD subunit
PMM0429	2	-2.60	0.53	0.38	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0435	2	-0.26	0.18	0.12	0.59	NADH dehydrogenase	putative NADH dehydrogenase (complex I) subunit (chain 2)
PMM0436	2	0.95	0.65	0.46	1.00	DNA replication, recombination, and repair	Prokaryotic DNA topoisomerase
PMM0441	2	1.07	0.92	0.65	0.40	Other	Aldo/keto reductase family
PMM0443	2	0.90	1.06	0.75	0.56	Conserved hypothetical protein	conserved hypothetical protein
PMM0445	2	0.89	0.00	0.00	0.96	Respiratory terminal oxidases	Cytochrome c oxidase, subunit I
PMM0446	2	2.49	0.60	0.43	0.00	Respiratory terminal oxidases	putative cytochrome c oxidase, subunit 2
PMM0447	2	4.49	0.09	0.06	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0448	2	0.26	0.87	0.62	0.66	Cobalamin, heme, phycobilin and porphyrin	putative protoheme IX farnesyltransferase
PMM0451	2	2.23	0.85	0.60	0.00	Other	possible Arenavirus glycoprotein
PMM0452	2	-2.16	0.75	0.53	0.00	Chaperones	GroEL2 protein (Chaperonin cpn60 2)
PMM0453	2	-4.26	1.63	1.15	0.00	Fatty acid, phospholipid and sterol metabolism	3-oxoacyl-[acyl-carrier protein] reductase
PMM0461	2	0.00	0.45	0.32	0.76	Cytochrome b6/f complex	Cytochrome f
PMM0462	2	-0.94	0.26	0.18	0.15	Cytochrome b6/f complex	Rieske iron-sulfur protein
PMM0465	2	0.10	0.30	0.21	0.84	Conserved hypothetical protein	hypothetical
PMM0468	2	-3.46	1.84	1.30	0.00	Photosystem I	Photosystem I PsaJ protein (subunit IX)
PMM0469	2	-2.40	0.57	0.40	0.00	Photosystem I	Photosystem I PsaF protein (subunit III)
PMM0470	2	-0.31	0.10	0.07	0.64	Other	probable o-sialoglycoprotein endopeptidase

PMM0471	2	-0.85	0.35	0.25	0.39	Adaptations and atypical conditions	possible high light inducible protein
PMM0472	2	-0.12	0.67	0.48	0.75	Transport and binding proteins	putative Na+/H+ antiporter, CPA1 family
PMM0473	2	-0.48	0.04	0.03	0.55	Aminoacyl tRNA synthetases and tRNA modification	Glutamyl-tRNA synthetase
PMM0474	2	-1.19	0.30	0.21	0.22	Conserved hypothetical protein	Conserved hypothetical protein
PMM0475	2	-1.10	0.14	0.10	0.08	Ribosomal proteins	Ribosomal protein L19
PMM0476	2	-1.15	0.85	0.60	0.40	Conserved hypothetical protein	conserved hypothetical protein
PMM0477	2	-0.42	0.39	0.27	0.90	Protein modification and translation factors	putative methionine aminopeptidase
PMM0478	2	-4.19	0.45	0.32	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0479	2	-0.28	1.31	0.92	0.57	Conserved hypothetical protein	conserved hypothetical protein
PMM0480	2	2.40	0.74	0.52	0.01	Conserved hypothetical protein	conserved hypothetical protein
PMM0481	2	-0.92	0.02	0.01	0.39	Conserved hypothetical protein	conserved hypothetical protein
PMM0482	2	1.62	1.26	0.89	0.36	Other	Band 7 protein
PMM0483	2	-0.60	0.41	0.29	0.37	Cobalamin, heme, phycobilin and porphyrin	glutamate-1-semialdehyde 2,1-aminomutase
PMM0485	2	NA	NA	NA	0.95	Conserved hypothetical protein	conserved hypothetical protein
PMM0491	2	3.43	1.29	0.91	0.00	Other	4a-hydroxytetrahydrobiopterin dehydratase (PCD)
PMM0492	2	-2.45	1.34	0.94	0.02	Conserved hypothetical protein	conserved hypothetical protein
PMM0493	2	-0.16	1.90	1.34	0.44	Other	Carboxypeptidase Taq (M32) metallopeptidase
PMM0494	2	-1.78	0.31	0.22	0.03	Phosphorus compounds	putative inorganic pyrophosphatase
PMM0495	2	0.59	1.73	1.22	1.00	Cobalamin, heme, phycobilin and porphyrin	Porphobilinogen deaminase
PMM0496	2	-0.15	0.09	0.07	0.64	RNA synthesis, modification, and DNA transcription	Putative principal RNA polymerase sigma factor
PMM0500	2	-0.25	1.12	0.79	0.50	Conserved hypothetical protein	conserved hypothetical protein
PMM0501	2	-0.96	1.14	0.81	0.96	Conserved hypothetical protein	conserved hypothetical protein
PMM0502	2	2.45	0.07	0.05	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0503	2	-1.94	1.91	1.35	0.22	Cobalamin, heme, phycobilin and porphyrin	possible precorrin-6X reductase
PMM0506	2	0.07	1.07	0.75	0.73	Purine ribonucleotide biosynthesis	Adenylosuccinate synthetase
PMM0507	2	0.90	1.01	0.71	1.00	Photosystem II	possible Photosystem II reaction center Psb27 protein
PMM0508	2	-0.61	0.34	0.24	0.54	Aminoacyl tRNA synthetases and tRNA modification	Prolyl-tRNA synthetase
PMM0510	2	-1.85	0.08	0.06	0.00	Transposon-related functions	possible Reverse transcriptase (RNA-dependent
PMM0511	2	-1.76	0.27	0.19	0.01	Other	Inorganic pyrophosphatase
PMM0515	2	-0.56	0.52	0.37	0.56	Cobalamin, heme, phycobilin and porphyrin	possible alpha-ribazole-5'-P phosphatase
PMM0519	2	1.76	0.38	0.27	0.12	Other	Transaldolase
PMM0520	2	-1.27	1.17	0.82	0.13	Other	NAD binding site
PMM0522	2	-0.84	0.74	0.52	0.28	Pyrimidine ribonucleotide biosynthesis	uridylate kinase
PMM0525	2	-1.01	1.62	1.14	0.09	Other	Ferrochelatase
PMM0526	2	0.36	0.24	0.17	0.78	Branched chain family	Acetolactate synthase large subunit
PMM0530	2	0.23	0.88	0.62	0.76	Ribosomal proteins	30S ribosomal protein S1 homolog B, putative Nbp1
PMM0532	2	0.72	1.20	0.85	0.55	Conserved hypothetical protein	conserved hypothetical protein
PMM0533	2	-0.73	0.69	0.49	0.42	Conserved hypothetical protein	conserved hypothetical protein
PMM0534	2	-1.66	1.53	1.08	0.05	Fatty acid, phospholipid and sterol metabolism	acetyl-CoA carboxylase, alpha subunit
PMM0536	2	-1.40	1.02	0.72	0.18	Folic acid	putative GTP cyclohydrolase I
PMM0537	2	0.07	0.17	0.12	0.92	Aromatic amino acid family	phosphoribosylanthranilate isomerase
PMM0540	2	-3.39	1.74	1.23	0.00	Photosystem I	possible photosystem I reaction centre subunit XII (PsaM)
PMM0541	2	0.38	0.04	0.03	0.91	Conserved hypothetical protein	conserved hypothetical protein
PMM0543	2	-0.15	0.23	0.16	0.86	Cobalamin, heme, phycobilin and porphyrin	Protochlorophyllide reductase iron-sulfur ATP-binding protein
PMM0544	2	0.48	0.72	0.51	0.81	Cobalamin, heme, phycobilin and porphyrin	Light-independent protochlorophyllide reductase subunit B
PMM0545	2	-0.29	0.05	0.03	1.00	Cobalamin, heme, phycobilin and porphyrin	Light-independent protochlorophyllide reductase subunit N
PMM0546	2	0.33	0.05	0.04	1.00	Conserved hypothetical protein	conserved hypothetical
PMM0548	2	0.39	0.42	0.30	1.00	Other	HAM1 family protein
PMM0549	2	-2.81	0.36	0.26	0.00	CO2 fixation	carboxysome shell protein CsoS1
PMM0550	2	-1.48	0.20	0.14	0.01	CO2 fixation	Ribulose bisphosphate carboxylase, large chain
PMM0551	2	-1.09	0.63	0.45	0.24	CO2 fixation	Ribulose bisphosphate carboxylase, small chain
PMM0552	2	-1.98	0.37	0.26	0.00	CO2 fixation	carboxysome shell protein CsoS2
PMM0554	2	-0.03	0.63	0.44	0.76	CO2 fixation	putative carboxysome peptide A
PMM0555	2	-0.13	0.46	0.32	0.70	CO2 fixation	putative carboxysome peptide B
PMM0556	2	Inf	NA	NA	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0557	2	-1.75	0.03	0.02	0.03	Conserved hypothetical protein	conserved hypothetical
PMM0558	2	1.33	1.00	0.71	0.30	Conserved hypothetical protein	conserved hypothetical protein
PMM0560	2	-0.82	0.49	0.34	0.26	Other	possible ATP phosphoribosyltransferase
PMM0561	2	-0.69	1.18	0.83	0.35	Transport and binding proteins	putative multidrug efflux ABC transporter
PMM0564	2	-0.50	0.42	0.30	0.56	Conserved hypothetical protein	conserved hypothetical protein
PMM0565	2	1.90	0.49	0.34	0.07	DNA replication, recombination, and repair	chromosomal replication initiator protein DnaA
PMM0570	2	1.19	0.09	0.07	0.48	NADH dehydrogenase	NADH dehydrogenase subunit NdhL (ndhL)
PMM0571	2	3.04	2.01	1.42	0.03	Conserved hypothetical protein	conserved hypothetical protein
PMM0573	2	-0.59	0.28	0.20	0.45	Conserved hypothetical protein	conserved hypothetical protein
PMM0574	2	0.10	0.79	0.56	0.77	Conserved hypothetical protein	conserved hypothetical protein
PMM0577	2	-0.12	0.52	0.37	0.83	RNA synthesis, modification, and DNA transcription	Putative type II alternative sigma factor, sigma70 family
PMM0579	2	1.20	0.84	0.59	0.67	Conserved hypothetical protein	conserved hypothetical protein
PMM0580	2	-0.41	1.22	0.87	0.48	Degradation of proteins, peptides, and glycopeptides	ATP-dependent Clp protease, Hsp 100, ATP-binding subunit ClpB
PMM0581	2	-0.59	1.36	0.96	0.97	Soluble electron carriers	plastocyanin
PMM0583	2	-3.46	0.65	0.46	0.00	Cobalamin, heme, phycobilin and porphyrin	Uroporphyrinogen decarboxylase (URO-D)
PMM0586	2	-0.02	0.84	0.60	0.82	Conserved hypothetical protein	conserved hypothetical
PMM0593	2	0.17	0.29	0.21	1.00	Other	Peptidase family M3
PMM0594	2	-0.21	0.62	0.44	0.65	NADH dehydrogenase	putative NADH Dehydrogenase (complex I) subunit (chain 4)
PMM0595	2	0.87	0.36	0.25	0.64	Aspartate family	Homoserine kinase:GHMP kinases putative ATP-binding domain
PMM0599	2	-3.19	0.74	0.53	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0601	2	-0.70	0.62	0.44	0.45	Transport and binding proteins	ABC transporter, substrate binding protein, possibly Mn
PMM0603	2	-1.08	0.11	0.08	0.29	Transport and binding proteins	ABC transporter component, possibly Mn transport
PMM0605	2	-3.78	1.23	0.87	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0609	2	0.22	0.57	0.40	0.86	Polysaccharides and glycoproteins	Putative ADPglucose--glucosyltransferase (GlgA)
PMM0613	2	-0.17	0.36	0.26	0.73	Aromatic amino acid family	EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
PMM0614	2	-2.22	0.60	0.42	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0615	2	-0.06	0.22	0.16	0.73	Other	Possible nitrilase
PMM0618	2	1.40	1.57	1.11	0.39	Carotenoid	polyprenyl synthetase; solanesyl diphosphate synthase (sds)
PMM0619	2	0.80	0.24	0.17	0.94	Pyruvate and acetyl-CoA metabolism	acetyl-coenzyme A synthetase
PMM0622	2	-0.12	1.22	0.86	0.67	Conserved hypothetical protein	conserved hypothetical protein
PMM0626	2	2.23	1.07	0.75	0.08	Conserved hypothetical protein	hypothetical
PMM0627	2	-1.00	0.53	0.38	0.94	Photosystem II	light-harvesting complex protein
PMM0628	2	0.68	0.58	0.41	1.00	Transport and binding proteins	possible sodium:solute symporter, ESS family
PMM0629	2	-0.78	0.81	0.58	0.27	Conserved hypothetical protein	conserved hypothetical protein
PMM0633	2	-2.08	2.45	1.73	0.00	Carotenoid	putative lycopene epsilon cyclase
PMM0637	2	-0.11	0.72	0.51	0.68	Regulatory functions	Ferric uptake regulator family
PMM0638	2	-1.10	0.68	0.48	0.36	Conserved hypothetical protein	conserved hypothetical protein
PMM0641	2	-0.86	0.64	0.45	0.19	Conserved hypothetical protein	conserved hypothetical protein
PMM0642	2	-0.82	0.26	0.18	0.42	Serine family / Sulfur assimilation	putative O-Acetyl homoserine sulfhydrylase
PMM0647	2	2.58	1.23	0.87	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0649	2	-2.37	0.25	0.18	0.00	Other	Pentapeptide repeats
PMM0651	2	0.04	0.38	0.27	0.75	Regulatory functions	possible VHS domain
PMM0652	2	-1.06	0.17	0.12	0.30	RNA synthesis, modification, and DNA transcription	possible 5'-3' exonuclease, C-terminal SAM fol
PMM0658	2	-1.28	1.48	1.05	0.56	Aminoacyl tRNA synthetases and tRNA modification	putative pseudouridylate synthase specific to ribosomal small subunit
PMM0659	2	-0.82	1.95	1.38	0.04	DNA replication, recombination, and repair	NAD-dependent DNA ligase N-terminus
PMM0660	2	0.46	1.77	1.25	0.82	Degradation of RNA	possible RNA recognition motif. (a.k.a. RRM, R
PMM0661	2	1.76	0.08	0.05	0.14	Purine ribonucleotide biosynthesis	ribonucleotide reductase (Class II)
PMM0664	2	0.08	0.93	0.66	0.77	Conserved hypothetical protein	conserved hypothetical protein
PMM0665	2	0.24	0.84	0.59	0.83	Other	Hsp33 protein
PMM0667	2	2.73	0.95	0.67	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0674	2	-0.16	0.92	0.65	0.65	Aspartate family	Aminotransferases class-I
PMM0681	2	1.66	0.37	0.26	0.10	Conserved hypothetical protein	conserved hypothetical protein
PMM0683	2	1.20	0.51	0.36	0.42	Purine ribonucleotide biosynthesis	phosphoribosylaminoimidazole carboxylase
PMM0684	2	2.77	0.22	0.16	0.01	Regulatory functions	possible Zinc finger, C2H2 type
PMM0685	2	3.20	0.55	0.39	0.00	Conserved hypothetical protein	hypothetical protein
PMM0687	2	2.70	2.03	1.43	0.01	Conserved hypothetical protein	conserved hypothetical
PMM0688	2	1.48	1.97	1.39	0.53	Protein modification and translation factors	possible Elongation factor Tu domain 2
PMM0689	2	4.28	1.87	1.32	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM0690	2	Inf	NA	NA	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM0691	2	0.23	3.69	2.61	0.21	Conserved hypothetical protein	conserved hypothetical protein
PMM0692	2	-0.85	0.06	0.04	1.00	Regulatory functions	possible DDT domain
PMM0693	2	-0.15	0.51	0.36	0.73	Other	possible Hepatitis C virus envelope glycoprote
PMM0697	2	#NAME?	NA	NA	1.00	DNA replication, recombination, and repair	possible D12 class N6 adenine-specific DNA met

PMM0698	2	0.69	0.64	0.45	0.71	Chaperones	possible DnaJ central domain (4 repeats)
PMM0699	2	-4.82	0.86	0.61	0.00	Conserved hypothetical protein	conserved hypothetical
PMM0700	2	-0.90	0.49	0.34	0.85	Conserved hypothetical protein	conserved hypothetical protein
PMM0703	2	1.18	1.07	0.75	0.33	Conserved hypothetical protein	conserved hypothetical protein
PMM0704	2	0.80	1.06	0.75	0.50	Regulatory functions	putative potassium channel, VIC family
PMM0705	2	1.30	1.77	1.25	0.47	Regulatory functions	two-component response regulator, phosphate
PMM0707	2	0.22	0.38	0.27	1.00	Other	possible Lipoprotein
PMM0708	2	1.56	0.48	0.34	0.25	Regulatory functions	putative secreted protein
PMM0709	2	0.63	0.01	0.01	0.92	Membranes, lipoproteins and porins	possible porin
PMM0710	2	-3.05	0.17	0.12	0.00	Transport and binding proteins	ABC transporter, substrate binding protein, phosphate
PMM0714	2	Inf	NA	NA	0.87	Regulatory functions	Bacterial regulatory proteins, ArsR family
PMM0717	2	-1.20	0.63	0.45	0.19	Conserved hypothetical protein	conserved hypothetical protein
PMM0719	2	-0.87	1.68	1.19	0.80	Conserved hypothetical protein	hypothetical
PMM0722	2	-0.80	0.14	0.10	1.00	Conserved hypothetical protein	hypothetical
PMM0725	2	0.13	0.97	0.68	0.75	Transport and binding proteins	putative phosphate ABC transporter, ATP binding subunit
PMM0726	2	2.25	1.36	0.96	0.06	Conserved hypothetical protein	hypothetical
PMM0732	2	-0.23	1.11	0.78	0.79	Other	possible Major surface glycoprotein
PMM0736	2	0.20	0.31	0.22	0.99	Other	possible Alpha-2-macroglobulin family N-termin
PMM0739	2	0.53	0.32	0.23	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0740	2	-0.29	0.13	0.09	0.56	Cytochrome b6/f complex	Cytochrome b6-f complex subunit VIII
PMM0741	2	-0.74	0.04	0.03	0.45	Conserved hypothetical protein	conserved hypothetical protein
PMM0742	2	1.04	0.18	0.13	0.71	Degradation of proteins, peptides, and glycopeptides	Clp protease subunit
PMM0743	2	-0.02	0.26	0.18	0.71	Cell division	FtsH ATP-dependent protease homolog
PMM0744	2	-1.52	0.15	0.11	0.24	Conserved hypothetical protein	conserved hypothetical protein
PMM0747	2	-3.03	1.73	1.22	0.00	Cobalamin, heme, phycobilin and porphyrin	ferredoxin-dependent biliverdin reductase
PMM0751	2	-2.72	0.08	0.06	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0753	2	-1.29	0.28	0.20	0.04	Ribosomal proteins	30S ribosomal protein S2
PMM0754	2	-2.94	1.63	1.15	0.00	Protein modification and translation factors	putative Elongation factor Ts
PMM0758	2	1.04	1.27	0.90	0.56	Serine family / Sulfur assimilation	Ferredoxin-sulfite reductase
PMM0760	2	-0.59	0.17	0.12	0.50	Cobalamin, heme, phycobilin and porphyrin	Aromatic-ring hydroxylase (flavoprotein monooxygenase)
PMM0762	2	-0.46	0.51	0.36	0.60	Aromatic amino acid family	tyrosine binding protein
PMM0766	2	-1.92	1.09	0.77	0.00	Other	Ribulose-phosphate 3-epimerase
PMM0767	2	-1.20	0.44	0.31	0.04	Surface polysaccharides, lipopolysaccharides and antigens	Fructose-1,6-bisphosphatase/sedoheptulose-1,7-bis phosphatase
PMM0769	2	-1.61	0.44	0.31	0.00	Other	ADP-glucose pyrophosphorylase
PMM0770	2	2.53	1.04	0.74	0.00	Pentose phosphate pathway	6-phosphogluconate dehydrogenase
PMM0772	2	-0.52	1.14	0.80	0.70	Conserved hypothetical protein	conserved hypothetical protein
PMM0774	2	1.25	0.34	0.24	0.44	Branched chain family	Dihydroxy-acid dehydratase
PMM0775	2	-1.95	1.96	1.38	0.30	Conserved hypothetical protein	conserved hypothetical
PMM0777	2	0.55	1.16	0.82	0.85	Conserved hypothetical protein	conserved hypothetical protein
PMM0779	2	1.03	0.61	0.43	0.80	Conserved hypothetical protein	conserved hypothetical protein
PMM0781	2	-1.55	0.45	0.32	0.01	Fatty acid, phospholipid and sterol metabolism	Fructose-bisphosphate/sedoheptulose-1,7-bisphosph ate aldolase
PMM0784	2	-1.99	0.82	0.58	0.00	Fatty acid, phospholipid and sterol metabolism	acetyl-CoA carboxylase, beta subunit
PMM0785	2	-3.91	1.09	0.77	0.00	CO2 fixation	phosphoribulokinase
PMM0790	2	1.21	0.10	0.07	0.35	Conserved hypothetical protein	conserved hypothetical protein
PMM0794	2	0.11	0.18	0.13	0.82	Conserved hypothetical protein	conserved hypothetical protein
PMM0797	2	-2.25	0.92	0.65	0.00	Nucleoproteins	possible mRNA binding protein
PMM0799	2	-2.18	1.81	1.28	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0800	2	0.63	1.46	1.03	0.64	Conserved hypothetical protein	conserved hypothetical protein
PMM0801	2	-1.39	0.62	0.44	0.10	Conserved hypothetical protein	conserved hypothetical protein
PMM0802	2	0.97	1.80	1.27	1.00	DNA replication, recombination, and repair	putative endonuclease
PMM0804	2	1.95	0.54	0.38	0.23	Other	ferritin
PMM0806	2	1.36	0.49	0.35	0.38	Regulatory functions	Bacterial regulatory proteins, Crp family
PMM0810	2	1.79	0.81	0.57	0.01	Conserved hypothetical protein	hypothetical
PMM0812	2	1.85	4.26	3.01	0.73	Conserved hypothetical protein	hypothetical
PMM0814	2	-1.40	0.13	0.09	0.04	Other	possible Cytochrome oxidase c subunit VIb
PMM0815	2	4.86	0.76	0.53	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM0816	2	4.64	1.86	1.32	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM0817	2	3.14	0.62	0.44	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM0818	2	2.92	0.78	0.55	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM0819	2	2.83	0.74	0.52	0.00	Conserved hypothetical protein	hypothetical
PMM0820	2	#NAME?	NA	NA	0.00	Aromatic amino acid family	possible EPSP synthase (3-phosphoshikimate 1-c
PMM0821	2	0.61	0.49	0.35	0.97	Conserved hypothetical protein	conserved hypothetical protein
PMM0824	2	0.52	0.03	0.02	0.99	Conserved hypothetical protein	conserved hypothetical protein
PMM0828	2	0.87	0.28	0.20	0.10	Other	S4 domain
PMM0829	2	0.69	0.64	0.46	0.94	Other	Triosephosphate isomerase
PMM0835	2	-0.96	0.93	0.66	0.48	Conserved hypothetical protein	conserved hypothetical protein
PMM0844	2	-1.58	0.41	0.29	0.07	Adaptations and atypical conditions	phytochrome-regulated gene
PMM0845	2	0.90	0.02	0.01	0.53	Conserved hypothetical protein	conserved hypothetical protein
PMM0846	2	0.43	0.52	0.37	1.00	Other	possible Uncharacterized secreted proteins, Ya
PMM0847	2	-0.03	1.46	1.03	0.98	Drug and analog sensitivity	putative acetazolamide conferring resistance protein Zam
PMM0851	2	-0.54	1.22	0.86	0.26	Other	Putative CbbY homolog
PMM0852	2	2.60	1.49	1.05	0.01	Conserved hypothetical protein	conserved hypothetical protein
PMM0853	2	-0.39	1.76	1.24	0.56	Ribosomal proteins	50S ribosomal protein L32
PMM0856	2	-0.27	0.30	0.21	0.91	Detoxification	thioredoxin peroxidase
PMM0857	2	-2.45	0.26	0.19	0.00	Other	possible Influenza RNA-dependent RNA polymeras
PMM0858	2	2.89	0.21	0.15	0.00	Conserved hypothetical protein	hypothetical
PMM0861	2	-1.21	0.09	0.06	1.00	Transport and binding proteins	possible Virion host shutoff protein
PMM0863	2	-0.20	1.01	0.71	0.70	Cobalamin, heme, phycobilin and porphyrin	putative cobinamide kinase
PMM0864	2	-1.70	1.77	1.25	0.04	Other	possible Fusion glycoprotein F0.
PMM0867	2	-0.48	0.82	0.58	0.64	Aminoacyl tRNA synthetases and tRNA modification	Methionyl-tRNA synthetase
PMM0869	2	-2.25	1.41	0.99	0.00	Ribosomal proteins	30S Ribosomal protein S18
PMM0870	2	-2.68	1.09	0.77	0.00	Ribosomal proteins	50S Ribosomal protein L33
PMM0872	2	-0.65	0.11	0.08	0.63	Other	possible Carboxylesterase
PMM0876	2	-3.82	3.57	2.52	0.01	Conserved hypothetical protein	conserved hypothetical
PMM0878	2	-1.03	0.69	0.49	0.42	Branched chain family	putative Branched-chain amino acid aminotransferase
PMM0881	2	0.28	2.45	1.74	0.64	Conserved hypothetical protein	conserved hypothetical protein
PMM0883	2	0.64	0.37	0.26	0.95	Conserved hypothetical protein	conserved hypothetical protein
PMM0893	2	-0.71	0.49	0.35	0.46	Riboflavin	possible GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase
PMM0894	2	-0.87	0.02	0.01	0.22	Protein modification and translation factors	Cyclophilin-type peptidyl-prolyl cis-trans isomerase
PMM0895	2	#NAME?	NA	NA	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0896	2	1.03	1.73	1.22	1.00	Chaperones	DnaJ2 protein
PMM0897	2	0.59	0.22	0.15	1.00	Chaperones	Molecular chaperone DnaK, heat shock protein hsp70
PMM0898	2	-0.35	0.96	0.68	0.71	Soluble electron carriers	ferredoxin, petF-like protein
PMM0899	2	1.39	0.34	0.24	0.23	Regulatory functions	Possible myo-inositol-1(or 4)-monophosphatase
PMM0901	2	-2.15	1.13	0.80	0.00	Chaperones	heat shock protein HtpG
PMM0902	2	-1.17	0.03	0.02	0.19	Ribosomal proteins	50S ribosomal protein L28
PMM0906	2	-0.14	2.19	1.55	0.46	Photosystem I	Photosystem I PsaK protein (subunit X)
PMM0907	2	-0.98	0.26	0.19	0.26	Sugars	1-deoxy-D-xylulose 5-phosphate synthase
PMM0910	2	1.74	1.17	0.83	0.20	Conserved hypothetical protein	conserved hypothetical membrane protein
PMM0912	2	0.16	0.64	0.45	0.76	Other	Pyruvate kinase
PMM0913	2	1.06	0.06	0.04	0.45	Transport and binding proteins	possible ABC transporter
PMM0919	2	0.50	0.12	0.09	0.88	Branched chain family	serine:pyruvate/alanine:glyoxylate aminotransferase
PMM0920	2	2.85	0.14	0.10	0.00	Glutamate family / Nitrogen assimilation	Glutamine synthetase, glutamate--ammonia ligase
PMM0922	2	0.42	0.56	0.40	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0923	2	-4.63	2.06	1.46	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0926	2	-1.68	0.28	0.20	0.02	Photosystem II	possible Photosystem II reaction center Psb28 protein
PMM0930	2	-0.98	0.18	0.13	0.27	Other	Pyruvate dehydrogenase E1 beta subunit
PMM0934	2	-0.25	0.52	0.36	0.94	Conserved hypothetical protein	conserved hypothetical protein
PMM0936	2	0.36	0.65	0.46	1.00	DNA replication, recombination, and repair	putative SOS mutagenesis protein UmuD
PMM0941	2	0.66	0.41	0.29	0.91	Other	possible cAMP phosphodiesterases class-II
PMM0942	2	0.93	0.45	0.32	0.69	DNA replication, recombination, and repair	putative holliday junction DNA helicase RuvA
PMM0943	2	-2.32	1.41	1.00	0.04	Ribosomal proteins	30S Ribosomal protein S15
PMM0946	2	-0.09	0.08	0.06	0.73	Aminoacyl tRNA synthetases and tRNA modification	Glutamyl-tRNA(Gln) amidotransferase A subunit
PMM0947	2	-1.49	0.14	0.10	0.27	Conserved hypothetical protein	conserved hypothetical protein
PMM0949	2	0.68	2.01	1.42	0.76	Conserved hypothetical protein	conserved hypothetical protein
PMM0950	2	-0.23	1.15	0.81	0.51	Other	No Cyanobase Name
PMM0953	2	1.21	0.72	0.51	0.49	Conserved hypothetical protein	conserved hypothetical protein
PMM0954	2	0.29	0.14	0.10	0.82	Transport and binding proteins	ABC transporter, multidrug efflux family

PMM0955	2	1.47	0.20	0.14	0.21	Protein modification and translation factors	Peptide methionine sulfoxide reductase
PMM0957	2	1.25	0.56	0.39	0.27	Regulatory functions	possible GRAM domain
PMM0958	2	0.80	0.91	0.64	0.53	Conserved hypothetical protein	conserved hypothetical
PMM0963	2	1.20	0.31	0.22	0.38	Nitrogen metabolism	Urease alpha subunit
PMM0964	2	2.37	1.71	1.21	0.01	Nitrogen metabolism	Urease beta subunit
PMM0965	2	2.60	0.35	0.25	0.00	Nitrogen metabolism	Urease gamma subunit
PMM0966	2	2.36	1.39	0.98	0.02	Nitrogen metabolism	urease accessory protein UreD
PMM0969	2	1.75	1.99	1.41	0.02	Nitrogen metabolism	urease accessory protein UreG
PMM0970	2	4.07	0.46	0.33	0.00	Transport and binding proteins	putative urea ABC transporter, substrate binding protein
PMM0971	2	2.37	0.98	0.69	0.00	Transport and binding proteins	putative urea ABC transporter
PMM0974	2	0.09	0.32	0.23	0.94	Transport and binding proteins	Putative ATP-binding subunit of urea ABC transport system
PMM0975	2	1.03	1.04	0.74	0.43	Conserved hypothetical protein	conserved hypothetical protein
PMM0982	2	0.54	0.31	0.22	0.82	DNA replication, recombination, and repair	HNH endonuclease:HNH nuclease
PMM0983	2	-1.42	1.06	0.75	0.07	Fatty acid, phospholipid and sterol metabolism	possible ATP synthase protein 8
PMM0987	2	-2.96	0.20	0.14	0.00	Ribosomal proteins	30S Ribosomal protein S21
PMM0988	2	2.25	2.32	1.64	0.01	Regulatory functions	Helix-hairpin-helix DNA-binding motif class 1
PMM0993	2	-3.79	1.24	0.88	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0996	2	3.51	1.48	1.04	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM0997	2	0.45	0.14	0.10	0.83	Conserved hypothetical protein	possible Protein of unknown function DUF67
PMM0998	2	1.53	0.24	0.17	0.19	Conserved hypothetical protein	conserved hypothetical protein
PMM0999	2	-0.17	0.20	0.14	1.00	Conserved hypothetical protein	hypothetical
PMM1003	2	-1.40	0.97	0.69	0.09	Photosystem II	possible Photosystem II reaction centre N prot
PMM1005	2	0.04	0.21	0.15	0.76	Regulatory functions	possible Legume lectins alpha domain
PMM1008	2	0.68	2.18	1.54	0.90	Conserved hypothetical protein	hypothetical
PMM1011	2	#NAME?	NA	NA	0.00	Conserved hypothetical protein	hypothetical
PMM1015	2	3.02	0.58	0.41	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1026	2	0.88	0.17	0.12	0.57	Conserved hypothetical protein	conserved hypothetical protein
PMM1028	2	#NAME?	NA	NA	0.00	Conserved hypothetical protein	conserved hypothetical
PMM102a	2	0.00	1.51	1.06	0.68	Other	No Cyanobase Name
PMM1030	2	-2.50	0.96	0.68	0.00	Regulatory functions	Ferric uptake regulator family
PMM1031	2	2.96	1.18	0.83	0.00	Transport and binding proteins	ABC transporter, ATP binding domain, possibly Mn transport
PMM1032	2	3.65	0.09	0.06	0.00	Transport and binding proteins	ABC transporter, substrate binding protein, possibly Mn.
PMM1033	2	0.15	0.33	0.23	0.76	Protein modification and translation factors	Cobalamin synthesis protein/P47K
PMM1037	2	Inf	NA	NA	1.00	Conserved hypothetical protein	conserved hypothetical
PMM1039	2	-1.55	0.14	0.10	0.07	Conserved hypothetical protein	conserved hypothetical protein
PMM1042	2	-1.63	0.13	0.09	0.01	Conserved hypothetical protein	conserved hpothetical protein
PMM1045	2	0.96	0.53	0.38	1.00	Conserved hypothetical protein	conserved hypothetical
PMM1054	2	1.17	0.41	0.29	0.40	DNA replication, recombination, and repair	Crossover junction endodeoxyribonuclease RuvC
PMM1055	2	-1.42	0.41	0.29	0.10	Cobalamin, heme, phycobilin and porphyrin	Protoporphyrin IX Magnesium chelatase, ChlI subunit
PMM1058	2	0.17	0.56	0.40	0.88	Cytochrome b6/f complex	Cytochrome b6/f complex, subunit V
PMM1060	2	0.41	0.58	0.41	1.00	Other	Glutamine amidotransferase class-I
PMM1061	2	-0.26	0.69	0.49	0.88	Thiamine	Thioredoxin
PMM1063	2	0.58	1.57	1.11	0.97	DNA replication, recombination, and repair	DNA gyrase/topoisomerase IV, subunit A
PMM1066	2	0.39	0.50	0.36	0.82	Branched chain family	2-isopropylmalate synthase
PMM1067	2	0.09	0.21	0.15	0.95	WD repeat proteins	possible Adenoviral fiber protein (repeat/shaf
PMM1069	2	-2.71	1.02	0.72	0.00	Folic acid	putuative bifunctional Methylenetetrahydrofolate dehydrogenase Methenyltetrahydrofolate/cyclohydrolase
PMM1074	2	2.52	0.89	0.63	0.01	Other	Glucose-6-phosphate dehydrogenase
PMM1075	2	1.14	0.33	0.24	0.51	Cytochrome b6/f complex	ferredoxin-NADP oxidoreductase (FNR)
PMM1077	2	0.56	0.07	0.05	0.94	Regulatory functions	two-component sensor histidine kinase
PMM1078	2	0.67	0.60	0.42	0.64	Conserved hypothetical protein	conserved hypothetical
PMM1079	2	-0.37	0.51	0.36	0.48	Regulatory functions	possible Villin headpiece domain
PMM1080	2	1.11	0.91	0.64	0.35	Other	Ribose-phosphate pyrophosphokinase
PMM1086	2	0.03	0.95	0.67	0.83	Fatty acid, phospholipid and sterol metabolism	Alpha/beta hydrolase fold:Esterase/lipase/thioesterase family...
PMM1088	2	0.27	0.12	0.08	0.75	Degradation of proteins, peptides, and glycopeptides	ClpC
PMM1090	2	0.45	0.82	0.58	1.00	Branched chain family	Diaminopimelate decarboxylase
PMM1091	2	0.33	0.14	0.10	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1092	2	0.74	0.34	0.24	0.80	Other	Undecaprenyl pyrophosphate synthetase (UPPS)
PMM1098	2	0.00	0.86	0.61	0.71	Photosystem II	photosystem II oxygen evolving complex protein PsbP
PMM1107	2	-0.22	0.12	0.08	0.67	Pyridoxine	Pyridoxal phosphate biosynthetic protein PdxJ
PMM1109	2	#NAME?	NA	NA	0.12	Conserved hypothetical protein	conserved hypothetical protein
PMM1111	2	-1.13	0.30	0.21	0.40	Other	Glutaredoxin-related protein
PMM1113	2	-0.82	0.11	0.08	0.35	Regulatory functions	two-component response regulator
PMM1116	2	-1.18	0.29	0.20	0.07	Cell division	NAD binding site:Glucose inhibited division protein A family
PMM1117	2	-1.20	0.15	0.11	0.17	Photosystem II	possible Photosystem II reaction center Y protein (PsbY)
PMM1118	2	1.46	0.00	0.00	1.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1119	2	1.63	0.34	0.24	0.59	Membranes, lipoproteins and porins	possible porin
PMM1121	2	1.74	0.31	0.22	1.00	Membranes, lipoproteins and porins	possible porin
PMM1123	2	2.08	0.84	0.59	0.13	Hydrogenase	putative hydrogenase accessory protein
PMM1124	2	0.45	0.70	0.49	0.85	Other	possible Natural resistance-associated macroph
PMM1125	2	#NAME?	NA	NA	0.08	Regulatory functions	possible Bacterial regulatory proteins, deoR f
PMM1128	2	1.87	0.26	0.18	0.02	Adaptations and atypical conditions	possible high light inducible protein
PMM1129	2	1.13	0.09	0.07	0.40	Regulatory functions	possible Notch (DSL) domain
PMM1131	2	0.35	0.91	0.65	0.94	Conserved hypothetical protein	conserved hypothetical protein
PMM1132	2	1.18	0.46	0.33	0.99	Conserved hypothetical protein	conserved hypothetical protein
PMM1133	2	0.43	0.23	0.16	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1134	2	2.49	0.38	0.27	0.00	Other	possible Phosphatidylinositol-specific phospho
PMM1135	2	2.58	0.68	0.48	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1138	2	0.41	1.20	0.85	1.00	Regulatory functions	probable GTP-binding protein
PMM1139	2	0.47	1.89	1.33	1.00	Drug and analog sensitivity	possible membrane fusion protein
PMM1145	2	1.14	0.15	0.10	0.42	Respiration	putative nicotinamide nucleotide transhydrogenase, subunit beta
PMM1146	2	1.42	0.19	0.13	0.34	Nicotinate and nicotinamide	putative nicotinamide nucleotide transhydrogenase, subunit alpha 2 (A2)
PMM1147	2	1.21	0.83	0.59	0.60	DNA replication, recombination, and repair	putative nicotinamide nucleotide transhydrogenase, subunit alpha 1 (A1)
PMM1148	2	-0.66	0.85	0.60	0.29	Protein modification and translation factors	possible EF-1 guanine nucleotide exchange doma
PMM1149	2	1.55	0.42	0.30	0.24	Conserved hypothetical protein	conserved hypothetical
PMM1150	2	1.54	0.86	0.61	0.19	Regulatory functions	putative thioredoxin reductase
PMM1151	2	3.46	1.58	1.12	0.00	Protein modification and translation factors	translation initiation factor IF-1
PMM1152	2	0.47	0.12	0.09	0.94	Photosystem II	putative chaperon-like protein for quinone binding in photosystem II
PMM1152a	2	0.43	0.08	0.06	0.80	Other	No Cyanobase Name
PMM1154	2	1.98	0.33	0.23	0.01	Branched chain family	Acetolactate synthase small subunit
PMM1156	2	-1.07	0.12	0.09	0.21	Photosystem I	photosystem I assembly related protein Ycf4
PMM1157	2	2.04	1.07	0.76	0.53	Photosystem II	Photosystem II PsbD protein (D2)
PMM1158	2	1.56	0.69	0.49	1.00	Photosystem II	Photosystem II PsbC protein (CP43)
PMM1165	2	-0.11	0.39	0.27	0.77	Aminoacyl tRNA synthetases and tRNA modification	Glycyl-tRNA synthetase alpha subunit
PMM1167	2	-0.30	0.66	0.47	0.65	Other	Macrophage migration inhibitory factor family
PMM1168	2	-0.13	0.41	0.29	0.72	Conserved hypothetical protein	conserved hypothetical protein
PMM1169	2	0.83	0.93	0.65	1.00	Conserved hypothetical protein	hypothetical
PMM1170	2	-0.57	1.07	0.76	0.62	Conserved hypothetical protein	conserved hypothetical protein
PMM1171	2	-2.64	1.03	0.73	0.00	Soluble electron carriers	Flavodoxin
PMM1174	2	0.14	0.83	0.59	0.77	Conserved hypothetical protein	hypothetical
PMM1176	2	0.26	1.78	1.26	0.72	Regulatory functions	possible Helix-turn-helix protein, copG family
PMM1179	2	-0.79	0.42	0.30	0.42	Regulatory functions	putative SMR family transporter, possible pecM homologue
PMM1180	2	-0.47	1.21	0.86	0.64	Degradation of proteins, peptides, and glycopeptides	signal peptide peptidase SppA (protease IV)
PMM1183	2	-1.49	0.48	0.34	0.03	Ribosomal proteins	50S ribosomal protein L34
PMM1184	2	-0.55	1.00	0.71	0.65	Degradation of RNA	Bacterial ribonuclease P protein component
PMM1185	2	-0.32	0.65	0.46	0.57	Conserved hypothetical protein	conserved hypothetical protein
PMM1186	2	0.36	0.09	0.06	0.78	Regulatory functions	Putative inner membrane protein; similar to 60 kDa inner membrane protein family
PMM1188	2	0.27	0.05	0.04	1.00	Aminoacyl tRNA synthetases and tRNA modification	Seryl-tRNA synthetase
PMM1190	2	-1.03	0.33	0.23	0.20	Ribosomal proteins	30S Ribosomal protein S14
PMM1191	2	-1.43	0.71	0.50	0.11	RNA synthesis, modification, and DNA transcription	polyribonucleotide nucleotidyltransferase
PMM1192	2	1.40	0.20	0.14	0.24	Other	CysQ protein homolog
PMM1204	2	0.76	0.19	0.13	0.59	Surface polysaccharides, lipopolysaccharides and antigens	glucose-1-phosphate cytidylyltransferase
PMM1205	2	-0.41	0.94	0.67	0.44	Sugars	NDP-hexose 3,4-dehydratase
PMM1229	2	-0.02	0.04	0.03	0.76	Respiration	Dehydrogenase, E1 component
PMM1234	2	0.46	1.32	0.93	1.00	Hydrogenase	Zinc-containing alcohol dehydrogenase superfamily
PMM1235	2	0.26	0.46	0.32	1.00	Transport and binding proteins	possible N-terminal fragment of transketolase
PMM1240	2	-4.52	1.41	1.00	0.00	Other	methyltransferase
PMM1241	2	1.35	0.27	0.19	0.28	Conserved hypothetical protein	hypothetical protein
PMM1244	2	-0.07	0.81	0.57	0.88	Conserved hypothetical protein	hypothetical protein

PMM1245	2	0.14	0.72	0.51	0.90	Conserved hypothetical protein	conserved hypothetical protein
PMM1250	2	0.21	0.55	0.39	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1251	2	0.03	0.59	0.42	0.73	Other	Carbamoyltransferase
PMM1252	2	0.07	1.19	0.84	0.81	Other	possible acetyltransferase
PMM1257	2	-1.75	0.59	0.42	0.13	Surface polysaccharides, lipopolysaccharides and antigens	possible dTDP-glucose 4,6-dehydratase
PMM1258	2	0.56	0.05	0.04	1.00	Pyridoxine	pyridoxal-phosphate-dependent aminotransferase
PMM1259	2	1.53	0.23	0.16	0.21	Pyridoxine	pyridoxal-phosphate-dependent aminotransferase
PMM1260	2	-0.14	0.53	0.38	0.70	Transport and binding proteins	Nucleoside-diphosphate-sugar epimerase
PMM1261	2	0.24	0.64	0.45	0.77	Sugars	UDP-glucose 6-dehydrogenase
PMM1262	2	1.33	0.51	0.36	0.64	Regulatory functions	SOS function regulatory protein, LexA repressor
PMM1264	2	-0.54	0.60	0.42	0.40	Cell division	cell division protein FtsH3
PMM1267	2	0.93	3.28	2.32	1.00	Conserved hypothetical protein	conserved hypothetical
PMM1269	2	-0.14	0.22	0.16	1.00	Transport and binding proteins	predicted sugar kinase
PMM1270	2	0.04	0.62	0.44	0.76	Aminoacyl tRNA synthetases and tRNA modification	Phenylalanyl-tRNA synthetase alpha chain
PMM1272	2	0.72	0.94	0.66	0.86	Conserved hypothetical protein	conserved hypothetical protein
PMM1273	2	0.08	1.01	0.71	0.78	Riboflavin	putative riboflavin kinase/FAD synthase
PMM1275	2	-0.39	1.66	1.18	1.00	Conserved hypothetical protein	DUF170
PMM1276	2	-2.34	1.25	0.88	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1277	2	-0.32	1.22	0.87	0.56	Conserved hypothetical protein	conserved hypothetical protein
PMM1283	2	0.93	0.07	0.05	0.98	Conserved hypothetical protein	conserved hypothetical protein
PMM1284	2	1.42	1.28	0.90	0.48	Adaptations and atypical conditions	PhoH-like phosphate starvation-inducible protein
PMM1285	2	-2.85	0.24	0.17	0.00	Ribosomal proteins	30S Ribosomal protein S16
PMM1286	2	0.01	0.91	0.64	0.77	Protein and peptide secretion	signal recognition particle protein (SRP54)
PMM1287	2	-0.33	0.38	0.27	0.64	Conserved hypothetical protein	conserved hypothetical protein
PMM1288	2	-1.00	0.56	0.40	0.37	Other	Pyruvate dehydrogenase E1 alpha subunit
PMM1289	2	0.53	0.01	0.01	0.76	Transport and binding proteins	Type II alternative RNA polymerase sigma factor, sigma-70 family
PMM1293	2	0.80	0.21	0.15	1.00	Other	FKBP-type peptidyl-prolyl cis-trans isomerase (PPIase)
PMM1294	2	0.13	0.47	0.33	0.74	Hydrogenase	putative nickel-containing superoxide dismutase precursor (NISOD)
PMM1296	2	0.42	0.10	0.07	0.85	Other	marine cyanobacterial conserved hypothetical
PMM1298	2	-3.62	0.10	0.07	0.00	Regulatory functions	putative dihydrolipoamide dehydrogenase
PMM1299	2	-1.17	0.01	0.00	0.23	RNA synthesis, modification, and DNA transcription	tRNA/rRNA methyltransferase (SpoU)
PMM1300	2	0.77	0.51	0.36	0.90	Degradation of RNA	UDP-N-glucosamine 1-carboxyvinyltransferase
PMM1301	2	1.14	2.29	1.62	0.95	Glutamate family / Nitrogen assimilation	Aminotransferase class-III pyridoxal-phosphate:Acetylornithin...
PMM1304	2	0.54	0.74	0.52	1.00	Other	possible cytosine deaminase
PMM1305	2	0.46	1.15	0.81	0.81	Conserved hypothetical protein	conserved hypothetical protein
PMM1307	2	1.04	0.03	0.02	0.91	Conserved hypothetical protein	conserved hypothetical protein
PMM1309	2	0.57	0.45	0.32	1.00	Cell division	Cell division protein FtsZ:Tubulin/FtsZ family
PMM1310	2	0.77	0.20	0.14	1.00	Regulatory functions	putative Ketopantoate hydroxymethyltransferase
PMM1312	2	2.68	0.55	0.39	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1313	2	1.75	0.35	0.25	0.15	Degradation of proteins, peptides, and glycopeptides	Clp protease proteolytic subunit
PMM1314	2	2.91	0.83	0.59	0.00	Degradation of proteins, peptides, and glycopeptides	Clp protease proteolytic subunit
PMM1315	2	-0.64	0.13	0.09	0.33	Branched chain family	Ketol-acid reductoisomerase
PMM1317	2	-0.10	1.32	0.93	0.71	Adaptations and atypical conditions	possible high light inducible protein
PMM1318	2	-1.04	2.80	1.98	0.17	Conserved hypothetical protein	conserved hypothetical
PMM1319	2	0.71	0.43	0.30	0.60	Drug and analog sensitivity	possible Beta-lactamase
PMM1321	2	2.11	0.66	0.46	1.00	Nucleoproteins	Bacterial histone-like DNA-binding protein
PMM1322	2	0.95	0.79	0.56	0.97	Other	Putative isoamylase
PMM1323	2	-1.10	0.51	0.36	0.26	Regulatory functions	putative GPH family sugar transporter
PMM1324	2	1.52	0.18	0.12	0.33	Transport and binding proteins	possible transporter, membrane component
PMM1325	2	0.51	0.18	0.13	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1327	2	-0.31	0.49	0.35	0.70	Conserved hypothetical protein	conserved hypothetical protein
PMM1330	2	-0.76	0.70	0.50	0.77	Conserved hypothetical protein	conserved hypothetical protein
PMM1331	2	0.21	0.83	0.59	0.94	Conserved hypothetical protein	conserved hypothetical protein
PMM1333	2	0.83	0.37	0.26	0.64	Protein modification and translation factors	Peptide methionine sulfoxide reductase
PMM1336	2	-2.69	0.17	0.12	0.00	Fatty acid, phospholipid and sterol metabolism	Putative (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase
PMM1339	2	0.04	0.05	0.03	0.71	Purine ribonucleotide biosynthesis	SAICAR synthetase
PMM1340	2	0.47	0.28	0.20	0.94	Purine ribonucleotide biosynthesis	phosphoribosylglycinamide synthetase
PMM1342	2	0.71	0.49	0.35	0.97	Other	possible circadian clock protein KaiC
PMM1343	2	1.70	3.05	2.16	0.91	Other	possible circadian oscillation regulator KaiB
PMM1344	2	-2.28	0.70	0.50	0.00	Ribosomal proteins	50S ribosomal protein L21
PMM1345	2	-3.13	0.31	0.22	0.00	Ribosomal proteins	50S ribosomal protein L27
PMM1346	2	-1.69	1.11	0.79	0.06	Conserved hypothetical protein	conserved hypothetical protein
PMM1349	2	1.44	1.08	0.76	0.42	Conserved hypothetical protein	conserved hypothetical protein
PMM1350	2	-2.65	1.09	0.77	0.00	Other	Pentapeptide repeats
PMM1351	2	0.86	0.55	0.39	0.62	Conserved hypothetical protein	conserved hypothetical protein
PMM1352	2	1.40	0.94	0.67	1.00	Soluble electron carriers	ferredoxin
PMM1354	2	0.01	0.42	0.30	0.69	Regulatory functions	putative D-3-phosphoglycerate dehydrogenase (PGDH)
PMM1355	2	1.37	0.58	0.41	0.20	Conserved hypothetical protein	conserved hypothetical protein
PMM1363	2	1.52	0.72	0.51	0.26	Conserved hypothetical protein	hypothetical
PMM1365	2	-0.98	1.02	0.72	0.20	Regulatory functions	possible MATH domain
PMM1368	2	1.81	1.77	1.25	0.37	Conserved hypothetical protein	conserved hypothetical protein
PMM1369	2	-1.97	1.81	1.28	0.00	Regulatory functions	GAF domain
PMM1372	2	-0.72	0.27	0.19	0.44	Conserved hypothetical protein	conserved hypothetical protein
PMM1375	2	-3.67	2.45	1.73	0.00	Conserved hypothetical protein	possible M protein repeat
PMM1376	2	0.48	0.84	0.59	0.88	Nucleoproteins	RNA-binding protein RbpD
PMM1377	2	-0.13	0.06	0.04	0.76	Other	possible dihydroflavonol-4-reductase (maize, petunia, tomato)...
PMM1382	2	0.80	1.95	1.38	1.00	Fatty acid, phospholipid and sterol metabolism	fatty acid desaturase, type 2
PMM1383	2	2.42	3.23	2.29	0.01	Conserved hypothetical protein	conserved hypothetical protein
PMM1384	2	3.47	0.32	0.22	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1385	2	3.72	0.58	0.41	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1387	2	1.77	0.81	0.57	0.23	Conserved hypothetical protein	hypothetical
PMM1388	2	1.25	0.90	0.64	0.36	Conserved hypothetical protein	conserved hypothetical protein
PMM1390	2	4.81	1.26	0.89	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1391	2	2.32	1.20	0.85	0.08	Regulatory functions	possible Helix-turn-helix protein, copG family
PMM1392	2	2.70	2.08	1.47	0.01	Branched chain family	possible Heat-labile enterotoxin alpha chain
PMM1394	2	0.49	1.05	0.74	0.70	Conserved hypothetical protein	hypothetical
PMM1395	2	2.55	0.26	0.19	0.00	Conserved hypothetical protein	hypothetical
PMM1396	2	4.17	0.20	0.14	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1397	2	3.91	0.37	0.26	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1398	2	3.64	1.29	0.91	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1399	2	3.36	0.76	0.54	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1400	2	-1.38	0.14	0.10	1.00	Other	possible Hemagglutinin-neuraminidase
PMM1401	2	-1.07	0.45	0.32	0.32	Conserved hypothetical protein	conserved hypothetical
PMM1402	2	-1.70	2.20	1.55	0.00	Conserved hypothetical protein	unnamed protein product
PMM1404	2	4.57	0.20	0.14	0.00	Adaptations and atypical conditions	possible high light inducible protein
PMM1405	2	0.07	0.78	0.55	0.81	Conserved hypothetical protein	hypothetical
PMM1407	2	1.53	0.48	0.34	0.17	Other	possible SRP19 protein
PMM1408	2	0.21	0.72	0.51	0.78	Conserved hypothetical protein	hypothetical
PMM1409	2	2.23	0.98	0.69	0.05	Other	possible Rubredoxin
PMM1412	2	2.02	0.41	0.29	0.06	Conserved hypothetical protein	conserved hypothetical protein
PMM1413	2	3.52	1.24	0.88	0.00	Conserved hypothetical protein	conserved hypothetical
PMM1416	2	0.86	0.19	0.13	0.97	Conserved hypothetical protein	conserved hypothetical
PMM1419	2	-0.15	1.32	0.93	0.74	Transport and binding proteins	possible ATP synthase B/B' CF(0)
PMM1422	2	0.89	0.01	0.01	0.64	Conserved hypothetical protein	conserved hypothetical protein
PMM1423	2	1.33	0.92	0.65	0.30	Conserved hypothetical protein	conserved hypothetical protein
PMM1424	2	0.00	0.11	0.08	0.76	Other	possible Uncharacterized protein family UPF003
PMM1427	2	2.46	0.57	0.40	0.00	Conserved hypothetical protein	conserved hypothetical
PMM1428	2	-0.36	0.39	0.28	0.64	Conserved hypothetical protein	conserved hypothetical protein
PMM1429	2	1.39	1.06	0.75	0.27	Conserved hypothetical protein	conserved hypothetical protein
PMM1430	2	0.51	0.30	0.21	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1431	2	-0.07	0.35	0.25	0.70	RNA synthesis, modification, and DNA transcription	putative DNA-directed RNA polymerase (omega chain)
PMM1434	2	1.43	0.67	0.47	0.46	Glycolysis	Phosphoglycerate mutase, co-factor-independent (iPGM)
PMM1435	2	1.74	1.25	0.89	0.13	Conserved hypothetical protein	conserved hypothetical protein
PMM1436	2	-2.12	0.68	0.48	0.12	Chaperones	GroEL protein (Chaperonin cpn60)
PMM1437	2	-2.63	0.66	0.47	0.00	Chaperones	GroES protein (Chaperonin cpn10)
PMM1438	2	-3.05	0.31	0.22	0.00	ATP synthase	ATP synthase beta subunit, central region:ATP synth...
PMM1440	2	-1.60	0.17	0.12	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1441	2	NA	NA	NA	0.00	Conserved hypothetical protein	hypothetical

PMM1442	2	1.57	1.19	0.84	0.16	Regulatory functions	putative aminopeptidase P
PMM1443	2	0.35	0.60	0.42	1.00	Conserved hypothetical protein	Domain of unknown function DUF21
PMM1449	2	1.36	1.41	1.00	0.27	Soluble electron carriers	ferredoxin
PMM1451	2	-3.00	1.24	0.88	0.00	ATP synthase	ATP synthase alpha subunit, central region:ATP synth...
PMM1452	2	-5.53	0.51	0.36	0.00	ATP synthase	ATP synthase, delta (OSCP) subunit
PMM1453	2	-5.25	0.32	0.22	0.00	ATP synthase	ATP synthase B/B' CF(0)
PMM1454	2	-4.69	0.02	0.01	0.00	ATP synthase	ATP synthase B/B' CF(0)
PMM1455	2	-4.17	0.13	0.09	0.00	Membranes, lipoproteins and porins	Eubacterial and plasma membrane ATP synthase subunit C:ATP sy...
PMM1456	2	-1.49	1.43	1.01	0.04	ATP synthase	ATP synthase A subunit
PMM1457	2	-3.20	0.77	0.54	0.00	Conserved hypothetical protein	possible ATP synthase subunit 1
PMM1459	2	0.29	1.08	0.76	0.77	Regulatory functions	putative c-type cytochrome biogenesis protein CcdA
PMM1462	2	0.01	0.77	0.54	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM1463	2	0.69	0.63	0.44	0.96	Other	Nitrogen regulatory protein P-II
PMM1477	2	2.22	1.30	0.92	0.01	Conserved hypothetical protein	conserved hypothetical
PMM1478	2	0.56	0.75	0.53	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1479	2	0.26	0.01	0.01	0.85	Conserved hypothetical protein	conserved hypothetical protein
PMM1480	2	0.86	0.10	0.07	0.55	Conserved hypothetical protein	conserved hypothetical protein
PMM1482	2	-0.22	2.22	1.57	0.88	Adaptations and atypical conditions	possible high light inducible protein
PMM1483	2	-0.86	0.16	0.11	0.25	RNA synthesis, modification, and DNA transcription	RNA polymerase beta prime subunit
PMM1484	2	0.21	0.23	0.16	0.76	RNA synthesis, modification, and DNA transcription	RNA polymerase gamma subunit
PMM1485	2	-0.06	0.16	0.12	0.64	RNA synthesis, modification, and DNA transcription	RNA polymerase beta subunit
PMM1487	2	-0.34	2.20	1.56	0.68	Ribosomal proteins	30s Ribosomal protein S20
PMM1489	2	0.23	0.75	0.53	1.00	Other	Ribose 5-phosphate isomerase
PMM1490	2	2.10	0.14	0.10	0.01	Degradation of proteins, peptides, and glycopeptides	Serine proteases, trypsin family:Chymotrypsin serine protease...
PMM1492	2	-0.50	0.49	0.35	0.45	RNA synthesis, modification, and DNA transcription	N utilization substance protein A
PMM1494	2	0.26	0.27	0.19	1.00	Protein modification and translation factors	Translation initiation factor IF-2
PMM1495	2	Inf	NA	NA	0.85	Conserved hypothetical protein	hypothetical
PMM1498	2	1.00	0.49	0.34	0.65	Conserved hypothetical protein	conserved hypothetical protein
PMM1499	2	0.30	0.19	0.14	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1500	2	1.35	0.20	0.14	0.51	Regulatory functions	putative aminotransferase
PMM1501	2	0.13	0.03	0.02	0.74	Other	S1 RNA binding domain:Ribonuclease E and G
PMM1504	2	0.40	0.66	0.47	0.80	Aromatic amino acid family	Chorismate mutase-Prephenate dehydratase
PMM1506	2	-0.62	0.09	0.07	0.53	Regulatory functions	ATP-dependent protease La (LON) domain
PMM1507	2	-1.19	0.65	0.46	0.15	Ribosomal proteins	30S ribosomal protein S10
PMM1508	2	0.08	0.26	0.19	0.87	Protein modification and translation factors	Elongation factor Tu
PMM1509	2	0.55	0.37	0.26	0.93	Protein modification and translation factors	Elongation factor G
PMM1510	2	-1.26	1.24	0.87	0.10	Ribosomal proteins	30S ribosomal protein S7
PMM1511	2	-3.43	0.79	0.56	0.00	Ribosomal proteins	30S ribosomal protein S12
PMM1512	2	0.81	0.08	0.05	1.00	Glutamate family / Nitrogen assimilation	Ferredoxin-dependent glutamate synthase, Fd-GOGAT
PMM1514	2	-0.11	0.76	0.54	0.69	Other	lipoic acid synthetase
PMM1515	2	1.15	1.12	0.79	0.45	Other	Site-specific recombinase
PMM1519	2	-1.31	1.09	0.77	0.01	Photosystem I	Photosystem I PsaL protein (subunit XI)
PMM1520	2	-2.01	0.87	0.62	0.00	Photosystem I	photosystem I subunit VIII (PsaI)
PMM1523	2	-0.97	0.05	0.04	0.40	Photosystem I	Photosystem I PsaB protein
PMM1524	2	-0.14	0.13	0.09	0.86	Photosystem I	Photosystem I PsaA protein
PMM1528	2	-0.37	0.02	0.02	0.66	DNA replication, recombination, and repair	HNH endonuclease family protein
PMM1530	2	-0.86	0.33	0.23	0.35	Ribosomal proteins	50S ribosomal protein L31
PMM1531	2	-0.84	0.31	0.22	1.00	Ribosomal proteins	30S ribosomal protein S9
PMM1532	2	-2.19	0.39	0.28	0.00	Ribosomal proteins	50S ribosomal protein L13
PMM1534	2	-0.82	1.09	0.77	0.23	Ribosomal proteins	50S ribosomal protein L17
PMM1535	2	-0.69	0.78	0.55	0.42	RNA synthesis, modification, and DNA transcription	Bacterial RNA polymerase, alpha chain
PMM1536	2	-2.80	0.13	0.09	0.00	Ribosomal proteins	30S ribosomal protein S11
PMM1537	2	-3.72	0.88	0.62	0.00	Ribosomal proteins	30S ribosomal protein S13
PMM1538	2	-3.41	0.89	0.63	0.00	Ribosomal proteins	50S Ribosomal protein L36
PMM1540	2	-0.68	0.01	0.01	0.48	Protein and peptide secretion	preprotein translocase SecY subunit
PMM1541	2	-0.55	0.97	0.69	0.41	Ribosomal proteins	50S ribosomal protein L15
PMM1542	2	-2.39	2.28	1.61	0.14	Ribosomal proteins	30S ribosomal protein S5
PMM1543	2	0.01	1.25	0.88	0.71	Ribosomal proteins	50S ribosomal protein L18
PMM1544	2	-0.76	0.19	0.14	0.42	Ribosomal proteins	50S ribosomal protein L6
PMM1545	2	-2.04	0.11	0.08	0.01	Ribosomal proteins	30S ribosomal protein S8
PMM1546	2	-1.09	1.25	0.88	0.13	Ribosomal proteins	50S ribosomal protein L5
PMM1548	2	0.07	0.08	0.05	0.77	Ribosomal proteins	50S Ribosomal protein L14
PMM1549	2	-0.61	0.37	0.26	0.73	Ribosomal proteins	30S Ribosomal protein S17
PMM1550	2	-1.70	0.06	0.04	0.13	Ribosomal proteins	50S ribosomal protein L29
PMM1551	2	-1.06	0.13	0.09	0.22	Ribosomal proteins	50S ribosomal protein L16
PMM1552	2	-2.26	0.40	0.28	0.00	Ribosomal proteins	30S ribosomal protein S3
PMM1553	2	-2.23	0.17	0.12	0.00	Ribosomal proteins	50S ribosomal protein L22
PMM1554	2	-2.06	0.57	0.41	0.00	Ribosomal proteins	30S Ribosomal protein S19
PMM1555	2	-2.44	0.14	0.10	0.00	Ribosomal proteins	50S ribosomal protein L2
PMM1556	2	-1.90	0.85	0.60	0.00	Ribosomal proteins	50S ribosomal protein L23
PMM1557	2	-1.91	0.19	0.13	0.00	Ribosomal proteins	50S ribosomal protein L4
PMM1558	2	-4.30	1.79	1.26	0.00	Ribosomal proteins	50S ribosomal protein L3
PMM1559	2	1.45	1.24	0.88	0.06	Conserved hypothetical protein	conserved hypothetical protein
PMM1562	2	2.54	0.23	0.16	0.02	DNA replication, recombination, and repair	RecA bacterial DNA recombination protein
PMM1563	2	-0.25	0.58	0.41	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1566	2	-0.13	0.58	0.41	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM1568	2	0.06	0.16	0.11	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM1570	2	-1.59	0.17	0.12	0.00	Cobalamin, heme, phycobilin and porphyrin	ATP:corrinoid adenosyltransferase BtuR/CobO/CobP
PMM1571	2	1.07	0.43	0.31	0.49	Conserved hypothetical protein	conserved hypothetical protein
PMM1575	2	1.21	0.21	0.15	0.37	Pyruvate and acetyl-CoA metabolism	Phosphoenolpyruvate carboxylase
PMM1578	2	-1.24	0.03	0.02	0.20	Photosystem I	Photosystem I protein PsaD
PMM1581	2	-0.22	1.02	0.72	0.56	Regulatory functions	MRP protein homolog
PMM1583	2	0.64	0.10	0.07	0.93	Conserved hypothetical protein	conserved hypothetical protein
PMM1585	2	-0.68	0.55	0.39	0.67	Conserved hypothetical protein	conserved hypothetical protein
PMM1588	2	1.27	0.35	0.25	0.42	Regulatory functions	possible Conserved carboxylase domain
PMM1594	2	0.95	0.28	0.20	0.64	Cobalamin, heme, phycobilin and porphyrin	Heme oxygenase
PMM1596	2	-0.02	0.60	0.42	0.76	Other	Isocitrate dehydrogenase
PMM1599	2	-0.18	0.05	0.04	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM1600	2	0.94	0.93	0.65	1.00	Transport and binding proteins	putative Na+/H+ antiporter, CPA2 family
PMM1601	2	2.52	0.31	0.22	0.00	Other	phosphorylase
PMM1602	2	1.14	0.53	0.38	0.53	Conserved hypothetical protein	conserved hypothetical protein
PMM1603	2	3.07	0.59	0.42	0.00	Regulatory functions	putative ribonuclease III
PMM1604	2	-1.88	0.17	0.12	0.02	Conserved hypothetical protein	conserved hypothetical protein
PMM1605	2	2.29	1.75	1.23	0.03	Protein modification and translation factors	possible 16S rRNA processing protein RimM
PMM1606	2	-1.28	1.33	0.94	0.12	Other	Glutamine--fructose-6-phosphate transaminase (isomerizing)
PMM1607	2	-1.79	0.48	0.34	0.00	Photosystem I	Photosystem I subunit PsaC
PMM1608	2	-2.11	1.02	0.72	0.00	Fatty acid, phospholipid and sterol metabolism	acyl carrier protein (ACP)
PMM1609	2	-2.59	0.30	0.21	0.00	Fatty acid, phospholipid and sterol metabolism	3-oxoacyl-[acyl-carrier-protein] synthase II
PMM1610	2	-1.80	0.11	0.08	0.00	Other	Transketolase
PMM1611	2	0.90	0.30	0.21	1.00	Thiamine	ThiC family
PMM1613	2	0.46	1.12	0.79	0.78	Other	Zinc metallopeptidase M20/M25/M40 family
PMM1615	2	2.44	0.14	0.10	0.00	DNA replication, recombination, and repair	Holliday junction DNA helicase RuvB
PMM1616	2	0.56	0.07	0.05	0.88	Other	tmRNA binding protein SmpB
PMM1617	2	-1.04	0.37	0.26	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1619	2	-0.05	0.35	0.25	1.00	Regulatory functions	two-component response regulator
PMM1622	2	0.58	0.65	0.46	1.00	Murein sacculus and peptidoglycan	Rod shape determining protein
PMM1623	2	3.39	0.08	0.05	0.00	DNA replication, recombination, and repair	single-stranded DNA-binding protein
PMM1625	2	1.37	0.70	0.49	0.52	Amino acids and amines	putative adenosylhomocysteinase
PMM1626	2	2.53	1.13	0.80	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1629	2	0.93	0.51	0.36	0.64	Transport and binding proteins	Type II alternative RNA polymerase sigma factor, sigma-70 family
PMM1630	2	-0.58	0.07	0.05	0.90	Transport and binding proteins	MgtE family, putative magnesium transport protein
PMM1634	2	1.76	0.67	0.47	0.12	DNA replication, recombination, and repair	DNA gyrase, subunit B
PMM1635	2	-1.11	0.20	0.14	0.21	Aminoacyl tRNA synthetases and tRNA modification	tRNA delta-2-isopentenylpyrophosphate (IPP) transferase
PMM1636	2	-0.72	0.52	0.37	0.50	Protein modification and translation factors	Translation Initiation factor 3
PMM1639	2	-0.16	0.27	0.19	0.64	Protein and peptide secretion	Preprotein translocase SecA subunit
PMM1640	2	0.01	1.92	1.36	0.98	Regulatory functions	putative acetyltransferase, GNAT family
PMM1642	2	0.75	0.04	0.03	1.00	Regulatory functions	possible transcription regulator
PMM1643	2	-0.70	0.56	0.40	0.27	Riboflavin	Putative 6,7-dimethyl-8-ribityllumazine synthase or riboflavin synthase beta chain

PMM1644	2	-2.09	0.92	0.65	0.00	Photosystem II	possible Photosystem II reaction center Z protein (PsbZ)
PMM1648	2	0.97	0.21	0.15	0.92	Branched chain family	Aspartate kinase
PMM1649	2	1.15	0.67	0.47	0.46	DNA replication, recombination, and repair	Excinuclease ABC subunit B (UvrB)
PMM1650	2	-1.53	0.21	0.15	0.07	Conserved hypothetical protein	conserved hypothetical protein
PMM1652	2	0.81	0.68	0.48	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1653	2	0.18	0.12	0.09	0.73	Aspartate family	Dihydrodipicolinate synthetase
PMM1655	2	-1.04	1.24	0.88	0.17	Other	FKBP-type peptidyl-prolyl cis-trans isomerase (PPIase)
PMM1656	2	-0.64	1.63	1.15	0.57	Degradation of proteins, peptides, and glycopeptides	Clp protease proteolytic subunit
PMM1657	2	0.37	0.85	0.60	0.74	Degradation of proteins, peptides, and glycopeptides	Clp protease ATP-binding subunit, ClpX
PMM1661	2	-2.05	1.33	0.94	0.00	Ribosomal proteins	50S ribosomal protein L35
PMM1662	2	-1.24	1.10	0.78	0.18	Ribosomal proteins	50S ribosomal protein L20
PMM1665	2	-0.86	1.14	0.80	0.33	Fatty acid, phospholipid and sterol metabolism	sulfolipid (UDP-sulfoquinovose) biosynthesis protein
PMM1667	2	1.06	0.26	0.18	0.58	Conserved hypothetical protein	conserved hypothetical protein
PMM1669	2	2.91	0.41	0.29	0.00	Regulatory functions	putative Glycine cleavage H-protein
PMM1671	2	0.59	0.74	0.52	0.96	Conserved hypothetical protein	conserved hypothetical protein
PMM1672	2	1.59	0.07	0.05	0.15	Fatty acid, phospholipid and sterol metabolism	Fatty acid desaturase, type 1
PMM1673	2	0.42	0.94	0.66	0.85	Ribosomal proteins	50S ribosomal protein L9
PMM1676	2	0.46	0.93	0.66	0.71	Conserved hypothetical protein	conserved hypothetical protein
PMM1678	2	2.21	0.81	0.57	0.02	Conserved hypothetical protein	conserved hypothetical protein
PMM1680	2	3.15	0.78	0.55	0.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1683	2	-0.33	0.36	0.26	0.64	Conserved hypothetical protein	conserved hypothetical
PMM1685	2	1.80	0.43	0.31	0.07	Regulatory functions	putative spermidine synthase
PMM1688	2	-0.18	0.05	0.03	0.71	Aminoacyl tRNA synthetases and tRNA modification	Aspartyl-tRNA synthetase
PMM1689	2	1.52	1.09	0.77	0.33	Pyrimidine ribonucleotide biosynthesis	Glutamine amidotransferase class-I:CTP synthase
PMM1694	2	1.19	1.53	1.08	0.40	Cobalamin, heme, phycobilin and porphyrin	putative uroporphyrin-III C-methyltransferase
PMM1697	2	-0.02	0.11	0.08	1.00	Transport and binding proteins	Type II alternative RNA polymerase sigma factor, sigma-70 family
PMM1700	2	2.96	0.64	0.45	0.00	Other	Aconitate hydratase B
PMM1702	2	-0.16	0.15	0.11	0.64	Purine ribonucleotide biosynthesis	formyltetrahydrofolate deformylase
PMM1703	2	0.89	0.20	0.14	0.57	Transport and binding proteins	NAD binding site:D-amino acid oxidase
PMM1704	2	-1.74	0.28	0.20	0.11	Chaperones	Molecular chaperone DnaK2, heat shock protein hsp70-2
PMM1706	2	-4.65	3.37	2.38	0.00	Ribosomal proteins	30S ribosomal protein S6
PMM1707	2	0.40	0.09	0.07	0.80	Glutamate family / Nitrogen assimilation	Argininosuccinate synthase
PMM1708	2	0.87	0.01	0.01	1.00	Conserved hypothetical protein	conserved hypothetical protein
PMM1716	2	0.04	1.21	0.86	0.69	Aspartate family	No Cyanobase Name
PMM1717	2	-2.23	0.21	0.15	0.58	Other	No Cyanobase Name
PMM1718	2	0.81	1.17	0.83	0.75	Other	No Cyanobase Name