

Table S5. Gene Expression For Genes with Top 50% Expression Values during 24 Hours Post Starvation

| Name    | Number | log2 Fold Change | Standard Deviation | Standard Error | p-value | Category  | Definition   |
|---------|--------|------------------|--------------------|----------------|---------|---|--|
| PMM0001 | 2      | 0.87             | 1.35               | 0.96           | 0.49    | DNA replication, recombination, and repair                  | DNA polymerase III, beta chain   |
| PMM0008 | 2      | -0.11            | 0.05               | 0.03           | 0.62    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0013 | 2      | -1.40            | 0.93               | 0.65           | 0.27    | Fatty acid, phospholipid and sterol metabolism              | RNA-binding region RNP-1 (RNA recognition motif)   |
| PMM0015 | 2      | 0.03             | 0.48               | 0.34           | 0.93    | Conserved hypothetical protein                              | Domain of unknown function DUF25   |
| PMM0016 | 2      | -0.88            | 1.81               | 1.28           | 0.08    | Chaperones  | Heat shock protein GrpE  |
| PMM0017 | 2      | 1.37             | 0.02               | 0.01           | 0.11    | Chaperones  | DnaJ protein   |
| PMM0020 | 2      | 0.87             | 0.05               | 0.03           | 0.46    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0023 | 2      | -0.62            | 1.18               | 0.84           | 0.28    | C02 fixation  | Glyceraldehyde 3-phosphate dehydrogenase(NADP+)(phosphorylating)   |
| PMM0025 | 2      | -0.59            | 0.21               | 0.15           | 0.40    | Protein modification and translation factors                | Cyclophilin-type peptidyl-prolyl cis-trans isomerase   |
| PMM0026 | 2      | -1.32            | 0.39               | 0.28           | 0.03    | Protein modification and translation factors                | Elongation factor P (EF-P)   |
| PMM0027 | 2      | 1.21             | 0.07               | 0.05           | 0.19    | Fatty acid, phospholipid and sterol metabolism              | Biotin / Lipoyl attachment:Acetyl-CoA biotin carboxyl carrier... possible Transcription factor TFID (or TATA-b |
| PMM0030 | 2      | 4.93             | 0.95               | 0.67           | 0.00    | Protein modification and translation factors                | HNH endonuclease:HNN nuclease  |
| PMM0031 | 2      | 1.13             | 0.35               | 0.25           | 0.33    | DNA replication, recombination, and repair                  | possible Bacterial type II secretion system pr   |
| PMM0032 | 2      | 1.07             | 0.68               | 0.48           | 0.46    | Protein and peptide secretion                               | conserved hypothetical protein   |
| PMM0033 | 2      | 1.11             | 0.46               | 0.33           | 1.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0034 | 2      | -0.22            | 0.17               | 0.12           | 0.57    | Conserved hypothetical protein                              | soluble hydrogenase small subunit  |
| PMM0035 | 2      | 1.83             | 0.09               | 0.06           | 0.02    | Hydrogenase   | Glutamine amidotransferase class-I:GMP synthase  |
| PMM0037 | 2      | 1.56             | 0.33               | 0.24           | 0.10    | Purine ribonucleotide biosynthesis                          | flavoprotein   |
| PMM0043 | 2      | -0.25            | 0.69               | 0.48           | 0.53    | Other   | Nucleoside diphosphate kinase  |
| PMM0046 | 2      | -2.59            | 0.10               | 0.07           | 0.00    | Interconversions and salvage of nucleosides and nucleotides | Glutamyl-tRNA (Gln) amidotransferase subunit B   |
| PMM0048 | 2      | -0.01            | 0.46               | 0.33           | 0.19    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0051 | 2      | 1.13             | 1.34               | 0.95           | 1.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0055 | 2      | 0.36             | 0.11               | 0.08           | 0.41    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0056 | 2      | -0.44            | 1.67               | 1.18           | 0.43    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0058 | 2      | 2.89             | 0.30               | 0.21           | 0.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0059 | 2      | 0.92             | 1.09               | 0.77           | 0.56    | Conserved hypothetical protein                              | soluble hydrogenase  |
| PMM0060 | 2      | -0.44            | 0.14               | 0.10           | 0.45    | Fatty acid, phospholipid and sterol metabolism              | YGGT family, conserved hypothetical integral membrane protein  |
| PMM0061 | 2      | -0.58            | 1.63               | 1.15           | 0.22    | Other   | photosystem II P88 protein   |
| PMM0062 | 2      | -2.24            | 0.44               | 0.31           | 0.00    | Photosystem II  | photosystem II P88 protein   |
| PMM0063 | 2      | 1.85             | 0.17               | 0.12           | 0.19    | Conserved hypothetical protein                              | possible high light inducible protein  |
| PMM0064 | 2      | 0.42             | 0.90               | 0.63           | 0.71    | Adaptations and atypical conditions                         | putative formylmethionine deformylase  |
| PMM0068 | 2      | 1.42             | 1.24               | 0.88           | 0.24    | Regulatory functions  | ABC transporter, membrane component  |
| PMM0073 | 2      | 0.01             | 0.61               | 0.43           | 0.63    | Transport and binding proteins                              | conserved hypothetical protein   |
| PMM0075 | 2      | 2.41             | 1.68               | 1.19           | 0.00    | Conserved hypothetical protein                              | possible 4'-phosphopantetheinyl transferase family protein   |
| PMM0078 | 2      | -0.79            | 0.32               | 0.22           | 0.23    | Other   | putative bacterioferritin conjugatory (BCP) protein  |
| PMM0079 | 2      | -2.29            | 0.49               | 0.35           | 0.00    | Transport and binding proteins                              | Phosphoadenosine phosphosulfate reductase  |
| PMM0081 | 2      | -0.55            | 1.18               | 0.83           | 0.38    | Serine family / Sulfur assimilation                         | putative NADH dehydrogenase, transport associated  |
| PMM0082 | 2      | 1.31             | 0.23               | 0.17           | 0.15    | Regulatory functions  | putative sodium/sulfate transporter, DASS family   |
| PMM0083 | 2      | -0.68            | 1.16               | 0.82           | 0.26    | Regulatory functions  | putative potassium channel, VIC family   |
| PMM0085 | 2      | 0.23             | 0.19               | 0.14           | 1.00    | Regulatory functions  | Conserved hypothetical protein   |
| PMM0086 | 2      | 0.22             | 0.13               | 0.09           | 1.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0087 | 2      | 3.49             | 1.13               | 0.80           | 0.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0088 | 2      | 1.45             | 0.66               | 0.47           | 0.15    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0091 | 2      | 0.64             | 0.24               | 0.17           | 1.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0092 | 2      | 2.56             | 0.44               | 0.31           | 0.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0093 | 2      | -0.41            | 0.61               | 0.43           | 0.82    | Adaptations and atypical conditions                         | possible high light inducible protein  |
| PMM0095 | 2      | -0.52            | 1.28               | 0.90           | 0.34    | Other   | similar to serum resistance locus brk8   |
| PMM0099 | 2      | 0.85             | 0.02               | 0.02           | 0.38    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0101 | 2      | 1.35             | 0.34               | 0.24           | 0.14    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0103 | 2      | -0.37            | 1.21               | 0.86           | 0.71    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0105 | 2      | 1.50             | 0.83               | 0.59           | 0.12    | Riboflavin  | RibD/rbG C-terminal domain   |
| PMM0106 | 2      | 0.75             | 0.60               | 0.42           | 0.91    | Other   | 6-pyruvoyl tetrahydropterin synthase   |
| PMM0111 | 2      | 0.72             | 0.32               | 0.22           | 0.47    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0114 | 2      | 1.13             | 0.16               | 0.12           | 0.23    | Conserved hypothetical protein                              | zeta-carotene desaturase   |
| PMM0115 | 2      | 1.17             | 0.19               | 0.13           | 0.41    | Carotenoid  | conserved hypothetical protein   |
| PMM0116 | 2      | 0.73             | 0.08               | 0.05           | 0.92    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0117 | 2      | 2.49             | 0.50               | 0.35           | 0.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0120 | 2      | 1.65             | 0.06               | 0.04           | 0.05    | Cell division   | putative cell division inhibitor   |
| PMM0121 | 2      | 0.91             | 1.38               | 0.98           | 0.59    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0123 | 2      | 1.40             | 0.32               | 0.22           | 0.14    | Serine family / Sulfur assimilation                         | O-acetylseringe (thiol)-lyase A  |
| PMM0124 | 2      | -0.10            | 0.70               | 0.50           | 0.50    | Conserved hypothetical protein                              | conserved hypothetical protein in cyanobacteria  |
| PMM0125 | 2      | -0.53            | 0.49               | 0.35           | 0.40    | Transport and binding proteins                              | possible ABC transporter, ATP-binding component  |
| PMM0126 | 2      | 0.06             | 0.02               | 0.02           | 0.77    | Other   | possible Herpesvirus Ul6 like  |
| PMM0128 | 2      | 0.39             | 0.80               | 0.57           | 1.00    | Regulatory functions  | two-component response regulator   |
| PMM0132 | 2      | -1.14            | 0.82               | 0.58           | 0.18    | Other   | cyanobacterial conserved hypothetical  |
| PMM0133 | 2      | 2.06             | 0.28               | 0.20           | 0.00    | Radiation sensitivity                                       | putative DNA repair protein RadA   |
| PMM0134 | 2      | -0.75            | 1.11               | 0.79           | 0.31    | Regulatory functions  | two-component response regulator   |
| PMM0136 | 2      | -1.67            | 0.95               | 0.67           | 0.02    | Fatty acid, phospholipid and sterol metabolism              | 3'-oxoacyl-[acyl-carrier-protein] synthase III   |
| PMM0137 | 2      | -0.48            | 0.43               | 0.31           | 0.48    | Fatty acid, phospholipid and sterol metabolism              | Malonyl coenzyme A-acyl carrier protein transacylase   |
| PMM0138 | 2      | 0.47             | 0.10               | 0.07           | 0.87    | Fatty acid, phospholipid and sterol metabolism              | putative 1-acyl-sn-glycerol-3-phosphate acyltransferase  |
| PMM0139 | 2      | -1.04            | 0.34               | 0.24           | 0.22    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0140 | 2      | 1.28             | 2.88               | 2.04           | 1.00    | Regulatory functions  | putative Ycf34   |
| PMM0142 | 2      | -1.75            | 1.28               | 0.90           | 0.00    | Fatty acid, phospholipid and sterol metabolism              | RNA-binding region RNP-1 (RNA recognition motif)   |
| PMM0143 | 2      | 1.05             | 0.30               | 0.21           | 0.46    | Carotenoid  | Squalene and phytene synthases   |
| PMM0144 | 2      | 2.34             | 0.62               | 0.44           | 0.00    | Carotenoid  | phytene desaturase   |
| PMM0145 | 2      | 1.97             | 0.05               | 0.03           | 0.01    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0146 | 2      | 2.10             | 0.49               | 0.34           | 0.01    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0147 | 2      | -0.34            | 0.00               | 0.00           | 0.50    | Regulatory functions  | putative Rubisco transcriptional regulator   |
| PMM0149 | 2      | 1.39             | 0.32               | 0.22           | 0.21    | NADH dehydrogenase  | putative NADH Dehydrogenase (complex I) subunit (chain 5)  |
| PMM0150 | 2      | 1.39             | 0.04               | 0.03           | 0.20    | NADH dehydrogenase  | putative NADH dehydrogenase subunit (chain 4)  |
| PMM0153 | 2      | -0.81            | 0.63               | 0.45           | 0.22    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0154 | 2      | -1.11            | 0.55               | 0.39           | 0.13    | Regulatory functions  | Bacterial regulatory protein, LuxR family  |
| PMM0159 | 2      | 0.38             | 0.09               | 0.06           | 0.75    | NADH dehydrogenase  | putative NADH Dehydrogenase subunit  |
| PMM0160 | 2      | 3.11             | 0.90               | 0.63           | 0.00    | NADH dehydrogenase  | putative respiratory-chain NADH dehydrogenase subunit  |
| PMM0163 | 2      | -2.03            | 0.28               | 0.20           | 0.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0164 | 2      | 1.36             | 0.16               | 0.12           | 0.20    | Aromatic amino acid family                                  | Tryptophan synthase, beta chain:Pyridoxal-5'-phosphate-depend...   |
| PMM0166 | 2      | -2.62            | 1.18               | 0.84           | 0.00    | Serine family / Sulfur assimilation                         | Adenylsulfate kinase   |
| PMM0172 | 2      | 1.45             | 0.82               | 0.58           | 0.07    | NADH dehydrogenase  | putative NADH dehydrogenase subunit  |
| PMM0179 | 2      | 1.33             | 1.71               | 1.21           | 0.30    | Other   | Glutaredoxin   |
| PMM0180 | 2      | 0.37             | 0.05               | 0.04           | 1.00    | Protein modification and translation factors                | peptide chain release factor RF-2  |
| PMM0184 | 2      | 1.10             | 0.25               | 0.18           | 0.20    | Aromatic amino acid family                                  | para-aminobenzoate synthase component II   |
| PMM0195 | 2      | 0.12             | 0.34               | 0.24           | 0.71    | Other   | Phosphoglycerate kinase  |
| PMM0200 | 2      | -1.01            | 0.22               | 0.16           | 0.34    | Degradation of RNA  | possibly ribonuclease HI   |
| PMM0201 | 2      | -2.30            | 0.06               | 0.04           | 0.00    | Ribosomal proteins  | SOS ribosomal protein L7/L12   |
| PMM0202 | 2      | -2.46            | 0.35               | 0.25           | 0.19    | Ribosomal proteins  | SOS ribosomal protein L10  |
| PMM0203 | 2      | -1.98            | 0.45               | 0.32           | 0.00    | Ribosomal proteins  | SOS ribosomal protein L1   |
| PMM0204 | 2      | -1.41            | 0.33               | 0.23           | 0.00    | Ribosomal proteins  | SOS ribosomal protein L11  |
| PMM0205 | 2      | 1.66             | 0.82               | 0.58           | 0.12    | RNA synthesis, modification, and DNA transcription          | transcription antitermination protein, NusG  |
| PMM0206 | 2      | -1.37            | 1.04               | 0.74           | 0.03    | Protein and peptide secretion                               | putative preprotein translocase, SecE subunit  |
| PMM0208 | 2      | -0.15            | 0.15               | 0.11           | 0.60    | Other   | Endopeptidase  |
| PMM0209 | 2      | -0.68            | 0.32               | 0.23           | 0.38    | Other   | possible kinase  |
| PMM0211 | 2      | -0.50            | 0.57               | 0.40           | 0.47    | Other   | FAD-dependent pyridine nucleotide-disulphide oxidoreductase  |
| PMM0212 | 2      | 3.18             | 1.65               | 1.17           | 0.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0213 | 2      | 1.40             | 1.07               | 0.75           | 0.19    | Transport and binding proteins                              | putative sodium-dependent bicarbonate transporter  |
| PMM0214 | 2      | -2.54            | 0.92               | 0.65           | 0.00    | Regulatory functions  | putative sulfate transporter   |
| PMM0216 | 2      | -1.52            | 0.09               | 0.06           | 0.22    | Adaptations and atypical conditions                         | Glyoxalase/Bleomycin resistance protein/Dioxxygenase superfamily   |
| PMM0218 | 2      | -0.05            | 0.56               | 0.40           | 0.50    | Other   | GTP1/OBG family  |
| PMM0219 | 2      | -0.37            | 1.21               | 0.86           | 0.57    | Conserved hypothetical protein                              | conserved hypothetical   |
| PMM0220 | 2      | 1.67             | 0.70               | 0.49           | 1.00    | Other   | No Cyanobase Name  |
| PMM0223 | 2      | 2.47             | 0.37               | 0.26           | 0.00    | Photosystem II  | Photosystem II PsB protein (D1)  |
| PMM0224 | 2      | 0.43             | 0.95               | 0.67           | 0.10    | Aromatic amino acid family                                  | Chorismate synthase  |
| PMM0226 | 2      | 0.18             | 0.13               | 0.09           | 0.77    | Cell division   | cell division protein FtsH2  |
| PMM0228 | 2      | -0.73            | 0.83               | 0.58           | 0.14    | Photosystem II  | Photosystem II manganese-stabilizing protein   |
| PMM0231 | 2      | -2.76            | 0.40               | 0.28           | 0.00    | Conserved hypothetical protein                              | conserved hypothetical protein   |
| PMM0235 | 2      | -0.52            | 1.04               | 0.73           | 0.72    | Aminoacyl tRNA synthetases and tRNA modification            | Glycyl-tRNA(Gln) amidotransferase subunit C  |
| PMM0237 | 2      | -0.21            | 0.06               | 0.04           | 0.75    | Conserved hypothetical protein                              | conserved hypothetical protein   |

|         |   |       |      |      |   |
|---------|---|-------|------|------|---|
| PMM0239 | 2 | -1.69 | 0.52 | 0.36 | 0.00 Conserved hypothetical protein                     |
| PMM0242 | 2 | 1.14  | 0.66 | 0.46 | 0.20 Thiamine   |
| PMM0243 | 2 | 0.16  | 0.59 | 0.42 | 1.00 Pyrimidine ribonucleotide biosynthesis             |
| PMM0244 | 2 | 0.06  | 0.22 | 0.15 | 0.60 Purine ribonucleotide biosynthesis                 |
| PMM0245 | 2 | 1.58  | 0.40 | 0.28 | 0.04 Cobalamin, heme, phycobilin and porphyrin          |
| PMM0246 | 2 | 2.17  | 1.70 | 1.20 | 0.00 Transport and binding proteins                     |
| PMM0251 | 2 | -2.79 | 0.26 | 0.18 | 0.00 Photosystem II                                     |
| PMM0252 | 2 | 2.28  | 0.23 | 0.16 | 0.00 Photosystem II                                     |
| PMM0253 | 2 | 0.28  | 0.54 | 0.38 | 1.00 Photosystem II                                     |
| PMM0254 | 2 | -0.13 | 0.11 | 0.08 | 0.61 Conserved hypothetical protein                     |
| PMM0258 | 2 | 1.81  | 0.56 | 0.39 | 0.02 Other  |
| PMM0259 | 2 | 0.28  | 0.69 | 0.49 | 1.00 Conserved hypothetical protein                     |
| PMM0260 | 2 | 1.27  | 2.31 | 1.64 | 0.40 Conserved hypothetical protein                     |
| PMM0263 | 2 | 2.26  | 0.23 | 0.16 | 1.00 Transport and binding proteins                     |
| PMM0264 | 2 | -1.32 | 0.69 | 0.49 | 0.09 Murein sacculus and peptidoglycan                  |
| PMM0265 | 2 | -1.03 | 0.56 | 0.40 | 0.19 Conserved hypothetical protein                     |
| PMM0267 | 2 | -1.67 | 0.16 | 0.12 | 0.06 Other  |
| PMM0268 | 2 | 0.06  | 0.12 | 0.09 | 0.88 Conserved hypothetical protein                     |
| PMM0272 | 2 | -4.18 | 1.09 | 0.77 | 0.00 Photosystem II                                     |
| PMM0273 | 2 | -1.10 | 0.50 | 0.35 | 0.14 Other  |
| PMM0275 | 2 | -1.17 | 0.96 | 0.68 | 0.04 Pyrimidine ribonucleotide biosynthesis             |
| PMM0278 | 2 | 0.03  | 0.10 | 0.07 | 0.91 Other  |
| PMM0279 | 2 | -0.79 | 1.38 | 0.98 | 0.19 Conserved hypothetical protein                     |
| PMM0282 | 2 | 0.41  | 1.50 | 1.06 | 0.70 Fatty acid, phospholipid and sterol metabolism     |
| PMM0284 | 2 | -1.39 | 0.24 | 0.17 | 0.05 Regulatory functions                               |
| PMM0286 | 2 | -1.23 | 0.26 | 0.18 | 0.13 Other  |
| PMM0289 | 2 | 1.24  | 0.13 | 0.10 | 0.21 Transport and binding proteins                     |
| PMM0290 | 2 | 1.16  | 0.33 | 0.23 | 0.33 Transport and binding proteins                     |
| PMM0293 | 2 | 0.82  | 0.24 | 0.17 | 0.50 NADH dehydrogenase                                 |
| PMM0294 | 2 | 1.32  | 0.75 | 0.53 | 0.27 NADH dehydrogenase                                 |
| PMM0295 | 2 | -0.84 | 0.43 | 0.30 | 0.21 Other  |
| PMM0296 | 2 | -1.56 | 0.42 | 0.30 | 0.01 Conserved hypothetical protein                     |
| PMM0297 | 2 | -0.52 | 0.26 | 0.18 | 0.86 Photosystem II                                     |
| PMM0298 | 2 | -0.69 | 0.26 | 0.19 | 0.87 Photosystem II                                     |
| PMM0299 | 2 | -1.15 | 0.23 | 0.16 | 0.06 Photosystem II                                     |
| PMM0300 | 2 | -1.16 | 0.01 | 0.01 | 0.16 Photosystem II                                     |
| PMM0301 | 2 | 1.82  | 0.08 | 0.06 | 0.04 Other  |
| PMM0305 | 2 | -2.06 | 1.49 | 1.05 | 0.03 Phycobilisome                                      |
| PMM0306 | 2 | -3.80 | 1.16 | 0.82 | 0.00 Phycobilisome                                      |
| PMM0307 | 2 | -3.44 | 0.68 | 0.48 | 0.00 Conserved hypothetical protein                     |
| PMM0308 | 2 | 0.95  | 0.70 | 0.49 | 0.51 Conserved hypothetical protein                     |
| PMM0309 | 2 | 0.04  | 0.54 | 0.38 | 1.00 Other  |
| PMM0311 | 2 | -1.65 | 0.74 | 0.53 | 0.01 Aspartate family                                   |
| PMM0312 | 2 | -1.75 | 0.43 | 0.31 | 0.00 Ribosomal proteins                                 |
| PMM0313 | 2 | -0.59 | 0.47 | 0.33 | 0.55 Conserved hypothetical protein                     |
| PMM0314 | 2 | -1.53 | 0.40 | 0.28 | 0.02 Photosystem II                                     |
| PMM0315 | 2 | -1.10 | 0.36 | 0.26 | 0.95 Photosystem II                                     |
| PMM0316 | 2 | 1.19  | 0.76 | 0.53 | 0.37 Soluble electron carriers                          |
| PMM0317 | 2 | -1.93 | 0.78 | 0.55 | 0.00 Photosystem II                                     |
| PMM0318 | 2 | -1.55 | 1.18 | 0.84 | 0.00 Cobalamin, heme, phycobilin and porphyrin          |
| PMM0321 | 2 | -0.27 | 0.33 | 0.23 | 0.51 Cell division                                      |
| PMM0324 | 2 | -0.54 | 1.55 | 1.09 | 0.41 Detoxification                                     |
| PMM0325 | 2 | -0.82 | 0.58 | 0.41 | 1.00 Cytochrome b6/f complex                            |
| PMM0326 | 2 | 0.37  | 0.11 | 0.08 | 1.00 Cytochrome b6/f complex                            |
| PMM0327 | 2 | 0.11  | 0.05 | 0.04 | 0.72 Other  |
| PMM0328 | 2 | -1.81 | 0.46 | 0.33 | 0.00 DNA replication, recombination, and repair         |
| PMM0329 | 2 | -2.13 | 0.33 | 0.23 | 0.00 Photosystem I                                      |
| PMM0333 | 2 | 1.01  | 0.96 | 0.68 | 0.34 Other  |
| PMM0334 | 2 | 2.84  | 1.79 | 1.27 | 0.00 Conserved hypothetical protein                     |
| PMM0336 | 2 | 1.33  | 0.38 | 0.27 | 0.27 Conserved hypothetical protein                     |
| PMM0337 | 2 | 8.45  | 0.19 | 0.14 | 0.00 Conserved hypothetical protein                     |
| PMM0338 | 2 | 0.55  | 0.29 | 0.20 | 0.89 Conserved hypothetical protein                     |
| PMM0339 | 2 | 0.41  | 0.70 | 0.50 | 0.00 Carotenoid   |
| PMM0341 | 2 | 1.50  | 0.16 | 0.11 | 0.19 Conserved hypothetical protein                     |
| PMM0342 | 2 | 1.21  | 0.05 | 0.04 | 0.36 Other  |
| PMM0343 | 2 | 0.98  | 1.21 | 0.85 | 0.68 Other  |
| PMM0345 | 2 | 0.19  | 0.03 | 0.02 | 0.80 Transport and binding proteins                     |
| PMM0346 | 2 | -6.53 | 2.46 | 1.74 | 0.00 Conserved hypothetical protein                     |
| PMM0347 | 2 | 0.09  | 0.22 | 0.16 | 0.58 Conserved hypothetical protein                     |
| PMM0348 | 2 | -0.77 | 1.08 | 0.77 | 0.97 Other  |
| PMM0350 | 2 | -1.37 | 1.82 | 1.29 | 0.57 Regulatory functions                               |
| PMM0351 | 2 | 1.24  | 1.76 | 1.24 | 0.33 Cobalamin, heme, phycobilin and porphyrin          |
| PMM0356 | 2 | -2.27 | 0.86 | 0.61 | 0.00 Fatty acid, phospholipid and sterol metabolism     |
| PMM0363 | 2 | 1.66  | 0.48 | 0.34 | 0.04 Regulatory functions                               |
| PMM0364 | 2 | 3.47  | 0.67 | 0.47 | 0.00 Other  |
| PMM0365 | 2 | 4.11  | 0.31 | 0.22 | 0.00 Other  |
| PMM0366 | 2 | 1.49  | 0.35 | 0.25 | 0.10 Transport and binding proteins                     |
| PMM0367 | 2 | 1.12  | 1.06 | 0.75 | 0.61 Conserved hypothetical protein                     |
| PMM0368 | 2 | 2.58  | 0.42 | 0.30 | 0.00 Conserved hypothetical protein                     |
| PMM0370 | 2 | 3.84  | 0.29 | 0.21 | 0.00 Transport and binding proteins                     |
| PMM0371 | 2 | 2.65  | 0.70 | 0.50 | 0.00 Transport and binding proteins                     |
| PMM0373 | 2 | -0.37 | 0.47 | 0.33 | 0.64 Other  |
| PMM0374 | 2 | 2.23  | 0.50 | 0.35 | 0.00 Other  |
| PMM0377 | 2 | 0.90  | 0.55 | 0.39 | 0.37 Conserved hypothetical protein                     |
| PMM0378 | 2 | 1.51  | 0.69 | 0.49 | 0.97 Conserved hypothetical protein                     |
| PMM0379 | 2 | -0.32 | 1.28 | 0.90 | 0.48 Conserved hypothetical protein                     |
| PMM0383 | 2 | 2.20  | 0.59 | 0.42 | 0.01 Transport and binding proteins                     |
| PMM0388 | 2 | 1.84  | 1.26 | 0.89 | 0.02 Chemotaxis   |
| PMM0395 | 2 | 1.96  | 0.35 | 0.25 | 0.08 Conserved hypothetical protein                     |
| PMM0400 | 2 | -1.52 | 1.82 | 1.29 | 0.16 Adaptations and atypical conditions                |
| PMM0403 | 2 | -0.16 | 1.03 | 0.73 | 0.43 Conserved hypothetical protein                     |
| PMM0405 | 2 | -1.43 | 0.12 | 0.09 | 0.03 Transport and binding proteins                     |
| PMM0407 | 2 | 0.06  | 0.54 | 0.38 | 0.84 Serine family / Sulfur assimilation                |
| PMM0410 | 2 | -1.68 | 0.68 | 0.48 | 0.00 Ribosomal proteins                                 |
| PMM0411 | 2 | 0.80  | 0.67 | 0.48 | 0.60 Conserved hypothetical protein                     |
| PMM0412 | 2 | -1.77 | 0.55 | 0.39 | 0.03 Conserved hypothetical protein                     |
| PMM0416 | 2 | -3.02 | 0.73 | 0.51 | 0.00 RNA synthesis, modification, and DNA transcription |
| PMM0417 | 2 | -1.53 | 0.04 | 0.03 | 0.07 Conserved hypothetical protein                     |
| PMM0418 | 2 | -0.21 | 1.49 | 1.06 | 1.00 Other  |
| PMM0428 | 2 | -1.57 | 0.55 | 0.39 | 0.02 Cobalamin, heme, phycobilin and porphyrin          |
| PMM0429 | 2 | -3.39 | 0.09 | 0.06 | 0.00 Conserved hypothetical protein                     |
| PMM0435 | 2 | -0.53 | 0.31 | 0.22 | 0.31 NADH dehydrogenase                                 |
| PMM0436 | 2 | 0.67  | 0.91 | 0.64 | 0.92 DNA replication, recombination, and repair         |
| PMM0441 | 2 | 1.26  | 0.09 | 0.06 | 0.19 Other  |
| PMM0443 | 2 | 1.15  | 0.04 | 0.03 | 0.20 Conserved hypothetical protein                     |
| PMM0445 | 2 | 0.95  | 0.38 | 0.27 | 1.00 Respiratory terminal oxidases                      |
| PMM0446 | 2 | 2.06  | 0.47 | 0.33 | 0.01 Respiratory terminal oxidases                      |
| PMM0447 | 2 | 3.76  | 0.63 | 0.45 | 0.00 Conserved hypothetical protein                     |
| PMM0448 | 2 | 0.16  | 0.38 | 0.27 | 0.99 Cobalamin, heme, phycobilin and porphyrin          |
| PMM0451 | 2 | 0.97  | 0.68 | 0.48 | 0.21 Other  |
| PMM0452 | 2 | -2.30 | 0.86 | 0.61 | 0.00 Chaperones   |
| PMM0453 | 2 | -4.63 | 1.51 | 1.07 | 0.00 Fatty acid, phospholipid and sterol metabolism     |
| PMM0461 | 2 | -0.34 | 0.09 | 0.06 | 0.50 Cytochrome b6/f complex                            |
| PMM0462 | 2 | -1.36 | 0.04 | 0.03 | 0.03 Cytochrome b6/f complex                            |
| PMM0465 | 2 | -0.92 | 1.16 | 0.82 | 0.20 Conserved hypothetical protein                     |
| PMM0468 | 2 | -2.93 | 0.32 | 0.23 | 0.00 Photosystem I                                      |
| PMM0469 | 2 | -3.27 | 0.30 | 0.21 | 0.00 Photosystem I                                      |
| PMM0470 | 2 | -0.75 | 0.57 | 0.40 | 0.27 Other  |

|         |   |           |      |      |   |
|---------|---|-----------|------|------|---|
| PMM0471 | 2 | -2.22     | 1.78 | 1.26 | 0.00 Adaptations and atypical conditions                              |
| PMM0472 | 2 | 0.88      | 0.81 | 0.58 | 0.85 Transport and binding proteins                                   |
| PMM0473 | 2 | -0.85     | 0.77 | 0.54 | 0.36 Aminoacyl tRNA synthetases and tRNA modification                 |
| PMM0474 | 2 | -0.68     | 0.71 | 0.50 | 0.95 Conserved hypothetical protein                                   |
| PMM0475 | 2 | -1.32     | 0.44 | 0.31 | 1.00 Conserved hypothetical protein                                   |
| PMM0476 | 2 | 0.32      | 0.34 | 0.24 | 0.87 Protein modification and translation factors                     |
| PMM0477 | 2 | -0.74     | 0.17 | 0.12 | 0.00 Conserved hypothetical protein                                   |
| PMM0478 | 2 | #NAME? NA | NA   | NA   | possible high light inducible protein                                 |
| PMM0479 | 2 | -0.75     | 0.52 | 0.36 | putative Na <sup>+</sup> /H <sup>+</sup> antiporter, CPA1 family      |
| PMM0480 | 2 | 1.61      | 0.06 | 0.05 | Glutamyl-tRNA synthetase  |
| PMM0481 | 2 | -1.18     | 0.18 | 0.13 | Conserved hypothetical protein  |
| PMM0482 | 2 | 0.78      | 0.53 | 0.37 | Ribosomal protein L19   |
| PMM0483 | 2 | -0.08     | 0.22 | 0.16 | conserved hypothetical protein  |
| PMM0485 | 2 | 0.96      | 1.36 | 0.96 | putative methionine aminopeptidase                                    |
| PMM0491 | 2 | 1.95      | 0.25 | 0.18 | conserved hypothetical protein  |
| PMM0492 | 2 | -1.14     | 0.48 | 0.34 | conserved hypothetical protein  |
| PMM0493 | 2 | -1.04     | 1.47 | 1.04 | Carboxypeptidase Tag (M32) metallopeptidase                           |
| PMM0494 | 2 | -1.69     | 1.94 | 1.37 | putative inorganic pyrophosphatase                                    |
| PMM0495 | 2 | 0.78      | 0.48 | 0.34 | Porphobilinogen deaminase   |
| PMM0496 | 2 | 0.80      | 0.96 | 0.68 | Putative principal RNA polymerase sigma factor                        |
| PMM0500 | 2 | -0.67     | 0.54 | 0.38 | conserved hypothetical protein  |
| PMM0501 | 2 | #NAME? NA | NA   | NA   | conserved hypothetical protein  |
| PMM0502 | 2 | 1.25      | 0.06 | 0.05 | conserved hypothetical protein  |
| PMM0503 | 2 | -0.54     | 1.07 | 0.76 | 0.20 Conserved hypothetical protein                                   |
| PMM0506 | 2 | -0.48     | 1.16 | 0.82 | 0.47 Cobalamin, heme, phycobilin and porphyrin                        |
| PMM0507 | 2 | -0.16     | 0.22 | 0.22 | 0.40 Purine ribonucleotide biosynthesis                               |
| PMM0508 | 2 | 0.14      | 1.00 | 0.71 | 0.65 Photosystem II   |
| PMM0510 | 2 | 2.09      | 0.20 | 0.14 | 0.84 Aminoacyl tRNA synthetases and tRNA modification                 |
| PMM0511 | 2 | -2.11     | 0.08 | 0.06 | 0.00 Transposon-related functions                                     |
| PMM0515 | 2 | -1.81     | 1.54 | 1.09 | 0.00 Other  |
| PMM0519 | 2 | 1.22      | 0.66 | 0.47 | 0.00 Cobalamin, heme, phycobilin and porphyrin                        |
| PMM0520 | 2 | -0.38     | 0.14 | 0.10 | 0.32 Other  |
| PMM0522 | 2 | -0.15     | 0.07 | 0.05 | 0.48 Other  |
| PMM0525 | 2 | -0.58     | 0.30 | 0.21 | 0.64 Pyrimidine ribonucleotide biosynthesis                           |
| PMM0526 | 2 | 0.48      | 0.04 | 0.03 | 0.37 Other  |
| PMM0530 | 2 | -0.37     | 0.14 | 0.10 | 1.00 Branched chain family  |
| PMM0532 | 2 | 0.14      | 0.39 | 0.27 | 0.37 Ribosomal proteins   |
| PMM0533 | 2 | -0.77     | 0.62 | 0.44 | 0.98 Conserved hypothetical protein                                   |
| PMM0534 | 2 | -1.42     | 0.31 | 0.22 | 0.28 Conserved hypothetical protein                                   |
| PMM0536 | 2 | -1.19     | 0.26 | 0.18 | 0.05 Fatty acid, phospholipid and sterol metabolism                   |
| PMM0537 | 2 | -0.39     | 0.97 | 0.68 | 0.40 Folic acid   |
| PMM0540 | 2 | -3.57     | 1.58 | 1.11 | 0.00 Photosystem I  |
| PMM0541 | 2 | -0.75     | 0.50 | 0.35 | 0.27 Conserved hypothetical protein                                   |
| PMM0543 | 2 | 0.07      | 0.31 | 0.22 | 0.75 Cobalamin, heme, phycobilin and porphyrin                        |
| PMM0544 | 2 | 0.25      | 0.41 | 0.29 | 0.69 Cobalamin, heme, phycobilin and porphyrin                        |
| PMM0545 | 2 | -1.10     | 0.09 | 0.06 | 0.19 Cobalamin, heme, phycobilin and porphyrin                        |
| PMM0546 | 2 | 1.78      | 0.34 | 0.24 | 0.02 Conserved hypothetical protein                                   |
| PMM0548 | 2 | 2.96      | 0.73 | 0.52 | 0.00 Other  |
| PMM0549 | 2 | -3.04     | 0.99 | 0.70 | 0.00 CO2 fixation   |
| PMM0550 | 2 | -1.28     | 0.23 | 0.16 | 0.11 CO2 fixation   |
| PMM0551 | 2 | -1.24     | 0.02 | 0.01 | 0.09 CO2 fixation   |
| PMM0552 | 2 | -2.02     | 0.19 | 0.13 | 0.00 CO2 fixation   |
| PMM0554 | 2 | -0.05     | 0.55 | 0.39 | 0.65 CO2 fixation   |
| PMM0555 | 2 | 0.20      | 1.31 | 0.93 | 0.81 CO2 fixation   |
| PMM0556 | 2 | -0.17     | 1.25 | 0.88 | 0.76 Conserved hypothetical protein                                   |
| PMM0557 | 2 | -1.28     | 1.11 | 0.78 | 0.01 Conserved hypothetical protein                                   |
| PMM0558 | 2 | -0.04     | 0.35 | 0.25 | 0.76 Conserved hypothetical protein                                   |
| PMM0560 | 2 | -1.09     | 0.22 | 0.15 | 1.00 Conserved hypothetical protein                                   |
| PMM0561 | 2 | -0.77     | 1.15 | 0.81 | 0.05 Other  |
| PMM0564 | 2 | -1.12     | 0.78 | 0.55 | 0.27 Transport and binding proteins                                   |
| PMM0565 | 2 | 0.93      | 0.56 | 0.40 | 0.16 Conserved hypothetical protein                                   |
| PMM0570 | 2 | 1.46      | 0.65 | 0.46 | 0.41 DNA replication, recombination, and repair                       |
| PMM0571 | 2 | 3.88      | 2.48 | 1.76 | 0.20 NADH dehydrogenase   |
| PMM0573 | 2 | -0.78     | 0.86 | 0.61 | 0.00 Conserved hypothetical protein                                   |
| PMM0574 | 2 | -0.64     | 0.73 | 0.51 | 0.25 Conserved hypothetical protein                                   |
| PMM0577 | 2 | -0.48     | 0.75 | 0.53 | 0.48 Conserved hypothetical protein                                   |
| PMM0579 | 2 | 1.12      | 0.05 | 0.03 | 0.85 RNA synthesis, modification, and DNA transcription               |
| PMM0580 | 2 | -1.05     | 0.24 | 0.17 | 0.48 Conserved hypothetical protein                                   |
| PMM0581 | 2 | -1.01     | 0.90 | 0.64 | 0.15 Degradation of proteins, peptides, and glycopeptides             |
| PMM0583 | 2 | -4.21     | 0.95 | 0.67 | 1.00 Solubil electron carriers  |
| PMM0586 | 2 | -0.78     | 0.26 | 0.18 | 0.00 Cobalamin, heme, phycobilin and porphyrin                        |
| PMM0593 | 2 | 0.50      | 0.01 | 0.01 | 0.30 Conserved hypothetical protein                                   |
| PMM0594 | 2 | 0.12      | 0.50 | 0.35 | 0.86 Other  |
| PMM0595 | 2 | 0.40      | 0.84 | 0.60 | 0.58 NADH dehydrogenase   |
| PMM0599 | 2 | -3.64     | 0.97 | 0.69 | 1.00 Aspartate family   |
| PMM0601 | 2 | -0.78     | 0.77 | 0.54 | 0.00 Conserved hypothetical protein                                   |
| PMM0603 | 2 | -1.02     | 0.55 | 0.39 | 0.33 Transport and binding proteins                                   |
| PMM0605 | 2 | -3.91     | 0.16 | 0.11 | 0.22 Transport and binding proteins                                   |
| PMM0609 | 2 | 0.10      | 0.26 | 0.18 | 0.00 Conserved hypothetical protein                                   |
| PMM0613 | 2 | -0.40     | 0.23 | 0.16 | 1.00 Polysaccharides and glycoproteins                                |
| PMM0614 | 2 | -0.73     | 0.20 | 0.14 | 0.48 Aromatic amino acid family                                       |
| PMM0615 | 2 | 0.39      | 1.02 | 0.72 | 0.34 Conserved hypothetical protein                                   |
| PMM0618 | 2 | 1.33      | 0.51 | 0.36 | 0.91 Other  |
| PMM0619 | 2 | 1.08      | 0.04 | 0.03 | 0.37 Carotenoid   |
| PMM0622 | 2 | -0.39     | 0.64 | 0.45 | 0.40 Pyruvate and acetyl-CoA metabolism                               |
| PMM0626 | 2 | 2.49      | 0.31 | 0.22 | 0.52 Conserved hypothetical protein                                   |
| PMM0627 | 2 | -1.55     | 0.29 | 0.21 | 0.00 Conserved hypothetical protein                                   |
| PMM0628 | 2 | 0.93      | 0.10 | 0.07 | 1.00 Photosystem II   |
| PMM0629 | 2 | -0.64     | 0.85 | 0.60 | 0.37 Transport and binding proteins                                   |
| PMM0633 | 2 | -1.55     | 1.10 | 0.78 | 0.48 Conserved hypothetical protein                                   |
| PMM0637 | 2 | 0.63      | 0.35 | 0.25 | 0.00 Regulatory functions   |
| PMM0638 | 2 | -0.30     | 0.18 | 0.13 | 0.54 Conserved hypothetical protein                                   |
| PMM0641 | 2 | -0.80     | 0.52 | 0.37 | 0.26 Conserved hypothetical protein                                   |
| PMM0642 | 2 | -0.10     | 0.93 | 0.66 | 0.62 Serrine family / Sulfur assimilation                             |
| PMM0647 | 2 | 0.73      | 0.55 | 0.39 | 0.51 Conserved hypothetical protein                                   |
| PMM0649 | 2 | -0.87     | 1.11 | 0.79 | 0.36 Other  |
| PMM0651 | 2 | 2.56      | 0.28 | 0.20 | 0.00 Regulatory functions   |
| PMM0652 | 2 | -0.54     | 0.43 | 0.30 | 0.48 RNA synthesis, modification, and DNA transcription               |
| PMM0658 | 2 | -0.91     | 0.95 | 0.67 | 0.36 Aminoacyl tRNA synthetases and tRNA modification                 |
| PMM0659 | 2 | 0.39      | 0.39 | 0.58 | 1.00 DNA replication, recombination, and repair                       |
| PMM0660 | 2 | -1.54     | 0.49 | 0.34 | 0.05 Degradation of RNA   |
| PMM0661 | 2 | 1.48      | 0.09 | 0.06 | 0.16 Purine ribonucleotide biosynthesis                               |
| PMM0664 | 2 | 0.18      | 0.18 | 0.13 | 1.00 Conserved hypothetical protein                                   |
| PMM0665 | 2 | 1.36      | 0.26 | 0.19 | 0.11 Other  |
| PMM0667 | 2 | 0.98      | 1.32 | 0.94 | 0.50 Conserved hypothetical protein                                   |
| PMM0674 | 2 | -0.34     | 0.51 | 0.36 | 0.55 Aspartate family   |
| PMM0681 | 2 | 2.30      | 0.22 | 0.16 | 0.00 Conserved hypothetical protein                                   |
| PMM0683 | 2 | 0.86      | 0.63 | 0.45 | 0.37 Purine ribonucleotide biosynthesis                               |
| PMM0684 | 2 | 3.38      | 0.04 | 0.03 | 0.00 Regulatory functions   |
| PMM0685 | 2 | 3.58      | 0.55 | 0.39 | 0.00 Conserved hypothetical protein                                   |
| PMM0687 | 2 | 3.13      | 0.68 | 0.48 | 0.00 Conserved hypothetical protein                                   |
| PMM0688 | 2 | 0.67      | 0.16 | 0.11 | 0.48 Protein modification and translation factors                     |
| PMM0689 | 2 | 3.44      | 0.77 | 0.54 | 0.00 Adaptations and atypical conditions                              |
| PMM0690 | 2 | 4.37      | 0.58 | 0.41 | 0.00 Adaptations and atypical conditions                              |
| PMM0691 | 2 | -1.54     | 1.35 | 0.96 | 0.01 Conserved hypothetical protein                                   |
| PMM0692 | 2 | -2.43     | 0.50 | 0.35 | 0.00 Regulatory functions   |
| PMM0693 | 2 | 1.17      | 1.59 | 1.12 | 0.25 Other  |
| PMM0697 | 2 | 1.08      | 2.01 | 1.42 | 0.47 DNA replication, recombination, and repair                       |
|         |   |           |      |      | possible high light inducible protein                                 |
|         |   |           |      |      | putative Na <sup>+</sup> /H <sup>+</sup> antiporter, CPA1 family      |
|         |   |           |      |      | Glutamyl-tRNA synthetase  |
|         |   |           |      |      | Conserved hypothetical protein  |
|         |   |           |      |      | Ribosomal protein L19   |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | putative methionine aminopeptidase                                    |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | Band 7 protein  |
|         |   |           |      |      | glutamate-1-semialdehyde 2,1-aminomutase                              |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | 4a-hydroxytetrahydrobiopterin dehydratase (PCD)                       |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | Carboxypeptidase Tag (M32) metallopeptidase                           |
|         |   |           |      |      | putative inorganic pyrophosphatase                                    |
|         |   |           |      |      | Porphobilinogen deaminase   |
|         |   |           |      |      | Putative principal RNA polymerase sigma factor                        |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | possible precorrin-6X reductase                                       |
|         |   |           |      |      | Adenylosuccinate synthetase   |
|         |   |           |      |      | possible Photosystem II reaction center Psb27 protein                 |
|         |   |           |      |      | Prolyl-RNA synthetase   |
|         |   |           |      |      | possible Reverse transcriptase (RNA-dependent                         |
|         |   |           |      |      | Inorganic pyrophosphatase   |
|         |   |           |      |      | possible alpha-ribazole-5'-P phosphatase                              |
|         |   |           |      |      | Transaldolase   |
|         |   |           |      |      | NAD binding site  |
|         |   |           |      |      | uridylate kinase  |
|         |   |           |      |      | Ferrochelatase  |
|         |   |           |      |      | Acetyl-CoA synthase large subunit                                     |
|         |   |           |      |      | 30S ribosomal protein S1 homolog B, putative Nbp1                     |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | putative GTP cyclohydrolase I   |
|         |   |           |      |      | phosphoribosylanthranilate isomerase                                  |
|         |   |           |      |      | possible photosystem I reaction centre subunit XII (PsA)              |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | Protocchlorophyll reductase iron-sulfur ATP-binding protein           |
|         |   |           |      |      | Light-independent protocchlorophyllide reductase subunit B            |
|         |   |           |      |      | Light-independent protocchlorophyllide reductase subunit N            |
|         |   |           |      |      | conserved hypothetical  |
|         |   |           |      |      | HAM1 family protein   |
|         |   |           |      |      | carboxysome shell protein CsoS1                                       |
|         |   |           |      |      | Ribulose bisphosphate carboxylase, large chain                        |
|         |   |           |      |      | Ribulose bisphosphate carboxylase, small chain                        |
|         |   |           |      |      | carboxysome shell protein CsoS2                                       |
|         |   |           |      |      | putative carboxysome peptide A  |
|         |   |           |      |      | putative carboxysome peptide B  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | possible ATP phosphoribosyltransferase                                |
|         |   |           |      |      | putative multidrug efflux ABC transporter                             |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | chromosomal replication initiator protein DnaA                        |
|         |   |           |      |      | NADH dehydrogenase subunit NdhL (ndhL)                                |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | Putative type II alternative sigma factor, sigma70 family             |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | ATP-dependent Clp protease, Hsp 100, ATP-binding subunit ClpB         |
|         |   |           |      |      | plastocyanin  |
|         |   |           |      |      | Uroporphyrinogen decarboxylase (URO-D)                                |
|         |   |           |      |      | conserved hypothetical  |
|         |   |           |      |      | Peptidase family M3   |
|         |   |           |      |      | putative NADH Dehydrogenase (complex I) subunit (chain 4)             |
|         |   |           |      |      | Homoserine kinase-GMP kinases putative ATP-binding domain             |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | ABC transporter, substrate binding protein, possibly Mn               |
|         |   |           |      |      | ABC transporter component, possibly Mn transport                      |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | Putative ADPglucose–glucosyltransferase (GlgA)                        |
|         |   |           |      |      | EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)          |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | Possible nitrilase  |
|         |   |           |      |      | polyPryenyl synthetase; solanensyl diphosphate synthase (sds)         |
|         |   |           |      |      | acetyl-coenzyme A synthetase  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | hypothetical  |
|         |   |           |      |      | light-harvesting complex protein                                      |
|         |   |           |      |      | possible sodium:solute symporter, ESS family                          |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | putative lycopene epsilon-acylcyclase                                 |
|         |   |           |      |      | Ferric uptake regulator family  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | putative O-Acetyl homoserine sulfhydrylase                            |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | Pentapeptide repeats  |
|         |   |           |      |      | possible VHS domain   |
|         |   |           |      |      | possible 5'-exonuclease, C-terminal SAM fol                           |
|         |   |           |      |      | putative pseudouridylate synthase specific to ribosomal small subunit |
|         |   |           |      |      | NAD-dependent DNA ligase N-terminus                                   |
|         |   |           |      |      | possible RNA recognition motif. (a.k.a. RRM, R                        |
|         |   |           |      |      | ribonucleotide reductase (Class II)                                   |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | Hsp33 protein   |
|         |   |           |      |      | conserved hypothetical protein  |
|         |   |           |      |      | Aminotransferases class-I   |
|         |   |           |      |      | conserved hypothetical protein  |
| </td    |   |           |      |      |   |

|         |   |       |      |      |  |  |
|---------|---|-------|------|------|--|--|
| PMM0698 | 2 | 2.19  | 1.55 | 1.09 | 0.00 Chaperones  | possible DnaJ central domain (4 repeats)                                     |
| PMM0699 | 2 | -2.12 | 1.79 | 1.26 | 0.01 Conserved hypothetical protein                            | conserved hypothetical   |
| PMM0700 | 2 | -0.39 | 0.51 | 0.36 | 0.60 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0703 | 2 | 0.61  | 0.68 | 0.48 | 0.80 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0704 | 2 | 1.87  | 0.28 | 0.20 | 0.01 Regulatory functions                                      | putative potassium channel, VIC family                                       |
| PMM0705 | 2 | 0.59  | 0.34 | 0.24 | 0.63 Regulatory functions                                      | two-component response regulator, phosphate                                  |
| PMM0707 | 2 | 1.29  | 0.56 | 0.40 | 0.13 Other   | possible Lipoprotein   |
| PMM0708 | 2 | 1.52  | 0.21 | 0.15 | 0.13 Regulatory functions                                      | putative secreted protein  |
| PMM0709 | 2 | 0.48  | 0.22 | 0.16 | 1.00 Membranes, lipoproteins and porins                        | possible porin   |
| PMM0710 | 2 | -4.00 | 0.03 | 0.02 | 0.00 Transport and binding proteins                            | ABC transporter, substrate binding protein, phosphate                        |
| PMM0714 | 2 | 1.61  | 1.51 | 1.07 | 0.27 Regulatory functions                                      | Bacterial regulatory proteins, ArsR family                                   |
| PMM0717 | 2 | -0.56 | 0.59 | 0.41 | 0.43 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0719 | 2 | 0.72  | 0.16 | 0.11 | 0.56 Conserved hypothetical protein                            | hypothetical   |
| PMM0722 | 2 | -0.08 | 2.95 | 2.08 | 0.97 Conserved hypothetical protein                            | hypothetical   |
| PMM0725 | 2 | 0.52  | 0.01 | 0.01 | 1.00 Transport and binding proteins                            | putative phosphate ABC transporter, ATP binding subunit                      |
| PMM0726 | 2 | 3.59  | 1.24 | 0.88 | 0.00 Conserved hypothetical protein                            | hypothetical   |
| PMM0732 | 2 | -0.35 | 0.58 | 0.41 | 0.53 Other   | possible Major surface glycoprotein  |
| PMM0736 | 2 | -0.48 | 1.09 | 0.77 | 0.50 Other   | possible Alpha-2-macroglobulin family N-terminal                             |
| PMM0739 | 2 | 1.04  | 0.21 | 0.15 | 0.33 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0740 | 2 | -0.11 | 0.15 | 0.10 | 0.48 Cytochrome b/f complex                                    | Cytochrome b-f complex subunit VIII  |
| PMM0741 | 2 | -0.07 | 0.72 | 0.51 | 0.63 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0742 | 2 | 1.24  | 0.62 | 0.44 | 0.38 Degradation of proteins, peptides, and glycopeptides      | Cip protease subunit   |
| PMM0743 | 2 | -0.83 | 0.16 | 0.11 | 0.28 Cell division   | FtsH ATP-dependent protease homolog  |
| PMM0744 | 2 | 0.21  | 3.01 | 2.13 | 0.65 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0747 | 2 | -2.43 | 0.58 | 0.41 | 0.00 Cobalamin, heme, phycobilin and porphyrin                 | ferredoxin dependent biliverdin reductase                                    |
| PMM0751 | 2 | -2.80 | 1.09 | 0.77 | 0.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0753 | 2 | -1.08 | 0.33 | 0.24 | 0.21 Ribosomal proteins  | 30S ribosomal protein S2   |
| PMM0754 | 2 | -1.27 | 0.86 | 0.61 | 0.03 Protein modification and translation factors              | putative Elongation factor Ts  |
| PMM0758 | 2 | 0.16  | 0.93 | 0.66 | 1.00 Serine family / Sulfur assimilation                       | ferredoxin-sulfite reductase   |
| PMM0760 | 2 | -0.97 | 0.16 | 0.11 | 0.18 Cobalamin, heme, phycobilin and porphyrin                 | Aromatic-ring hydroxylase (flavoprotein monooxygenase)                       |
| PMM0762 | 2 | -0.48 | 0.01 | 0.01 | 0.46 Aromatic amino acid family                                | tyrosine binding protein   |
| PMM0766 | 2 | -2.40 | 1.46 | 1.04 | 0.00 Other   | Ribulose-phosphate 3-epimerase   |
| PMM0767 | 2 | -1.48 | 0.36 | 0.25 | 0.01 Surface polysaccharides, lipopolysaccharides and antigens | Fructose-1,6-bisphosphatase/sedoheptulose-1,7-bis phosphatase                |
| PMM0769 | 2 | -1.95 | 0.20 | 0.14 | 0.00 Other   | ADP-glucose pyrophosphorylase  |
| PMM0770 | 2 | 1.60  | 0.51 | 0.36 | 0.11 Pentose phosphate pathway                                 | 6-phosphogluconate dehydrogenase   |
| PMM0772 | 2 | 0.56  | 1.20 | 0.85 | 0.69 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0774 | 2 | 1.22  | 0.41 | 0.29 | 0.28 Branched chain family                                     | Dihydroxy-acid dehydratase   |
| PMM0775 | 2 | 0.14  | 0.97 | 0.68 | 0.95 Conserved hypothetical protein                            | conserved hypothetical   |
| PMM0777 | 2 | 0.36  | 0.18 | 0.12 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0779 | 2 | -0.80 | 3.07 | 2.17 | 0.35 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0781 | 2 | -1.53 | 0.68 | 0.48 | 0.00 Fatty acid, phospholipid and sterol metabolism            | Fructose-bisphosphate/sedoheptulose-1,7-bisphosphate aldolase                |
| PMM0784 | 2 | -0.74 | 1.17 | 0.82 | 0.37 Fatty acid, phospholipid and sterol metabolism            | acetyl-CoA carboxylase, beta subunit   |
| PMM0785 | 2 | -4.13 | 1.35 | 0.96 | 0.00 CO2 fixation  | phosphoribulokinase  |
| PMM0790 | 2 | 0.24  | 0.03 | 0.02 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0794 | 2 | -0.25 | 0.46 | 0.33 | 0.55 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0797 | 2 | -2.70 | 1.56 | 1.11 | 0.00 Nucleoprotein   | possible mRNA binding protein  |
| PMM0799 | 2 | -2.96 | 1.34 | 0.95 | 0.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0800 | 2 | -1.86 | 0.09 | 0.07 | 0.03 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0801 | 2 | -2.19 | 2.14 | 1.51 | 0.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0802 | 2 | 1.29  | 0.70 | 0.49 | 0.24 DNA replication, recombination, and repair                | putative endonuclease  |
| PMM0804 | 2 | 1.40  | 0.49 | 0.34 | 1.00 Other   | ferritin   |
| PMM0806 | 2 | 1.62  | 1.11 | 0.78 | 0.00 Regulatory functions                                      | Bacterial regulatory proteins, Crp family                                    |
| PMM0810 | 2 | 1.63  | 0.53 | 0.38 | 0.07 Conserved hypothetical protein                            | hypothetical   |
| PMM0812 | 2 | 2.40  | 0.26 | 0.19 | 0.00 Conserved hypothetical protein                            | hypothetical   |
| PMM0814 | 2 | -1.09 | 0.80 | 0.57 | 0.18 Other   | possible Cytochrome oxidase c subunit Vib                                    |
| PMM0815 | 2 | 3.08  | 0.52 | 0.37 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein  |
| PMM0816 | 2 | 4.01  | 0.53 | 0.37 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein  |
| PMM0817 | 2 | 3.66  | 0.29 | 0.21 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein  |
| PMM0818 | 2 | 4.26  | 0.12 | 0.08 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein  |
| PMM0819 | 2 | 3.96  | 0.08 | 0.05 | 0.00 Conserved hypothetical protein                            | hypothetical   |
| PMM0820 | 2 | -1.60 | 0.10 | 0.07 | 0.11 Aromatic amino acid family                                | possible EPSP synthase (3-phosphoshikimate 1-c                               |
| PMM0821 | 2 | 0.56  | 0.07 | 0.05 | 0.79 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0824 | 2 | -0.23 | 0.33 | 0.23 | 0.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0828 | 2 | 0.79  | 0.54 | 0.38 | 0.55 Other   | S4 domain  |
| PMM0829 | 2 | 0.32  | 0.10 | 0.07 | 1.00 Other   | Triosephosphate isomerase  |
| PMM0835 | 2 | -4.13 | 0.91 | 0.64 | 0.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0844 | 2 | -1.49 | 0.43 | 0.31 | 0.02 Adaptations and atypical conditions                       | phytochrome-regulated gene   |
| PMM0845 | 2 | -0.06 | 0.82 | 0.58 | 0.53 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0846 | 2 | -0.25 | 0.47 | 0.33 | 0.50 Other   | possible Uncharacterized secreted proteins, Ya                               |
| PMM0847 | 2 | -0.83 | 0.19 | 0.14 | 0.28 Drug and analog sensitivity                               | putative acetazolamide conferring resistance protein Zam                     |
| PMM0851 | 2 | -2.07 | 0.86 | 0.61 | 0.00 Other   | Putative CbbP homolog  |
| PMM0852 | 2 | 2.40  | 0.07 | 0.05 | 0.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0853 | 2 | -1.36 | 1.18 | 0.83 | 0.01 Ribosomal proteins  | 50S ribosomal protein L32  |
| PMM0856 | 2 | -0.77 | 0.77 | 0.54 | 0.96 Detoxification  | thioredoxin peroxidase   |
| PMM0857 | 2 | -3.70 | 0.89 | 0.63 | 0.00 Other   | possible Influenza RNA-dependent RNA polymeras                               |
| PMM0858 | 2 | 2.80  | 0.33 | 0.23 | 0.00 Conserved hypothetical protein                            | hypothetical   |
| PMM0861 | 2 | -0.83 | 0.10 | 0.07 | 0.91 Transport and binding proteins                            | possible Virion host shutoff protein   |
| PMM0863 | 2 | -0.70 | 0.19 | 0.14 | 0.33 Cobalamin, heme, phycobilin and porphyrin                 | putative cobinamide kinase   |
| PMM0864 | 2 | -2.44 | 1.71 | 1.21 | 0.00 Other   | possible Fusion glycoprotein F0.   |
| PMM0867 | 2 | -0.53 | 1.56 | 1.10 | 0.37 Aminocycl tRNA synthetases and tRNA modification          | Methionyl-tRNA synthetase  |
| PMM0869 | 2 | -2.64 | 0.80 | 0.57 | 0.00 Ribosomal proteins  | 30S ribosomal protein S18  |
| PMM0870 | 2 | -3.22 | 0.17 | 0.12 | 0.00 Ribosomal proteins  | 50S Ribosomal protein L33  |
| PMM0872 | 2 | -0.38 | 0.17 | 0.12 | 0.84 Other   | possible Carboxylesterase  |
| PMM0876 | 2 | -2.18 | 0.09 | 0.06 | 0.00 Conserved hypothetical protein                            | conserved hypothetical   |
| PMM0878 | 2 | 0.13  | 0.05 | 0.03 | 0.00 Branched chain family                                     | putative Branched-chain amino acid aminotransferase                          |
| PMM0881 | 2 | -0.16 | 1.16 | 0.82 | 0.54 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0883 | 2 | 0.49  | 0.68 | 0.48 | 0.89 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0893 | 2 | 0.21  | 1.37 | 0.97 | 0.76 Riboflavin  | possible GTP cyclohydrolase II / 3,4-dihydroxy-2-butane 4-phosphate synthase |
| PMM0894 | 2 | -1.60 | 0.13 | 0.09 | 0.00 Protein modification and translation factors              | Cyclophilin-type peptidyl-prolyl cis-trans isomerase                         |
| PMM0895 | 2 | -0.52 | 2.55 | 1.80 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0896 | 2 | 1.14  | 0.42 | 0.30 | 0.17 Chaperones  | DnaJ protein   |
| PMM0897 | 2 | 0.62  | 0.06 | 0.04 | 1.00 Chaperones  | Molecular chaperone DnaK, heat shock protein hsp70                           |
| PMM0898 | 2 | -0.67 | 0.30 | 0.22 | 0.35 Soluble electron carriers                                 | ferredoxin, petF-like protein  |
| PMM0899 | 2 | 0.27  | 0.82 | 0.58 | 1.00 Regulatory functions                                      | phospho myo-inositol(4 or)-monophosphatase                                   |
| PMM0901 | 2 | -1.84 | 0.68 | 0.48 | 0.00 Chaperones  | heat shock protein HtpG  |
| PMM0902 | 2 | -0.84 | 0.32 | 0.23 | 0.21 Ribosomal proteins  | 50S ribosomal protein L28  |
| PMM0906 | 2 | -1.96 | 0.34 | 0.24 | 0.00 Photosystem I   | Photosystem I Psk protein (subunit X)  |
| PMM0907 | 2 | -1.06 | 0.12 | 0.08 | 0.17 Sugars  | 1-deoxy-D-xylulose 5-phosphate synthase                                      |
| PMM0910 | 2 | 0.84  | 1.18 | 0.84 | 0.86 Conserved hypothetical protein                            | conserved hypothetical membrane protein                                      |
| PMM0912 | 2 | 0.09  | 0.35 | 0.25 | 0.63 Other   | Pyruvate kinase  |
| PMM0913 | 2 | 0.51  | 0.69 | 0.49 | 1.00 Transport and binding proteins                            | possible ABC transporter   |
| PMM0919 | 2 | 0.26  | 0.46 | 0.32 | 0.83 Branched chain family / Nitrogen assimilation             | serine:pyruvate/alanine:glyoxylate aminotransferase                          |
| PMM0920 | 2 | 2.45  | 0.57 | 0.41 | 0.00 Glutamated family / Nitrogen assimilation                 | Glutamine synthetase, glutamate-ammonia ligase                               |
| PMM0922 | 2 | 0.14  | 2.04 | 1.44 | 0.96 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0923 | 2 | -3.12 | 0.36 | 0.25 | 0.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0926 | 2 | -0.45 | 0.29 | 0.20 | 0.51 Photosystem II  | possible Photosystem II reaction center Psb28 protein                        |
| PMM0930 | 2 | -2.02 | 0.98 | 0.70 | 0.00 Other   | Pyruvate dehydrogenase E1 beta subunit                                       |
| PMM0934 | 2 | -0.04 | 0.89 | 0.63 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0936 | 2 | 2.30  | 2.05 | 1.45 | 0.03 DNA replication, recombination, and repair                | putative SOS mutagenesis protein UmuD  |
| PMM0941 | 2 | -0.26 | 0.23 | 0.16 | 0.59 Other   | possible CMP phosphodiesterases class-II                                     |
| PMM0942 | 2 | -1.15 | 0.08 | 0.06 | 0.15 DNA replication, recombination, and repair                | putative holliday junction DNA helicase RuvA                                 |
| PMM0943 | 2 | -1.77 | 0.30 | 0.21 | 0.00 Ribosomal proteins  | 30S Ribosomal protein S15  |
| PMM0946 | 2 | 0.83  | 0.03 | 0.02 | 0.79 Aminoacyl tRNA synthetases and tRNA modification          | Glutamyl-tRNA(Gln) amidotransferase A subunit                                |
| PMM0947 | 2 | -0.10 | 3.08 | 2.18 | 0.35 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0949 | 2 | 0.68  | 1.34 | 0.94 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0950 | 2 | 0.02  | 1.15 | 0.81 | 0.48 Other   | No Cyanobase Name  |
| PMM0953 | 2 | -1.61 | 0.50 | 0.36 | 0.15 Conserved hypothetical protein                            | conserved hypothetical protein   |
| PMM0954 | 2 | 0.16  | 0.46 | 0.33 | 1.00 Transport and binding proteins                            | ABC transporter, multidrug efflux family                                     |

|          |       |           |      |      |  |   |
|----------|-------|-----------|------|------|--|---|
| PMM0955  | 2     | 0.06      | 0.30 | 0.22 | 1.00 Protein modification and translation factors<br>0.06 Regulatory functions | Peptide methionine sulfoxide reductase<br>possible GRAM domain  |
| PMM0957  | 2     | 1.49      | 0.47 | 0.33 | 0.21 Conserved hypothetical protein  | conserved hypothetical  |
| PMM0958  | 2     | 1.11      | 0.47 | 0.33 | 0.05 Nitrogen metabolism   | Urease alpha subunit  |
| PMM0963  | 2     | 1.66      | 0.65 | 0.46 | 0.00 Nitrogen metabolism   | Urease beta subunit   |
| PMM0964  | 2     | 2.33      | 0.34 | 0.10 | 0.00 Nitrogen metabolism   | Urease gamma subunit  |
| PMM0965  | 2     | 3.08      | 0.72 | 0.51 | 0.00 Nitrogen metabolism   | urease accessory protein UreD   |
| PMM0966  | 2     | 1.05      | 0.25 | 0.18 | 0.29 Nitrogen metabolism   | urease accessory protein UreG   |
| PMM0969  | 2     | 1.85      | 0.94 | 0.66 | 0.05 Nitrogen metabolism   | putative urea ABC transporter, substrate binding protein  |
| PMM0970  | 2     | 2.80      | 0.27 | 0.19 | 0.01 Transport and binding proteins  | putative urea ABC transporter   |
| PMM0971  | 2     | 1.39      | 0.38 | 0.27 | 0.08 Transport and binding proteins  | Putative ATP-binding subunit of urea ABC transport system   |
| PMM0974  | 2     | -0.46     | 0.93 | 0.66 | 0.94 Transport and binding proteins  | conserved hypothetical protein  |
| PMM0975  | 2     | -0.21     | 0.74 | 0.53 | 0.59 Conserved hypothetical protein  | HNH endonuclease:HNN nuclease   |
| PMM0982  | 2     | -0.41     | 0.03 | 0.02 | 0.52 DNA replication, recombination, and repair                                | possible ATP synthase protein 8   |
| PMM0983  | 2     | -1.41     | 0.06 | 0.04 | 0.05 Fatty acid, phospholipid and sterol metabolism                            | 30S Ribosomal protein S21   |
| PMM0987  | 2     | -3.56     | 0.79 | 0.56 | 0.00 Ribosomal proteins  | Helix-hairpin-helix DNA-binding motif class 1   |
| PMM0988  | 2     | 0.60      | 1.04 | 0.74 | 1.00 Regulatory functions  | conserved hypothetical protein  |
| PMM0993  | 2     | -3.24     | 1.72 | 1.22 | 0.00 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM0996  | 2     | 2.19      | 0.81 | 0.57 | 0.01 Conserved hypothetical protein  | possible Protein of unknown function DUF67  |
| PMM0997  | 2     | 0.20      | 0.39 | 0.28 | 0.65 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM0998  | 2     | 1.58      | 0.61 | 0.43 | 0.03 Conserved hypothetical protein  | hypothetical  |
| PMM0999  | 2     | -1.94     | 0.67 | 0.47 | 0.02 Conserved hypothetical protein  | possible Photosystem II reaction centre N prot  |
| PMM1003  | 2     | -3.57     | 1.13 | 0.80 | 0.00 Photosystem II  | possible Legume lectins alpha domain  |
| PMM1005  | 2     | -1.37     | 0.30 | 0.21 | 0.06 Regulatory functions  | hypothetical  |
| PMM1008  | 2     | -0.14     | 0.57 | 0.40 | 0.71 Conserved hypothetical protein  | hypothetical  |
| PMM1011  | 2     | -3.04     | 2.02 | 1.43 | 0.00 Conserved hypothetical protein  | hypothetical  |
| PMM1015  | 2     | 4.10      | 2.14 | 1.52 | 0.00 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1026  | 2     | 0.43      | 0.11 | 0.08 | 1.00 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1028  | 2     | #NAME? NA | NA   | NA   | 0.00 Conserved hypothetical protein  | conserved hypothetical  |
| PMM102a  | 2     | -0.90     | 0.64 | 0.46 | 0.16 Other   | No Cyanobase Name   |
| PMM1030  | 2     | -1.22     | 0.40 | 0.29 | 0.06 Regulatory functions  | Ferric uptake regulator family  |
| PMM1031  | 2     | 3.74      | 0.47 | 0.33 | 0.00 Transport and binding proteins  | ABC transporter, ATP binding domain, possibly Mn transport  |
| PMM1032  | 2     | 3.48      | 0.24 | 0.17 | 0.00 Transport and binding proteins  | ABC transporter, substrate binding protein, possibly Mn.  |
| PMM1033  | 2     | 0.50      | 0.52 | 0.36 | 1.00 Protein modification and translation factors                              | Cobalamin synthesis protein/P47K  |
| PMM1037  | 2 Inf | NA        | NA   | NA   | 0.00 Conserved hypothetical protein  | conserved hypothetical  |
| PMM1039  | 2     | -0.91     | 0.28 | 0.20 | 0.21 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1042  | 2     | -1.21     | 0.66 | 0.47 | 0.03 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1045  | 2     | 0.83      | 0.83 | 0.59 | 0.47 Conserved hypothetical protein  | conserved hypothetical  |
| PMM1054  | 2     | 1.01      | 0.13 | 0.09 | 0.33 DNA replication, recombination, and repair                                | Crossover junction endodeoxyribonuclease RuvC   |
| PMM1055  | 2     | -1.54     | 0.50 | 0.36 | 0.04 Cobalamin, heme, phycobilin and porphyrin                                 | Protoporphyrin IX Magnesium chelatase, Chl subunit  |
| PMM1058  | 2     | -3.20     | 0.39 | 0.28 | 0.00 Cytochrome b6/f complex   | Cytochrome b6/f complex, subunit V  |
| PMM1060  | 2     | 0.75      | 0.60 | 0.43 | 1.00 Other   | Glutamine amidotransferase class-I  |
| PMM1061  | 2     | 0.17      | 0.54 | 0.38 | 0.80 Thiamine  | Thioredoxin   |
| PMM1063  | 2     | 1.26      | 1.01 | 0.71 | 0.60 DNA replication, recombination, and repair                                | DNA gyrase/opolysomerase IV, subunit A  |
| PMM1066  | 2     | 0.51      | 0.84 | 0.60 | 1.00 Branched chain family   | 2-isopropylmalate synthase  |
| PMM1067  | 2     | -0.05     | 0.89 | 0.63 | 0.57 WD repeat proteins  | possible Adenoviral fiber protein (repeat/shaf  |
| PMM1069  | 2     | -2.35     | 1.00 | 0.70 | 0.00 Folic acid  | putative bifunctional Methylenetetrahydrofolate dehydrogenase Methenyltetrahydrofolate/cyclohydrolase |
| PMM1074  | 2     | 1.48      | 0.11 | 0.08 | 0.15 Other   | Glucose-6-phosphate dehydrogenase   |
| PMM1075  | 2     | 1.16      | 0.09 | 0.06 | 0.68 Cytochrome b6/f complex   | ferredoxin-NADP oxidoreductase (FNR)  |
| PMM1077  | 2     | 0.85      | 0.55 | 0.39 | 0.94 Regulatory functions  | two-component sensor histidine kinase   |
| PMM1078  | 2     | 0.38      | 0.60 | 0.42 | 0.87 Conserved hypothetical protein  | conserved hypothetical  |
| PMM1079  | 2     | -0.95     | 1.18 | 0.83 | 0.16 Regulatory functions  | possible Villin headpiece domain  |
| PMM1080  | 2     | 0.27      | 1.38 | 0.98 | 1.00 Other   | Ribose-phosphate pyrophosphokinase  |
| PMM1086  | 2     | 0.10      | 0.32 | 0.23 | 1.00 Fatty acid, phospholipid and sterol metabolism                            | Alpha/beta hydrolase fold:Esterase/lipase/thioesterase family...                                      |
| PMM1088  | 2     | 0.40      | 0.40 | 0.28 | 0.84 Degradation of proteins, peptides, and glycopeptides                      | CipC  |
| PMM1090  | 2     | 0.21      | 0.47 | 0.34 | 0.80 Branched chain family   | Diaminopimelate decarboxylase   |
| PMM1091  | 2     | 0.61      | 1.45 | 1.02 | 0.65 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1092  | 2     | 0.63      | 0.39 | 0.28 | 0.91 Other   | Undecaprenyl pyrophosphate synthetase (UPPS)  |
| PMM1098  | 2     | 0.17      | 0.83 | 0.59 | 0.78 Photosystem II  | photosystem II oxygen evolving complex protein PsbP   |
| PMM1107  | 2     | 0.10      | 0.26 | 0.19 | 0.81 Pyridoxine  | Pyridoxal phosphate biosynthetic protein PdxK   |
| PMM1109  | 2     | -2.65     | 0.02 | 0.02 | 0.00 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1111  | 2     | 1.31      | 1.16 | 0.82 | 0.20 Other   | Glutaredoxin-related protein  |
| PMM1113  | 2     | -0.74     | 0.61 | 0.43 | 0.31 Regulatory functions  | two-component response regulator  |
| PMM1116  | 2     | -1.47     | 0.56 | 0.40 | 0.00 Cell division   | NAD binding Glucose inhibited division protein A family   |
| PMM1117  | 2     | -1.86     | 0.30 | 0.21 | 0.00 Photosystem II  | possible Photosystem II reaction center Y protein (PsbY)  |
| PMM1118  | 2     | 1.52      | 0.20 | 0.14 | 0.36 Adaptations and atypical conditions                                       | possible high light inducible protein   |
| PMM1119  | 2     | 1.98      | 0.42 | 0.30 | 1.00 Membranes, lipoproteins and porins  | possible porin  |
| PMM1121  | 2     | 2.04      | 0.26 | 0.19 | 1.00 Membranes, lipoproteins and porins  | possible porin  |
| PMM1123  | 2     | 2.04      | 0.43 | 0.30 | 0.07 Hydrogenase   | putative hydrogenase accessory protein  |
| PMM1124  | 2     | 0.65      | 0.03 | 0.02 | 1.00 Other   | possible Natural resistance-associated macroph  |
| PMM1125  | 2     | -3.35     | 0.70 | 0.50 | 0.00 Regulatory functions  | possible Bacterial regulatory proteins, deoR f  |
| PMM1128  | 2     | 1.68      | 0.25 | 0.18 | 0.03 Adaptations and atypical conditions                                       | possible high light inducible protein   |
| PMM1129  | 2     | 0.29      | 0.11 | 0.08 | 1.00 Regulatory functions  | possible Notch (DSL) domain   |
| PMM1131  | 2     | 0.34      | 0.06 | 0.04 | 1.00 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1132  | 2     | 1.35      | 0.38 | 0.27 | 0.39 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1133  | 2     | 0.33      | 0.82 | 0.58 | 1.00 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1134  | 2     | 2.87      | 0.55 | 0.39 | 0.00 Other   | possible Phosphatidylinositol-specific phospho  |
| PMM1135  | 2     | 2.56      | 0.17 | 0.12 | 0.00 Adaptations and atypical conditions                                       | possible high light inducible protein   |
| PMM1138  | 2     | 0.62      | 0.85 | 0.60 | 0.98 Regulatory functions  | probable GTP-binding protein  |
| PMM1139  | 2     | 0.10      | 0.42 | 0.30 | 0.84 Drug and analog sensitivity   | possible membrane fusion protein  |
| PMM1145  | 2     | 0.02      | 0.43 | 0.31 | 0.89 Respiration   | putative nicotinamide nucleotide transhydrogenase, subunit beta                                       |
| PMM1146  | 2     | 2.09      | 1.55 | 1.09 | 0.04 Nicotinate and nicotinamide   | putative nicotinamide nucleotide transhydrogenase, subunit alpha 2 (A2)                               |
| PMM1147  | 2     | 0.74      | 1.09 | 0.77 | 1.00 DNA replication, recombination, and repair                                | putative nicotinamide nucleotide transhydrogenase, subunit alpha 1 (A1)                               |
| PMM1148  | 2     | -1.11     | 0.03 | 0.02 | 0.05 Protein modification and translation factors                              | possible EF-1 guanine nucleotide exchange doma  |
| PMM1149  | 2     | 2.92      | 0.19 | 0.14 | 0.00 Conserved hypothetical protein  | conserved hypothetical  |
| PMM1150  | 2     | 2.30      | 0.19 | 0.13 | 0.00 Regulatory functions  | putative thioredoxin reductase  |
| PMM1151  | 2     | 3.28      | 0.16 | 0.11 | 0.00 Protein modification and translation factors                              | translation initiation factor IF-1  |
| PMM1152  | 2     | 0.27      | 0.66 | 0.47 | 0.86 Photosystem II  | putative chaperon-like protein for quinone binding in photosystem II                                  |
| PMM1152a | 2     | 0.46      | 1.06 | 0.75 | 0.85 Other   | No Cyanobase Name   |
| PMM1154  | 2     | 1.38      | 0.76 | 0.54 | 0.21 Branched chain family   | Acetylacetate synthase small subunit  |
| PMM1156  | 2     | -0.37     | 0.20 | 0.14 | 0.37 Photosystem I   | photosystem I assembly related protein Ycf4   |
| PMM1157  | 2     | 1.58      | 0.39 | 0.27 | 1.00 Photosystem II  | Photosystem II Pbd protein (D2)   |
| PMM1158  | 2     | 0.88      | 0.06 | 0.04 | 0.97 Photosystem II  | Photosystem II Pbc protein (CP43)   |
| PMM1165  | 2     | 0.69      | 0.40 | 0.28 | 0.69 Aminoacyl RNA synthetases and tRNA modification                           | Glycyl-tRNA synthetase alpha subunit  |
| PMM1167  | 2     | -0.17     | 0.15 | 0.11 | 0.76 Other   | Macropage migration inhibitory factor family  |
| PMM1168  | 2     | 0.84      | 0.78 | 0.55 | 0.37 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1169  | 2     | -0.07     | 1.00 | 0.71 | 0.50 Conserved hypothetical protein  | hypothetical  |
| PMM1170  | 2     | -1.32     | 0.65 | 0.46 | 0.08 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1171  | 2     | -2.69     | 1.39 | 0.98 | 0.00 Soluble electron carriers   | Flavodoxin  |
| PMM1174  | 2     | -1.27     | 1.71 | 1.21 | 0.12 Conserved hypothetical protein  | hypothetical  |
| PMM1176  | 2     | -0.39     | 0.30 | 0.21 | 0.52 Regulatory functions  | possible Helix-turn-helix protein, copG family  |
| PMM1179  | 2     | 1.73      | 0.25 | 0.17 | 0.01 Regulatory functions  | putative SMR family transporter, possible pecM homologue  |
| PMM1180  | 2     | -0.39     | 0.16 | 0.11 | 0.47 Degradation of proteins, peptides, and glycopeptides                      | signal peptide peptidase SppA (protease IV)   |
| PMM1183  | 2     | -2.22     | 1.26 | 0.89 | 0.00 Ribosomal proteins  | SOS ribosomal protein L34   |
| PMM1184  | 2     | -1.31     | 0.66 | 0.46 | 0.09 Degradation of RNA  | Bacterial ribonuclease P protein component  |
| PMM1185  | 2     | -0.71     | 0.32 | 0.23 | 0.32 Conserved hypothetical protein  | conserved hypothetical protein  |
| PMM1186  | 2     | 0.61      | 0.18 | 0.13 | 0.93 Regulatory functions  | Putative inner membrane protein; similar to 60 kDa inner membrane protein family                      |
| PMM1188  | 2     | -0.49     | 0.47 | 0.33 | 0.42 Aminoacyl RNA synthetases and tRNA modification                           | Seryl-tRNA synthetase   |
| PMM1190  | 2     | -0.80     | 0.59 | 0.41 | 0.18 Ribosomal proteins  | 30S Ribosomal protein S14   |
| PMM1191  | 2     | -1.33     | 0.42 | 0.30 | 0.09 RNA synthesis, modification, and DNA transcription                        | polyribonucleotide nucleotidyltransferase   |
| PMM1192  | 2     | -0.29     | 1.07 | 0.76 | 0.53 Other   | CysQ protein homolog  |
| PMM1204  | 2     | 2.54      | 1.39 | 0.98 | 0.00 Surface polysaccharides, lipopolysaccharides and antigens                 | glucose-1-phosphate cytidylyltransferase  |
| PMM1205  | 2     | -0.49     | 0.36 | 0.25 | 0.46 Sugars  | NDP-hexose 3,4-dehydratase  |
| PMM1229  | 2     | -0.15     | 0.17 | 0.12 | 0.59 Respiration   | Dehydrogenase, E1 component   |
| PMM1234  | 2     | 0.33      | 0.18 | 0.13 | 1.00 Hydrogenase   | Zinc-containing alcohol dehydrogenase superfamily   |
| PMM1235  | 2     | 0.70      | 1.11 | 0.78 | 0.61 Transport and binding proteins  | possible N-terminal fragment of transketolase   |
| PMM1240  | 2     | -4.39     | 2.28 | 1.61 | 0.00 Other   | methyltransferase   |
| PMM1241  | 2     | 0.85      | 0.15 | 0.11 | 0.36 Conserved hypothetical protein  | hypothetical protein  |
| PMM1244  | 2     | 0.73      | 0.80 | 0.57 | 0.60 Conserved hypothetical protein  | hypothetical protein  |

|         |   |       |      |      |  |   |
|---------|---|-------|------|------|--|---|
| PMM1245 | 2 | 0.39  | 0.89 | 0.63 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1250 | 2 | -0.12 | 0.30 | 0.22 | 0.58 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1251 | 2 | 0.89  | 0.28 | 0.20 | 0.84 Other   | Carbamoyltransferase  |
| PMM1252 | 2 | -0.79 | 0.67 | 0.47 | 0.22 Other   | possible acetyltransferase  |
| PMM1257 | 2 | -1.08 | 0.79 | 0.56 | 0.15 Surface polysaccharides, lipopolysaccharides and antigens | possible dTDP-glucose 4,6-dehydratase                             |
| PMM1258 | 2 | 0.90  | 0.02 | 0.02 | 0.69 Pyridoxine  | pyridoxal-phosphate-dependent aminotransferase                    |
| PMM1259 | 2 | 3.51  | 0.69 | 0.49 | 0.00 Pyridoxine  | pyridoxal-phosphate-dependent aminotransferase                    |
| PMM1260 | 2 | -0.41 | 0.90 | 0.64 | 0.48 Transport and binding proteins                            | Nucleoside-diphosphate-sugar epimerase                            |
| PMM1261 | 2 | -0.22 | 0.72 | 0.51 | 0.53 Sugars  | UDP-glucose 6-dehydrogenase                                       |
| PMM1262 | 2 | 2.02  | 0.23 | 0.16 | 0.02 Regulatory functions                                      | SOS function regulatory protein, LexA repressor                   |
| PMM1264 | 2 | -0.56 | 0.99 | 0.70 | 0.22 Cell division   | cell division protein FtsH3                                       |
| PMM1267 | 2 | -0.84 | 1.51 | 1.07 | 0.12 Conserved hypothetical protein                            | conserved hypothetical  |
| PMM1269 | 2 | -0.37 | 0.09 | 0.07 | 1.00 Transport and binding proteins                            | predicted sugar kinase  |
| PMM1270 | 2 | -0.52 | 0.33 | 0.24 | 0.46 Aminocycl rRNA synthetases and tRNA modification          | Phenylalanyl-tRNA synthetase alpha chain                          |
| PMM1272 | 2 | 1.96  | 1.72 | 1.22 | 0.14 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1273 | 2 | -0.05 | 0.41 | 0.29 | 0.60 Riboflavin  | putative riboflavin kinase/FAD synthase                           |
| PMM1275 | 2 | -1.23 | 1.18 | 0.84 | 0.43 Conserved hypothetical protein                            | DUF170  |
| PMM1276 | 2 | -2.96 | 0.47 | 0.33 | 0.00 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1277 | 2 | -0.03 | 0.49 | 0.35 | 0.61 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1283 | 2 | 0.84  | 0.03 | 0.02 | 0.94 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1284 | 2 | 0.21  | 0.54 | 0.38 | 1.00 Adaptations and atypical conditions                       | PhoB-like phosphate starvation-inducible protein                  |
| PMM1285 | 2 | -3.29 | 1.21 | 0.85 | 0.00 Ribosomal proteins  | 30S Ribosomal protein S16   |
| PMM1286 | 2 | -0.26 | 0.66 | 0.46 | 0.55 Protein and peptide secretion                             | signal recognition particle protein (SRP54)                       |
| PMM1287 | 2 | 0.02  | 0.26 | 0.18 | 0.63 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1288 | 2 | -0.68 | 0.19 | 0.14 | 0.97 Other   | Pyruvate dehydrogenase E1 alpha subunit                           |
| PMM1289 | 2 | 0.47  | 0.70 | 0.49 | 0.91 Transport and binding proteins                            | Type II alternative RNA polymerase sigma factor, sigma-70 family  |
| PMM1293 | 2 | 0.15  | 0.58 | 0.41 | 0.61 Other   | FKBP-type peptidyl-prolyl cis-trans isomerase (PPIase)            |
| PMM1294 | 2 | 0.60  | 0.33 | 0.23 | 1.00 Hydrogenase   | putative nickel-containing superoxide dismutase precursor (NISOD) |
| PMM1296 | 2 | 0.90  | 0.50 | 0.35 | 1.00 Other   | marine cyanobacterial conserved hypothetical                      |
| PMM1298 | 2 | -2.51 | 0.37 | 0.26 | 0.00 Regulatory functions                                      | putative dihydrolipoamide dehydrogenase                           |
| PMM1299 | 2 | -0.68 | 0.71 | 0.51 | 0.30 RNA synthesis, modification, and DNA transcription        | tRNA/rRNA methyltransferase (SpoU)                                |
| PMM1300 | 2 | 0.83  | 0.16 | 0.11 | 0.82 Degradation of RNA  | UDP-N-glucosamine 1-carboxyvinyltransferase                       |
| PMM1301 | 2 | 0.94  | 0.43 | 0.30 | 0.94 Glutamate family / Nitrogen assimilation                  | Aminotransferase class-III pyridoxal-phosphate:Acetylornithin...  |
| PMM1304 | 2 | 0.86  | 0.69 | 0.49 | 0.54 Other   | possible cytosine deaminase                                       |
| PMM1305 | 2 | 0.55  | 0.81 | 0.57 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1307 | 2 | 1.07  | 0.15 | 0.10 | 0.35 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1309 | 2 | 0.73  | 0.39 | 0.28 | 1.00 Cell division   | Cell division protein FtsZ:Tubulin/FtsZ family                    |
| PMM1310 | 2 | 1.42  | 0.02 | 0.01 | 0.18 Regulatory functions                                      | putative Ketopantate hydroxymethyltransferase                     |
| PMM1312 | 2 | 2.02  | 0.73 | 0.52 | 0.04 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1313 | 2 | 1.71  | 0.18 | 0.13 | 0.07 Degradation of proteins, peptides, and glycopeptides      | Cip protease proteolytic subunit                                  |
| PMM1314 | 2 | 3.00  | 0.79 | 0.56 | 0.00 Degradation of proteins, peptides, and glycopeptides      | Cip protease proteolytic subunit                                  |
| PMM1315 | 2 | -0.69 | 0.06 | 0.04 | 0.41 Branched chain family                                     | Ketol-acid reductoisomerase                                       |
| PMM1317 | 2 | -1.63 | 0.36 | 0.25 | 0.03 Adaptations and atypical conditions                       | possible high light inducible protein                             |
| PMM1318 | 2 | -1.94 | 0.36 | 0.25 | 0.00 Conserved hypothetical protein                            | conserved hypothetical  |
| PMM1319 | 2 | 0.58  | 1.28 | 0.90 | 0.81 Drug and analog sensitivity                               | possible Beta-lactamase   |
| PMM1321 | 2 | 1.98  | 0.29 | 0.21 | 0.28 Nucleoprotein   | Bacterial histone-like DNA-binding protein                        |
| PMM1322 | 2 | 1.09  | 0.29 | 0.20 | 0.55 Other   | Putative Isoamylase   |
| PMM1323 | 2 | -0.31 | 0.29 | 0.21 | 0.55 Regulatory functions                                      | putative GPH family sugar transporter                             |
| PMM1324 | 2 | 0.72  | 0.22 | 0.16 | 0.51 Transport and binding proteins                            | possible transporter, membrane component                          |
| PMM1325 | 2 | 0.38  | 0.43 | 0.30 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1327 | 2 | 2.39  | 1.03 | 0.73 | 0.01 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1330 | 2 | 0.11  | 1.70 | 1.20 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1331 | 2 | -0.46 | 0.56 | 0.40 | 0.48 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1333 | 2 | 0.99  | 0.35 | 0.25 | 0.56 Protein modification and translation factors              | conserved hypothetical protein                                    |
| PMM1336 | 2 | -1.34 | 0.26 | 0.18 | 0.09 Fatty acid, phospholipid and sterol metabolism            | Peptide methionine sulfoxide reductase                            |
| PMM1339 | 2 | -0.70 | 0.34 | 0.24 | 0.33 Purine ribonucleotide biosynthesis                        | Putative [3R]-hydroxymyristoyl-[acyl carrier protein] dehydratase |
| PMM1340 | 2 | 0.52  | 0.02 | 0.01 | 0.86 Purine ribonucleotide biosynthesis                        | SAICAR synthetase   |
| PMM1342 | 2 | 0.24  | 0.34 | 0.24 | 1.00 Other   | phosphorylorynlvinamide synthetase                                |
| PMM1343 | 2 | -1.03 | 1.02 | 0.72 | 0.19 Other   | possible circadian clock protein KaiC                             |
| PMM1344 | 2 | -2.59 | 0.50 | 0.36 | 0.00 Ribosomal proteins  | possible circadian oscillation regulator KaiB                     |
| PMM1345 | 2 | -2.84 | 0.51 | 0.36 | 0.00 Ribosomal proteins  | 50S ribosomal protein L21   |
| PMM1346 | 2 | -2.29 | 1.06 | 0.75 | 0.00 Conserved hypothetical protein                            | 50S ribosomal protein L27   |
| PMM1349 | 2 | 0.86  | 0.56 | 0.39 | 0.88 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1350 | 2 | -3.37 | 1.45 | 1.02 | 0.00 Other   | Pentapeptide repeats  |
| PMM1351 | 2 | 2.52  | 0.15 | 0.11 | 0.00 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1352 | 2 | 1.08  | 0.68 | 0.48 | 0.96 Soluble electron carriers                                 | ferredoxin  |
| PMM1354 | 2 | 0.26  | 0.18 | 0.13 | 0.82 Regulatory functions                                      | putative D-3-phosphoglycerate dehydrogenase (PGDH)                |
| PMM1355 | 2 | 1.03  | 0.74 | 0.52 | 0.17 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1363 | 2 | 0.03  | 2.11 | 1.49 | 1.00 Conserved hypothetical protein                            | hypothetical  |
| PMM1365 | 2 | -0.28 | 2.50 | 1.77 | 0.23 Regulatory functions                                      | possible MATH domain  |
| PMM1368 | 2 | 0.26  | 0.13 | 0.09 | 1.00 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1369 | 2 | -2.66 | 0.08 | 0.06 | 0.00 Regulatory functions                                      | GAF domain  |
| PMM1372 | 2 | -0.35 | 0.85 | 0.60 | 0.40 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1375 | 2 | -2.86 | 0.97 | 0.68 | 0.00 Conserved hypothetical protein                            | possible M protein repeat   |
| PMM1376 | 2 | -0.31 | 0.96 | 0.68 | 0.64 Nucleoprotein   | RNA-binding protein RbpD  |
| PMM1377 | 2 | 1.21  | 0.16 | 0.11 | 0.20 Other   | possible dihydroflavonol-4-reductase (maize, petunia, tomato)...  |
| PMM1382 | 2 | 1.11  | 0.56 | 0.40 | 0.27 Fatty acid, phospholipid and sterol metabolism            | fatty acid desaturase type 2                                      |
| PMM1383 | 2 | 1.60  | 0.78 | 0.55 | 0.08 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1384 | 2 | 3.00  | 0.06 | 0.04 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein                             |
| PMM1385 | 2 | 2.89  | 0.09 | 0.06 | 0.01 Adaptations and atypical conditions                       | possible high light inducible protein                             |
| PMM1387 | 2 | 1.02  | 1.86 | 1.32 | 0.43 Conserved hypothetical protein                            | hypothetical  |
| PMM1388 | 2 | 1.93  | 1.72 | 1.21 | 0.01 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1390 | 2 | 4.01  | 0.83 | 0.59 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein                             |
| PMM1391 | 2 | 0.04  | 0.25 | 0.18 | 1.00 Regulatory functions                                      | possible Helix-turn-helix protein, copG family                    |
| PMM1392 | 2 | 1.40  | 1.70 | 1.21 | 0.33 Branched chain family                                     | possible Heat-labile enterotoxin alpha chain                      |
| PMM1394 | 2 | -0.25 | 1.00 | 0.71 | 0.61 Conserved hypothetical protein                            | hypothetical  |
| PMM1395 | 2 | 2.15  | 0.77 | 0.55 | 0.00 Conserved hypothetical protein                            | hypothetical  |
| PMM1396 | 2 | 3.09  | 0.41 | 0.29 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein                             |
| PMM1397 | 2 | 3.91  | 0.14 | 0.10 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein                             |
| PMM1398 | 2 | 3.56  | 0.15 | 0.11 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein                             |
| PMM1399 | 2 | 3.99  | 0.63 | 0.44 | 0.00 Adaptations and atypical conditions                       | possible high light inducible protein                             |
| PMM1400 | 2 | -1.52 | 0.62 | 0.44 | 0.60 Other   | possible high light inducible protein                             |
| PMM1401 | 2 | -2.27 | 0.04 | 0.03 | 0.00 Conserved hypothetical protein                            | possible Hemagglutinin-neuraminidase                              |
| PMM1402 | 2 | -1.52 | 0.57 | 0.40 | 0.17 Conserved hypothetical protein                            | conserved hypothetical  |
| PMM1404 | 2 | 5.09  | 0.38 | 0.27 | 0.00 Adaptations and atypical conditions                       | unnamed protein product   |
| PMM1405 | 2 | 0.65  | 0.69 | 0.48 | 0.66 Conserved hypothetical protein                            | possible high light inducible protein                             |
| PMM1407 | 2 | 0.90  | 0.26 | 0.18 | 0.31 Other   | hypothetical  |
| PMM1408 | 2 | 0.06  | 0.15 | 0.10 | 0.65 Conserved hypothetical protein                            | possible SRP19 protein  |
| PMM1409 | 2 | 3.07  | 0.30 | 0.21 | 0.00 Other   | hypothetical  |
| PMM1412 | 2 | 2.86  | 1.28 | 0.91 | 0.00 Conserved hypothetical protein                            | possible Rubredoxin   |
| PMM1413 | 2 | 1.24  | 1.32 | 0.93 | 0.32 Conserved hypothetical protein                            | conserved hypothetical  |
| PMM1416 | 2 | 0.43  | 0.10 | 0.07 | 0.88 Conserved hypothetical protein                            | conserved hypothetical  |
| PMM1419 | 2 | -0.79 | 0.83 | 0.58 | 0.31 Transport and binding proteins                            | possible ATP synthase B/B' CF(0)                                  |
| PMM1422 | 2 | 1.16  | 0.22 | 0.15 | 0.22 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1423 | 2 | 0.79  | 0.76 | 0.54 | 0.56 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1424 | 2 | 0.43  | 0.28 | 0.20 | 1.00 Other   | possible Uncharacterized protein family UPF003                    |
| PMM1427 | 2 | 3.23  | 0.33 | 0.23 | 0.00 Conserved hypothetical protein                            | conserved hypothetical  |
| PMM1428 | 2 | 1.17  | 2.48 | 1.75 | 0.84 Conserved hypothetical protein                            | conserved hypothetical  |
| PMM1429 | 2 | 1.50  | 0.59 | 0.42 | 0.10 Conserved hypothetical protein                            | conserved hypothetical  |
| PMM1430 | 2 | 0.33  | 0.97 | 0.68 | 0.66 Conserved hypothetical protein                            | conserved hypothetical  |
| PMM1431 | 2 | -0.02 | 0.23 | 0.16 | 0.67 RNA synthesis, modification, and DNA transcription        | putative DNA-directed RNA polymerase (omega chain)                |
| PMM1434 | 2 | 0.78  | 0.30 | 0.21 | 1.00 Glycolysis  | Phosphoglycerate mutase, co-factor-independent (IPGM)             |
| PMM1435 | 2 | 1.03  | 0.08 | 0.06 | 0.33 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1436 | 2 | -1.86 | 0.30 | 0.21 | 0.07 Chaperones  | GroEL protein (Chaperonin cpn60)                                  |
| PMM1437 | 2 | -2.01 | 0.22 | 0.15 | 0.03 Chaperones  | GroES protein (Chaperonin cpn10)                                  |
| PMM1438 | 2 | -3.18 | 0.88 | 0.62 | 0.00 ATP synthase  | ATP synthase beta subunit, central region:ATP synth...            |
| PMM1440 | 2 | -1.68 | 0.34 | 0.24 | 0.01 Conserved hypothetical protein                            | conserved hypothetical protein                                    |
| PMM1441 | 2 | -1.90 | 1.62 | 1.15 | 0.00 Conserved hypothetical protein                            | hypothetical  |

|         |   |           |      |      |   |  |
|---------|---|-----------|------|------|---|--|
| PMM1442 | 2 | 1.73      | 0.59 | 0.42 | 0.04 Regulatory functions                                 | putative aminopeptidase P  |
| PMM1443 | 2 | 0.46      | 0.56 | 0.39 | 0.93 Conserved hypothetical protein                       | Domain of unknown function DUF21   |
| PMM1449 | 2 | 1.41      | 0.96 | 0.68 | 0.09 Soluble electron carriers                            | ferredoxin   |
| PMM1451 | 2 | -3.17     | 0.32 | 0.23 | 0.00 ATP synthase   | ATP synthase alpha subunit, central region:ATP synth...                            |
| PMM1452 | 2 | -4.69     | 0.60 | 0.43 | 0.00 ATP synthase   | ATP synthase, delta (OSCP) subunit   |
| PMM1453 | 2 | -5.56     | 0.25 | 0.17 | 0.00 ATP synthase   | ATP synthase B/B' CfO  |
| PMM1454 | 2 | -4.92     | 0.56 | 0.40 | 0.00 ATP synthase   | ATP synthase B/B' CfO  |
| PMM1455 | 2 | -4.35     | 0.18 | 0.13 | 0.00 Membranes, lipoproteins and porins                   | Eubacterial and plasma membrane ATP synthase subunit C:ATP sy...                   |
| PMM1456 | 2 | -2.29     | 0.44 | 0.31 | 0.00 ATP synthase   | ATP synthase A subunit   |
| PMM1457 | 2 | -3.62     | 0.24 | 0.17 | 0.00 Conserved hypothetical protein                       | possible ATP synthase subunit 1  |
| PMM1459 | 2 | 0.36      | 0.55 | 0.39 | 1.00 Regulatory functions                                 | putative c-type cytochrome biogenesis protein CcdA                                 |
| PMM1462 | 2 | -0.10     | 0.44 | 0.31 | 1.00 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1463 | 2 | 0.69      | 0.67 | 0.47 | 0.56 Other  | Nitrogen regulatory protein P-II   |
| PMM1477 | 2 | 2.42      | 0.98 | 0.70 | 0.00 Conserved hypothetical protein                       | conserved hypothetical   |
| PMM1478 | 2 | 1.15      | 0.48 | 0.34 | 0.39 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1479 | 2 | 0.98      | 0.45 | 0.32 | 1.00 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1480 | 2 | 1.00      | 0.26 | 0.19 | 0.24 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1482 | 2 | -1.82     | 0.80 | 0.57 | 0.23 Adaptations and atypical conditions                  | possible high light inducible protein  |
| PMM1483 | 2 | -0.46     | 0.42 | 0.30 | 0.33 RNA synthesis, modification, and DNA transcription   | RNA polymerase beta prime subunit  |
| PMM1484 | 2 | 0.15      | 0.03 | 0.02 | 0.66 RNA synthesis, modification, and DNA transcription   | RNA polymerase gamma subunit   |
| PMM1485 | 2 | 0.21      | 0.49 | 0.35 | 0.88 RNA synthesis, modification, and DNA transcription   | RNA polymerase beta subunit  |
| PMM1487 | 2 | -0.97     | 1.52 | 1.07 | 0.17 Ribosomal proteins                                   | 30S Ribosomal protein S20  |
| PMM1489 | 2 | 0.42      | 0.56 | 0.40 | 1.00 Other  | Ribose 5-phosphate isomerase   |
| PMM1490 | 2 | 2.79      | 0.39 | 0.28 | 0.00 Degradation of proteins, peptides, and glycopeptides | Serine proteases, trypsin family:Chymotrypsin serine protease...                   |
| PMM1492 | 2 | -0.07     | 0.21 | 0.15 | 0.51 RNA synthesis, modification, and DNA transcription   | N utilization substance protein A  |
| PMM1494 | 2 | -0.02     | 0.89 | 0.63 | 0.72 Protein modification and translation factors         | Translation initiation factor IF-2   |
| PMM1495 | 2 | -0.69     | 1.26 | 0.89 | 0.55 Conserved hypothetical protein                       | hypothetical   |
| PMM1498 | 2 | 1.35      | 0.42 | 0.29 | 0.33 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1499 | 2 | 0.96      | 0.07 | 0.05 | 0.29 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1500 | 2 | 1.03      | 0.14 | 0.10 | 0.36 Regulatory functions                                 | putative aminotransferase  |
| PMM1501 | 2 | -0.37     | 0.39 | 0.27 | 0.39 Other  | S1 RNA binding domain:ribonuclease E and G   |
| PMM1504 | 2 | -0.84     | 0.77 | 0.54 | 0.21 Aromatic amino acid family                           | Chorismate mutase-Prephenate dehydratase   |
| PMM1506 | 2 | -0.89     | 0.18 | 0.13 | 0.25 Regulatory functions                                 | ATP-dependent protease La (LON) domain   |
| PMM1507 | 2 | -2.01     | 0.43 | 0.30 | 0.00 Ribosomal proteins                                   | 30S ribosomal protein S10  |
| PMM1508 | 2 | -0.17     | 0.39 | 0.28 | 0.78 Protein modification and translation factors         | Elongation factor Tu   |
| PMM1509 | 2 | 0.03      | 0.08 | 0.06 | 0.84 Protein modification and translation factors         | Elongation factor G  |
| PMM1510 | 2 | -0.19     | 0.55 | 0.39 | 0.58 Ribosomal proteins                                   | 30S ribosomal protein S7   |
| PMM1511 | 2 | -3.29     | 0.10 | 0.07 | 0.00 Ribosomal proteins                                   | 30S ribosomal protein S12  |
| PMM1512 | 2 | 0.94      | 0.35 | 0.25 | 0.40 Glutamate family / Nitrogen assimilation             | Ferrodoxin-dependent glutamate synthase, Fd-GOGAT                                  |
| PMM1514 | 2 | 0.74      | 1.74 | 1.23 | 0.87 Other  | lipoic acid synthetase   |
| PMM1515 | 2 | 0.05      | 0.88 | 0.62 | 1.00 Other  | Site-specific recombinase  |
| PMM1519 | 2 | -2.00     | 0.02 | 0.01 | 0.00 Photosystem I  | Photosystem I Psal protein (subunit XI)  |
| PMM1520 | 2 | -2.68     | 0.84 | 0.59 | 0.00 Photosystem I  | photosystem I subunit VIII (Psal)  |
| PMM1523 | 2 | -1.56     | 0.56 | 0.40 | 0.02 Photosystem I  | Photosystem I Psab protein   |
| PMM1524 | 2 | -0.59     | 0.20 | 0.14 | 0.94 Photosystem I  | Photosystem I Psaa protein   |
| PMM1528 | 2 | 0.17      | 0.46 | 0.33 | 1.00 DNA replication, recombination, and repair           | HNH endonuclease family protein  |
| PMM1530 | 2 | -1.07     | 0.14 | 0.10 | 0.15 Ribosomal proteins                                   | 50S ribosomal protein L31  |
| PMM1531 | 2 | -0.87     | 0.40 | 0.28 | 1.00 Ribosomal proteins                                   | 30S ribosomal protein S9   |
| PMM1532 | 2 | -2.98     | 0.01 | 0.00 | 0.00 Ribosomal proteins                                   | 50S ribosomal protein L13  |
| PMM1534 | 2 | -1.33     | 0.27 | 0.19 | 0.02 Ribosomal proteins                                   | 50S ribosomal protein L17  |
| PMM1535 | 2 | -0.84     | 0.50 | 0.35 | 0.21 RNA synthesis, modification, and DNA transcription   | Bacterial RNA polymerase, alpha chain  |
| PMM1536 | 2 | -3.01     | 0.15 | 0.11 | 0.00 Ribosomal proteins                                   | 30S ribosomal protein S11  |
| PMM1537 | 2 | -4.16     | 0.29 | 0.20 | 0.00 Ribosomal proteins                                   | 30S ribosomal protein S13  |
| PMM1538 | 2 | -4.17     | 0.82 | 0.58 | 0.00 Ribosomal proteins                                   | 50S Ribosomal protein L36  |
| PMM1540 | 2 | -0.70     | 0.18 | 0.13 | 0.36 Protein and peptide secretion                        | preprotein translocase SecY subunit  |
| PMM1541 | 2 | -3.24     | 0.81 | 0.57 | 0.00 Ribosomal proteins                                   | 50S ribosomal protein L15  |
| PMM1542 | 2 | -2.83     | 0.02 | 0.02 | 0.00 Ribosomal proteins                                   | 30S ribosomal protein S5   |
| PMM1543 | 2 | -0.99     | 0.77 | 0.55 | 0.27 Ribosomal proteins                                   | 50S ribosomal protein L18  |
| PMM1544 | 2 | -1.87     | 0.36 | 0.25 | 0.00 Ribosomal proteins                                   | 50S ribosomal protein L6   |
| PMM1545 | 2 | -1.00     | 0.42 | 0.30 | 0.21 Ribosomal proteins                                   | 30S ribosomal protein S8   |
| PMM1546 | 2 | -0.19     | 0.90 | 0.63 | 0.51 Ribosomal proteins                                   | 50S ribosomal protein L5   |
| PMM1548 | 2 | -0.36     | 0.43 | 0.30 | 0.69 Ribosomal proteins                                   | 50S ribosomal protein L14  |
| PMM1549 | 2 | #NAME? NA | NA   | NA   | 0.07 Ribosomal proteins                                   | 30S ribosomal protein L17  |
| PMM1550 | 2 | -1.93     | 0.75 | 0.53 | 0.13 Ribosomal proteins                                   | 50S ribosomal protein L29  |
| PMM1551 | 2 | -1.02     | 0.04 | 0.03 | 0.19 Ribosomal proteins                                   | 50S ribosomal protein L16  |
| PMM1552 | 2 | -2.56     | 0.06 | 0.04 | 0.00 Ribosomal proteins                                   | 30S ribosomal protein S3   |
| PMM1553 | 2 | -2.42     | 0.76 | 0.54 | 0.00 Ribosomal proteins                                   | 50S ribosomal protein L22  |
| PMM1554 | 2 | -2.15     | 0.69 | 0.49 | 0.00 Ribosomal proteins                                   | 30S Ribosomal protein S19  |
| PMM1555 | 2 | -2.54     | 0.59 | 0.42 | 0.00 Ribosomal proteins                                   | 50S ribosomal protein L2   |
| PMM1556 | 2 | -2.11     | 0.03 | 0.02 | 0.00 Ribosomal proteins                                   | 50S ribosomal protein L23  |
| PMM1557 | 2 | -1.14     | 0.29 | 0.21 | 0.13 Ribosomal proteins                                   | 50S ribosomal protein L4   |
| PMM1558 | 2 | -4.05     | 1.61 | 1.14 | 0.00 Ribosomal proteins                                   | 50S ribosomal protein L3   |
| PMM1559 | 2 | 0.68      | 0.44 | 0.31 | 0.65 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1562 | 2 | 3.38      | 0.66 | 0.47 | 0.00 DNA replication, recombination, and repair           | RecA bacterial DNA recombination protein   |
| PMM1563 | 2 | -1.20     | 0.71 | 0.50 | 1.00 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1566 | 2 | 0.33      | 0.33 | 0.23 | 1.00 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1568 | 2 | 0.07      | 0.10 | 0.07 | 0.56 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1570 | 2 | -1.16     | 0.23 | 0.16 | 0.16 Cobalamin, heme, phycobilin and porphyrin            | ATP:corrinoid adenosyltransferase BtuR/CobD/CobP                                   |
| PMM1571 | 2 | 1.08      | 0.95 | 0.67 | 0.51 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1575 | 2 | 0.51      | 0.06 | 0.04 | 1.00 Pyruvate and acetyl-CoA metabolism                   | Phosphoenolpyruvate carboxylase  |
| PMM1578 | 2 | -1.59     | 0.46 | 0.32 | 0.03 Photosystem I  | Photosystem I protein Psab   |
| PMM1581 | 2 | 0.63      | 0.05 | 0.04 | 0.77 Regulatory functions                                 | MRP protein homolog  |
| PMM1583 | 2 | 0.53      | 0.07 | 0.05 | 0.94 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1585 | 2 | -1.67     | 0.21 | 0.15 | 0.08 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1588 | 2 | 1.70      | 0.27 | 0.19 | 0.08 Regulatory functions                                 | possible Conserved carboxylase domain  |
| PMM1594 | 2 | 0.62      | 0.21 | 0.15 | 1.00 Cobalamin, heme, phycobilin and porphyrin            | Heme oxygenase   |
| PMM1596 | 2 | -0.25     | 0.71 | 0.50 | 0.52 Other  | Isocitrate dehydrogenase   |
| PMM1599 | 2 | -0.17     | 0.08 | 0.06 | 0.61 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1600 | 2 | 0.74      | 0.33 | 0.24 | 0.97 Transport and binding proteins                       | putative Na <sup>+</sup> /H <sup>+</sup> antiporter, CPA2 family                   |
| PMM1601 | 2 | 2.14      | 0.09 | 0.06 | 0.01 Other  | phosphorylase  |
| PMM1602 | 2 | 1.45      | 0.33 | 0.23 | 0.19 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1603 | 2 | 2.15      | 1.32 | 0.93 | 0.00 Regulatory functions                                 | putative ribonuclease III  |
| PMM1604 | 2 | -1.43     | 0.91 | 0.64 | 0.02 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1605 | 2 | 1.89      | 1.01 | 0.71 | 0.05 Protein modification and translation factors         | possible 16S rRNA processing protein RimM  |
| PMM1606 | 2 | -0.50     | 0.40 | 0.28 | 0.36 Other  | Glutamine-fructose-6-phosphate transaminase (isomerizing)                          |
| PMM1607 | 2 | -2.05     | 0.82 | 0.58 | 0.00 Photosystem I  | Photosystem I subunit Psab   |
| PMM1608 | 2 | -3.46     | 0.83 | 0.59 | 0.00 Fatty acid, phospholipid and sterol metabolism       | acyl carrier protein (ACP)   |
| PMM1609 | 2 | -3.09     | 0.47 | 0.33 | 0.00 Fatty acid, phospholipid and sterol metabolism       | 3-oxoacyl-[acyl-carrier-protein] synthase II                                       |
| PMM1610 | 2 | -1.86     | 0.70 | 0.49 | 0.00 Other  | Transketolase  |
| PMM1611 | 2 | 1.65      | 0.15 | 0.11 | 0.15 Thiamine   | ThiC family  |
| PMM1613 | 2 | 0.92      | 0.23 | 0.17 | 0.40 Other  | Zinc metallopeptidase M20/M25/M40 family   |
| PMM1615 | 2 | 2.15      | 1.06 | 0.75 | 0.01 DNA replication, recombination, and repair           | Holliday junction DNA helicase RuvB  |
| PMM1616 | 2 | 0.80      | 0.39 | 0.28 | 0.45 Other  | tRNA binding protein SmpB  |
| PMM1617 | 2 | -1.28     | 0.12 | 0.08 | 0.50 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1619 | 2 | -0.29     | 0.27 | 0.19 | 0.82 Regulatory functions                                 | two-component response regulator   |
| PMM1622 | 2 | 1.39      | 0.48 | 0.34 | 0.15 Murine sacculus and peptidoglycan                    | Rod shape determining protein  |
| PMM1623 | 2 | 3.08      | 0.94 | 0.67 | 0.00 DNA replication, recombination, and repair           | single-stranded DNA-binding protein  |
| PMM1625 | 2 | 0.64      | 0.40 | 0.28 | 1.00 Amino acids and amines                               | putative adenosylhomocysteine  |
| PMM1626 | 2 | 2.25      | 0.32 | 0.23 | 0.00 Conserved hypothetical protein                       | conserved hypothetical protein   |
| PMM1629 | 2 | 1.20      | 0.00 | 0.00 | 0.21 Transport and binding proteins                       | Type II alternative RNA polymerase sigma factor, sigma-70 family                   |
| PMM1630 | 2 | -0.14     | 0.05 | 0.03 | 0.77 Transport and binding proteins                       | MgtE family, putative magnesium transport protein                                  |
| PMM1634 | 2 | 1.25      | 0.85 | 0.60 | 0.28 DNA replication, recombination, and repair           | DNA gyrase, subunit B  |
| PMM1635 | 2 | -0.23     | 0.67 | 0.47 | 0.50 Aminoacyl tRNA synthetases and tRNA modification     | tRNA delta-2-isopentenylpyrophosphate (IPP) transferase                            |
| PMM1636 | 2 | -0.60     | 0.58 | 0.41 | 0.89 Protein modification and translation factors         | Translation Initiation factor 3  |
| PMM1639 | 2 | -0.17     | 0.42 | 0.29 | 0.51 Protein and peptide secretion                        | Preprotein translocase SecA subunit  |
| PMM1640 | 2 | 0.23      | 1.20 | 0.85 | 1.00 Regulatory functions                                 | putative acetyltransferase, GNAT family  |
| PMM1642 | 2 | 0.15      | 0.24 | 0.17 | 1.00 Regulatory functions                                 | possible transcription regulator   |
| PMM1643 | 2 | -1.75     | 0.85 | 0.60 | 0.00 Riboflavin   | Putative 6,7-dimethyl-8-ribityllumazine synthase or riboflavin synthase beta chain |

|         |   |       |      |      |   |  |
|---------|---|-------|------|------|---|--|
| PMM1644 | 2 | -3.40 | 1.11 | 0.78 | 0.00 Photosystem II                                       | possible Photosystem II reaction center Z protein (PsbZ)         |
| PMM1648 | 2 | 0.28  | 0.08 | 0.06 | 0.78 Branched chain family                                | Aspartate kinase   |
| PMM1649 | 2 | 0.32  | 0.29 | 0.20 | 1.00 DNA replication, recombination, and repair           | Exonuclease ABC subunit B (UvrB)                                 |
| PMM1650 | 2 | -1.45 | 0.12 | 0.09 | 0.03 Conserved hypothetical protein                       | conserved hypothetical protein                                   |
| PMM1652 | 2 | 0.55  | 0.43 | 0.30 | 1.00 Conserved hypothetical protein                       | conserved hypothetical protein                                   |
| PMM1653 | 2 | 0.37  | 0.21 | 0.15 | 0.88 Aspartate family                                     | Dihydrodipicolinate synthetase                                   |
| PMM1655 | 2 | -1.37 | 1.55 | 1.09 | 0.01 Other  | FKBP-type peptidyl-prolyl cis-trans isomerase (PPase)            |
| PMM1656 | 2 | -0.28 | 2.12 | 1.50 | 0.20 Degradation of proteins, peptides, and glycopeptides | Clp protease proteolytic subunit                                 |
| PMM1657 | 2 | -0.82 | 0.34 | 0.24 | 0.15 Degradation of proteins, peptides, and glycopeptides | Clp protease ATP-binding subunit, ClpX                           |
| PMM1661 | 2 | -2.81 | 1.16 | 0.82 | 0.00 Ribosomal proteins                                   | 50S ribosomal protein L35  |
| PMM1662 | 2 | -2.32 | 1.34 | 0.94 | 0.00 Ribosomal proteins                                   | 50S ribosomal protein L20  |
| PMM1665 | 2 | -1.72 | 0.13 | 0.09 | 0.00 Fatty acid, phospholipid and sterol metabolism       | sulfolipase (UDP-sulfoquinovose) biosynthesis protein            |
| PMM1667 | 2 | 0.69  | 0.39 | 0.28 | 0.71 Conserved hypothetical protein                       | conserved hypothetical protein                                   |
| PMM1669 | 2 | 2.25  | 0.94 | 0.67 | 0.00 Regulatory functions                                 | putative Glycine cleavage H-protein                              |
| PMM1671 | 2 | 2.53  | 0.94 | 0.66 | 0.00 Conserved hypothetical protein                       | conserved hypothetical protein                                   |
| PMM1672 | 2 | 2.04  | 0.51 | 0.36 | 0.01 Fatty acid, phospholipid and sterol metabolism       | Fatty acid desaturase, type 1                                    |
| PMM1673 | 2 | -0.32 | 0.70 | 0.49 | 0.53 Ribosomal proteins                                   | 50S ribosomal protein L9   |
| PMM1676 | 2 | 0.94  | 1.22 | 0.86 | 0.73 Conserved hypothetical protein                       | conserved hypothetical protein                                   |
| PMM1678 | 2 | 0.96  | 0.53 | 0.37 | 0.41 Conserved hypothetical protein                       | conserved hypothetical protein                                   |
| PMM1680 | 2 | 3.09  | 0.94 | 0.66 | 0.00 Conserved hypothetical protein                       | conserved hypothetical protein                                   |
| PMM1683 | 2 | -1.16 | 0.28 | 0.20 | 0.10 Conserved hypothetical protein                       | conserved hypothetical protein                                   |
| PMM1685 | 2 | 1.94  | 0.13 | 0.09 | 0.00 Regulatory functions                                 | conserved hypothetical protein                                   |
| PMM1688 | 2 | 0.00  | 0.14 | 0.10 | 0.65 Aminocycl RNA synthetases and tRNA modification      | putative spermidine synthase                                     |
| PMM1689 | 2 | 1.44  | 0.24 | 0.17 | 0.15 Pyrimidine ribonucleotide biosynthesis               | Aspartyl-tRNA synthetase   |
| PMM1694 | 2 | 1.50  | 0.62 | 0.44 | 0.06 Cobalamin, heme, phycobilin and porphyrin            | Glutamine amidotransferase class-I:CTP synthase                  |
| PMM1697 | 2 | -0.69 | 0.48 | 0.24 | 0.37 Transport and binding proteins                       | putative uroporphyrin-III C-methyltransferase                    |
| PMM1700 | 2 | 3.80  | 0.42 | 0.30 | 0.00 Other  | Type II alternative RNA polymerase sigma factor, sigma-70 family |
| PMM1702 | 2 | -0.68 | 0.07 | 0.05 | 0.25 Purine ribonucleotide biosynthesis                   | Aconitase hydratase B  |
| PMM1703 | 2 | 1.45  | 0.05 | 0.04 | 0.07 Transport and binding proteins                       | formyltetrahydrofolate deformylase                               |
| PMM1704 | 2 | -1.72 | 0.74 | 0.52 | 0.13 Chaperones   | NAD binding site-D-amino acid oxidase                            |
| PMM1706 | 2 | -2.20 | 2.23 | 1.58 | 0.00 Ribosomal proteins                                   | Molecular chaperone DnaK2, heat shock protein hsp70-2            |
| PMM1707 | 2 | 0.62  | 0.76 | 0.54 | 0.88 Glutamate family / Nitrogen assimilation             | 30S ribosomal protein S6   |
| PMM1708 | 2 | 0.12  | 0.65 | 0.46 | 0.79 Conserved hypothetical protein                       | Argininosuccinate synthetase                                     |
| PMM1716 | 2 | 0.86  | 0.82 | 0.58 | 0.39 Aspartate family                                     | conserved hypothetical protein                                   |
| PMM1717 | 2 | -3.05 | 0.42 | 0.30 | 0.00 Other  | No Cyanobase Name  |
| PMM1718 | 2 | -0.73 | 0.89 | 0.63 | 0.76 Other  | No Cyanobase Name  |