**Figure 3-sourcet data 1.** List of the proteins identified in the proteome of *T. ammonificans* grown under nitrate reducing conditions.

| **Locus** | **Product name** | ***Gene Name*** | **Accession number** | **MW (kDa)** | **NSAF %** |
| --- | --- | --- | --- | --- | --- |
| Theam\_0001 | anthranilate synthase component I | *trpE* | YP\_004150616.1 | 55 | **0.09** |
| Theam\_0005 | glycosyl transferase group 1 | *alg1* | YP\_004150620.1 | 64 | **0.09** |
| Theam\_0007 | DNA polymerase III, beta subunit | *dnaN* | YP\_004150622.1 | 39 | **0.25** |
| Theam\_0010 | Polyprenyl synthetase | *ggpps* | YP\_004150625.1 | 32 | **0.10** |
| Theam\_0011 | deoxyxylulose-5-phosphate synthase | *dxs* | YP\_004150626.1 | 68 | **0.02** |
| Theam\_0025 | phage protein |  | YP\_004150640.1 | 40 | **0.04** |
| Theam\_0045 | hypothetical protein |  | YP\_004150660.1 | 9 | **0.02** |
| Theam\_0050 | hypothetical protein |  | YP\_004150665.1 | 35 | **0.03** |
| Theam\_0051 | hypothetical protein |  | YP\_004150666.1 | 33 | **0.01** |
| Theam\_0069 | Rhodanese domain protein |  | YP\_004150684.1 | 14 | **1.06** |
| Theam\_0070 | regulatory protein ArsR | *arsR* | YP\_004150685.1 | 14 | **0.04** |
| Theam\_0071 | carbonic anhydrase | *cah* | YP\_004150686.1 | 25 | **0.04** |
| Theam\_0073 | methylthioadenosine phosphorylase | *mtaP* | YP\_004150688.1 | 32 | **0.58** |
| Theam\_0074 | 50S ribosomal Protein L19 (hypothetical protein) | *rpL19* | YP\_004150689.1 | 11 | **0.09** |
| Theam\_0075 | imidazoleglycerol phosphate synthase, cyclase subunit | *hisF* | YP\_004150690.1 | 27 | **0.06** |
| Theam\_0076 | thiamine biosynthesis protein ThiC | *thiC* | YP\_004150691.1 | 48 | **0.23** |
| Theam\_0077 | thiazole biosynthesis enzyme | *thi1* | YP\_004150692.1 | 29 | **1.13** |
| Theam\_0078 | hypothetical protein |  | YP\_004150693.1 | 48 | **0.06** |
| Theam\_0079 | amidohydrolase | *ah* | YP\_004150694.1 | 45 | **0.02** |
| Theam\_0080 | orotate phosphoribosyltransferase | *pyrE* | YP\_004150695.1 | 22 | **0.10** |
| Theam\_0081 | Polyprenyl synthetase | *idsB* | YP\_004150696.1 | 36 | **0.11** |
| Theam\_0084 | NAD-dependent epimerase/dehydratase |  | YP\_004150699.1 | 37 | **0.05** |
| Theam\_0085 | chromosome segregation protein SMC | *smc* | YP\_004150700.1 | 134 | **0.01** |
| Theam\_0088 | ribosome recycling factor | *frr* | YP\_004150703.1 | 21 | **0.03** |
| Theam\_0089 | uridylate kinase | *pyrH* | YP\_004150704.1 | 26 | **0.19** |
| Theam\_0090 | translation elongation factor Ts | *tsf* | YP\_004150705.1 | 22 | **0.46** |
| Theam\_0091 | ribosomal protein S2 | *rpsB\_bact* | YP\_004150706.1 | 33 | **0.46** |
| Theam\_0092 | 5-oxoprolinase (ATP-hydrolyzing) | *opla* | YP\_004150707.1 | 56 | **0.03** |
| Theam\_0093 | 5-oxoprolinase (ATP-hydrolyzing) | *opla* | YP\_004150708.1 | 71 | **0.11** |
| Theam\_0094 | ubiquinone/menaquinone biosynthesis methyltransferase | *men\_ubi* | YP\_004150709.1 | 24 | **0.01** |
| Theam\_0095 | hypothetical protein |  | YP\_004150710.1 | 44 | **0.00** |
| Theam\_0098 | apurinic endonuclease Apn1 | *nfo* | YP\_004150713.1 | 32 | **0.02** |
| Theam\_0100 | hypothetical protein |  | YP\_004150715.1 | 13 | **0.10** |
| Theam\_0101 | hypothetical protein |  | YP\_004150716.1 | 15 | **0.02** |
| Theam\_0102 | hypothetical protein |  | YP\_004150717.1 | 22 | **0.02** |
| Theam\_0103 | hypothetical protein |  | YP\_004150718.1 | 12 | **0.05** |
| Theam\_0104 | beta-lactamase domain protein |  | YP\_004150719.1 | 32 | **0.09** |
| Theam\_0105 | Roadblock/LC7 family protein |  | YP\_004150720.1 | 13 | **0.01** |
| Theam\_0106 | pyrimidine-nucleoside phosphorylase | *pynp* | YP\_004150721.1 | 46 | **0.05** |
| Theam\_0108 | AMMECR1 domain protein |  | YP\_004150723.1 | 22 | **0.03** |
| Theam\_0122 | outer membrane assembly lipoprotein YfiO | *yfiO* | YP\_004150737.1 | 37 | **0.01** |
| Theam\_0126 | protein of unknown function DUF481 |  | YP\_004150741.1 | 25 | **0.03** |
| Theam\_0129 | histone family protein DNA-binding protein |  | YP\_004150744.1 | 11 | **0.13** |
| Theam\_0132 | non-canonical NTP pyrophosphatase rdgB/HAM1 family | *rdgB* | YP\_004150747.1 | 22 | **0.12** |
| Theam\_0133 | ribonuclease PH | *RNasePH* | YP\_004150748.1 | 26 | **0.06** |
| Theam\_0136 | ATP-dependent Clp protease, proteolytic subunit ClpP | *clpP* | YP\_004150751.1 | 22 | **0.31** |
| Theam\_0137 | 3,4-dihydroxy-2-butanone 4-phosphate synthase | *ribA* | YP\_004150752.1 | 48 | **0.03** |
| Theam\_0139 | diguanylate phosphodiesterase CDS |  | YP\_004150753.1 | 77 | **0.00** |
| Theam\_0140 | shikimate 5-dehydrogenase | *aroE* | YP\_004150754.1 | 30 | **0.05** |
| Theam\_0142 | ribosomal protein L27 | *rpl27* | YP\_004150756.1 | 9 | **0.17** |
| Theam\_0143 | ribosomal protein L21 | *rpl21* | YP\_004150757.1 | 11 | **0.46** |
| Theam\_0145 | inosine-5'-monophosphate dehydrogenase | *impdh* | YP\_004150759.1 | 53 | **0.53** |
| Theam\_0146 | argininosuccinate lyase | *argH* | YP\_004150760.1 | 52 | **0.15** |
| Theam\_0147 | Transketolase domain-containing protein |  | YP\_004150761.1 | 32 | **0.11** |
| Theam\_0148 | Transketolase central region |  | YP\_004150762.1 | 34 | **0.36** |
| Theam\_0149 | carboxyl-terminal protease | *prc* | YP\_004150763.1 | 49 | **0.02** |
| Theam\_0151 | hypothetical protein |  | YP\_004150765.1 | 37 | **0.02** |
| Theam\_0155 | Radical SAM domain protein |  | YP\_004150769.1 | 40 | **0.00** |
| Theam\_0157 | chemotaxis sensory transducer |  | YP\_004150771.1 | 68 | **0.06** |
| Theam\_0159 | dihydroorotate dehydrogenase family protein | *pyrD1* | YP\_004150773.1 | 32 | **0.11** |
| Theam\_0161 | Tetratricopeptide TPR\_1 repeat-containing protein |  | YP\_004150775.1 | 67 | **0.01** |
| Theam\_0163 | peptidase M17 leucyl aminopeptidase domain protein |  | YP\_004150777.1 | 52 | **0.03** |
| Theam\_0165 | chemotaxis sensory transducer |  | YP\_004150779.1 | 86 | **0.02** |
| Theam\_0168 | phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase | *hisA* | YP\_004150782.1 | 27 | **0.15** |
| Theam\_0170 | quinolinate synthetase complex, A subunit | *nadA* | YP\_004150784.1 | 35 | **0.01** |
| Theam\_0171 | GMP synthase, large subunit | *guaA* | YP\_004150785.1 | 59 | **0.12** |
| Theam\_0179 | adenylosuccinate synthetase | *purA* | YP\_004150793.1 | 48 | **0.09** |
| Theam\_0180 | histidyl-tRNA synthetase 2 | *hisS2* | YP\_004150794.1 | 48 | **0.01** |
| Theam\_0181 | threonine synthase | *thrC* | YP\_004150795.1 | 38 | **0.16** |
| Theam\_0182 | dihydrodipicolinate synthase | *dapA* | YP\_004150796.1 | 32 | **0.35** |
| Theam\_0183 | hypothetical protein |  | YP\_004150797.1 | 40 | **0.00** |
| Theam\_0184 | dihydrodipicolinate reductase | *dapB* | YP\_004150798.1 | 28 | **0.26** |
| Theam\_0188 | hypothetical protein |  | YP\_004150802.1 | 101 | **0.01** |
| Theam\_0190 | homoserine dehydrogenase | *ak1h* | YP\_004150804.1 | 47 | **0.09** |
| Theam\_0191 | aminotransferase class I and II |  | YP\_004150805.1 | 46 | **0.09** |
| Theam\_0195 | TonB-dependent receptor plug |  | YP\_004150809.1 | 67 | **0.08** |
| Theam\_0197 | Citryl-CoA lyase | *citE* | YP\_004150811.1 | 37 | **0.06** |
| Theam\_0198 | LysR substrate-binding | *lysR* | YP\_004150812.1 | 34 | **0.01** |
| Theam\_0201 | 3-isopropylmalate dehydratase, large subunit | *haco* | YP\_004150815.1 | 46 | **0.13** |
| Theam\_0205 | nicotinate (nicotinamide) nucleotide adenylyltransferase |  | YP\_004150819.1 | 25 | **0.03** |
| Theam\_0206 | Phosphoglycerate kinase | *pgk* | YP\_004150820.1 | 45 | **0.17** |
| Theam\_0210 | Peptidoglycan-binding lysin domain |  | YP\_004150824.1 | 45 | **0.00** |
| Theam\_0215 | methionyl-tRNA formyltransferase | *fmt* | YP\_004150829.1 | 35 | **0.02** |
| Theam\_0217 | protein of unknown function DUF89 |  | YP\_004150831.1 | 34 | **0.03** |
| Theam\_0218 | phosphoribosylaminoimidazole carboxylase, catalytic subunit | *purE* | YP\_004150832.1 | 17 | **0.21** |
| Theam\_0220 | translation elongation factor P | *efp* | YP\_004150834.1 | 21 | **0.06** |
| Theam\_0221 | acetyl-CoA carboxylase, biotin carboxyl carrier protein | *accB* | YP\_004150835.1 | 16 | **0.23** |
| Theam\_0222 | acetyl-CoA carboxylase, biotin carboxylase | *accC* | YP\_004150836.1 | 49 | **0.03** |
| Theam\_0223 | Like-Sm ribonucleoprotein core |  | YP\_004150837.1 | 17 | **0.04** |
| Theam\_0227 | aminotransferase class V - serine glyoxylate | *sgt* | YP\_004150841.1 | 42 | **0.17** |
| Theam\_0228 | peptidylprolyl isomerase FKBP-type |  | YP\_004150842.1 | 16 | **0.05** |
| Theam\_0229 | flavin reductase domain protein FMN-binding |  | YP\_004150843.1 | 21 | **0.11** |
| Theam\_0230 | UbiD family decarboxylase | *ubid* | YP\_004150844.1 | 56 | **0.00** |
| Theam\_0231 | NIF3 containing protein of unknown function DUF34 |  | YP\_004150845.1 | 28 | **0.04** |
| Theam\_0233 | ATP-dependent protease La | *lon* | YP\_004150847.1 | 92 | **0.03** |
| Theam\_0234 | UTP-glucose-1-phosphate uridylyltransferase | *galU* | YP\_004150848.1 | 34 | **0.12** |
| Theam\_0235 | protein of unknown function Met10 |  | YP\_004150849.1 | 45 | **0.02** |
| Theam\_0237 | carbamoyl-phosphate synthase, small subunit | *cpsS* | YP\_004150851.1 | 42 | **0.08** |
| Theam\_0238 | periplasmic solute binding protein |  | YP\_004150852.1 | 32 | **0.03** |
| Theam\_0239 | glutamine amidotransferase of anthranilate synthase | *trpG\_papA* | YP\_004150853.1 | 21 | **0.02** |
| Theam\_0244 | dihydrouridine synthase DuS | *dus* | YP\_004150858.1 | 35 | **0.03** |
| Theam\_0245 | ribosomal protein S15 | *S15* | YP\_004150859.1 | 11 | **0.09** |
| Theam\_0246 | polyribonucleotide nucleotidyltransferase | *pnp* | YP\_004150860.1 | 79 | **0.19** |
| Theam\_0247 | deoxyUTP pyrophosphatase | *dut* | YP\_004150861.1 | 32 | **0.06** |
| Theam\_0250 | 2-isopropylmalate synthase | *leuA* | YP\_004150864.1 | 56 | **0.20** |
| Theam\_0252 | ribosomal protein S12 | *rpsL* | YP\_004150866.1 | 14 | **0.27** |
| Theam\_0253 | ribosomal protein S7 | *rpsG* | YP\_004150867.1 | 18 | **0.07** |
| Theam\_0254 | translation elongation factor G | *efG* | YP\_004150868.1 | 78 | **0.88** |
| Theam\_0256 | ribosomal protein S10 | *rpsJ* | YP\_004150870.1 | 12 | **0.96** |
| Theam\_0257 | 50S ribosomal protein L3 | *rpl3* | YP\_004150871.1 | 22 | **0.34** |
| Theam\_0258 | ribosomal protein L4/L1e | *rpsE* | YP\_004150872.1 | 24 | **0.14** |
| Theam\_0259 | Ribosomal protein L25/L23 | *rplL* | YP\_004150873.1 | 12 | **0.44** |
| Theam\_0260 | ribosomal protein L2 | *rplB* | YP\_004150874.1 | 30 | **0.26** |
| Theam\_0261 | ribosomal protein S19 | *rpsS* | YP\_004150875.1 | 11 | **0.08** |
| Theam\_0262 | ribosomal protein L22 | *rplV* | YP\_004150876.1 | 15 | **0.38** |
| Theam\_0263 | ribosomal protein S3 | *rpsC* | YP\_004150877.1 | 27 | **0.29** |
| Theam\_0264 | ribosomal protein L16 | *rplP* | YP\_004150878.1 | 16 | **0.36** |
| Theam\_0266 | 30S ribosomal protein S17 | *rps17* | YP\_004150880.1 | 12 | **0.18** |
| Theam\_0267 | ribosomal protein L14 | *rplN* | YP\_004150881.1 | 13 | **1.18** |
| Theam\_0268 | ribosomal protein L24 | *rplX* | YP\_004150882.1 | 13 | **0.13** |
| Theam\_0269 | 50S ribosomal protein L5 | *rpl5* | YP\_004150883.1 | 21 | **0.56** |
| Theam\_0271 | ribosomal protein S8 | *rps8* | YP\_004150885.1 | 16 | **0.44** |
| Theam\_0272 | ribosomal protein L6 | *rpl6* | YP\_004150886.1 | 20 | **0.23** |
| Theam\_0273 | ribosomal protein L18 | *rpl18* | YP\_004150887.1 | 14 | **0.39** |
| Theam\_0274 | ribosomal protein S5 | *rpsE* | YP\_004150888.1 | 20 | **0.34** |
| Theam\_0275 | ribosomal protein L30 | *rpmD* | YP\_004150889.1 | 7 | **0.19** |
| Theam\_0276 | ribosomal protein L15 | *rplO* | YP\_004150890.1 | 17 | **0.04** |
| Theam\_0278 | adenylate kinase | *adk* | YP\_004150892.1 | 21 | **0.27** |
| Theam\_0279 | methionine aminopeptidase, type I | *map1* | YP\_004150893.1 | 28 | **0.02** |
| Theam\_0282 | 30S ribosomal protein S13 | *rps13* | YP\_004150896.1 | 14 | **0.37** |
| Theam\_0283 | 30S ribosomal protein S11 | *rps11* | YP\_004150897.1 | 14 | **0.16** |
| Theam\_0284 | ribosomal protein S4 | *rpsD* | YP\_004150898.1 | 25 | **0.24** |
| Theam\_0285 | DNA-directed RNA polymerase, alpha subunit | *rpoA* | YP\_004150899.1 | 35 | **0.22** |
| Theam\_0286 | ribosomal protein L17 | *rpl17* | YP\_004150900.1 | 15 | **0.24** |
| Theam\_0288 | septum site-determining protein MinD | *minD* | YP\_004150902.1 | 29 | **0.01** |
| Theam\_0291 | spermidine synthase | *speE* | YP\_004150905.1 | 33 | **0.14** |
| Theam\_0292 | protein of unknown function DUF43 |  | YP\_004150906.1 | 40 | **0.30** |
| Theam\_0295 | purine or other phosphorylase family 1 |  | YP\_004150909.1 | 33 | **0.00** |
| Theam\_0297 | ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5 | *ctc* | YP\_004150911.1 | 22 | **0.10** |
| Theam\_0298 | peptidyl-tRNA hydrolase | *pth* | YP\_004150912.1 | 21 | **0.03** |
| Theam\_0299 | ribosomal protein S6 | *S6* | YP\_004150913.1 | 15 | **0.34** |
| Theam\_0301 | ribosomal protein S18 | *S18* | YP\_004150915.1 | 10 | **0.02** |
| Theam\_0303 | ribosomal protein L9 | *rpl9* | YP\_004150917.1 | 17 | **0.13** |
| Theam\_0304 | S-adenosylmethionine decarboxylase related | *speD* | YP\_004150918.1 | 20 | **0.21** |
| Theam\_0306 | endoribonuclease L-PSP | *lpsp* | YP\_004150920.1 | 14 | **0.06** |
| Theam\_0307 | regulatory protein ArsR | *arsR* | YP\_004150921.1 | 12 | **0.06** |
| Theam\_0308 | acetyl-CoA carboxylase, carboxyl transferase, beta subunit | *accD* | YP\_004150922.1 | 31 | **0.01** |
| Theam\_0310 | transcription-repair coupling factor | *mfd* | YP\_004150924.1 | 119 | **0.00** |
| Theam\_0311 | Ankyrin |  | YP\_004150925.1 | 26 | **0.01** |
| Theam\_0313 | hypothetical protein |  | YP\_004150927.1 | 43 | **0.01** |
| Theam\_0315 | excinuclease ABC, A subunit | *uvra* | YP\_004150929.1 | 105 | **0.00** |
| Theam\_0316 | DsrE family protein |  | YP\_004150930.1 | 13 | **0.24** |
| Theam\_0324 | CMP/dCMP deaminase zinc-binding |  | YP\_004150938.1 | 14 | **0.07** |
| Theam\_0325 | response regulator receiver |  | YP\_004150939.1 | 26 | **0.03** |
| Theam\_0326 | hypothetical protein |  | YP\_004150940.1 | 22 | **0.06** |
| Theam\_0327 | Glutamate synthase (ferredoxin) | *gltA* | YP\_004150941.1 | 159 | **0.17** |
| Theam\_0328 | phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase | *purH* | YP\_004150942.1 | 59 | **0.14** |
| Theam\_0331 | alanine racemase | *alr* | YP\_004150945.1 | 39 | **0.01** |
| Theam\_0332 | ribosomal L11 methyltransferase | *rpl11* | YP\_004150946.1 | 30 | **0.01** |
| Theam\_0333 | PHP domain protein |  | YP\_004150947.1 | 31 | **0.01** |
| Theam\_0334 | Protein of unknown function DUF2081 |  | YP\_004150948.1 | 74 | **0.00** |
| Theam\_0337 | heat shock protein HslVU, ATPase subunit HslU | *hslU* | YP\_004150951.1 | 55 | **0.01** |
| Theam\_0338 | peptidase M24 | *pM24* | YP\_004150952.1 | 38 | **0.03** |
| Theam\_0342 | CRISPR-associated protein, Csx11 family |  | YP\_004150956.1 | 123 | **0.00** |
| Theam\_0344 | CRISPR-associated RAMP protein, Cmr1 family |  | YP\_004150958.1 | 50 | **0.00** |
| Theam\_0347 | 3-isopropylmalate dehydratase, small subunit | *leuA* | YP\_004150961.1 | 18 | **0.19** |
| Theam\_0348 | 3-isopropylmalate dehydrogenase | *leuB* | YP\_004150962.1 | 40 | **0.38** |
| Theam\_0349 | aspartate-semialdehyde dehydrogenase | *dhaS* | YP\_004150963.1 | 37 | **0.23** |
| Theam\_0350 | hypothetical protein |  | YP\_004150964.1 | 14 | **0.02** |
| Theam\_0351 | metal-dependent hydrolase |  | YP\_004150965.1 | 25 | **0.18** |
| Theam\_0354 | Peptidase M23 | *pM23* | YP\_004150968.1 | 39 | **0.00** |
| Theam\_0356 | TrkA-N domain protein |  | YP\_004150970.1 | 48 | **0.03** |
| Theam\_0357 | cytochrome c-type biogenesis protein CcsB | *ccsB* | YP\_004150971.1 | 38 | **0.01** |
| Theam\_0358 | ResB family protein |  | YP\_004150972.1 | 50 | **0.00** |
| Theam\_0360 | metal dependent phophohydrolase | *hdig* | YP\_004150974.1 | 55 | **0.01** |
| Theam\_0362 | ATPase AAA-2 domain protein |  | YP\_004150976.1 | 94 | **0.01** |
| Theam\_0363 | protein of unknown function DUF558 |  | YP\_004150977.1 | 26 | **0.07** |
| Theam\_0365 | Appr-1-p processing domain protein |  | YP\_004150979.1 | 19 | **0.12** |
| Theam\_0373 | 2-isopropylmalate synthase/homocitrate synthase family protein | *leu1* | YP\_004150987.1 | 60 | **0.16** |
| Theam\_0374 | aspartate kinase | *aspK* | YP\_004150988.1 | 44 | **0.40** |
| Theam\_0375 | molybdenum cofactor synthesis domain protein | *moeA* | YP\_004150989.1 | 44 | **0.00** |
| Theam\_0376 | glyceraldehyde-3-phosphate dehydrogenase | *gapor* | YP\_004150990.1 | 75 | **0.01** |
| Theam\_0377 | N-acetyl-gamma-glutamyl-phosphate reductase | *argC* | YP\_004150991.1 | 39 | **0.09** |
| Theam\_0378 | ribosomal protein S9 | *rps9* | YP\_004150992.1 | 15 | **0.44** |
| Theam\_0379 | ribosomal protein L13 | *rplM* | YP\_004150993.1 | 16 | **0.02** |
| Theam\_0385 | ribulose-phosphate 3-epimerase | *rpe* | YP\_004150999.1 | 24 | **0.13** |
| Theam\_0386 | ribose-phosphate pyrophosphokinase | *rpppk* | YP\_004151000.1 | 34 | **0.73** |
| Theam\_0389 | pyridoxal phosphate biosynthetic protein PdxJ | *pdxJ* | YP\_004151003.1 | 27 | **0.22** |
| Theam\_0392 | acyl carrier protein | *acp* | YP\_004151006.1 | 9 | **0.10** |
| Theam\_0393 | 3-oxoacyl-(acyl-carrier-protein) reductase | *fabG* | YP\_004151007.1 | 26 | **0.07** |
| Theam\_0397 | hypothetical protein |  | YP\_004151011.1 | 24 | **0.12** |
| Theam\_0398 | phosphodiesterase, MJ0936 family |  | YP\_004151012.1 | 18 | **0.08** |
| Theam\_0400 | Conserved TM helix repeat-containing protein |  | YP\_004151014.1 | 41 | **0.01** |
| Theam\_0404 | HI0933 family protein |  | YP\_004151017.1 | 57 | **0.01** |
| Theam\_0410 | regulatory protein LuxR | *luxR* | YP\_004151023.1 | 22 | **0.01** |
| Theam\_0412 | thymidylate kinase | *kthY* | YP\_004151025.1 | 24 | **0.05** |
| Theam\_0414 | TrkA-C domain protein |  | YP\_004151027.1 | 18 | **0.01** |
| Theam\_0415 | hypothetical protein |  | YP\_004151028.1 | 23 | **0.01** |
| Theam\_0417 | PSP1 domain protein |  | YP\_004151030.1 | 35 | **0.01** |
| Theam\_0418 | hypothetical protein |  | YP\_004151031.1 | 52 | **0.19** |
| Theam\_0423 | NapA nitrate reductase periplasmic molybdopterin oxidoreductase  | *napA* | YP\_004151036.1 | 101 | **0.10** |
| Theam\_0429 | arginine biosynthesis bifunctional protein ArgJ | *argJ* | YP\_004151042.1 | 41 | **0.20** |
| Theam\_0430 | tRNA (guanine-N1-)-methyltransferase | *trmD* | YP\_004151043.1 | 41 | **0.01** |
| Theam\_0431 | cysteine synthase | *cysK* | YP\_004151044.1 | 33 | **0.10** |
| Theam\_0433 | hypothetical protein |  | YP\_004151046.1 | 15 | **0.04** |
| Theam\_0436 | tryptophan synthase, alpha subunit | *trpA* | YP\_004151049.1 | 29 | **0.20** |
| Theam\_0437 | twin-arginine translocation protein, TatA/E family subunit | *tatAE* | YP\_004151050.1 | 9 | **0.70** |
| Theam\_0439 | transcription termination factor Rho | *rho* | YP\_004151052.1 | 48 | **0.04** |
| Theam\_0440 | phosphoheptose isomerase | *gmhA* | YP\_004151053.1 | 22 | **0.09** |
| Theam\_0441 | predicted fructose-bisphosphate aldolase | *fba* | YP\_004151054.1 | 28 | **1.71** |
| Theam\_0442 | Radical SAM domain protein |  | YP\_004151055.1 | 63 | **0.00** |
| Theam\_0445 | ABC transporter related for Fe-S assembly | *sufC* | YP\_004151058.1 | 27 | **0.14** |
| Theam\_0446 | SufBD protein for Fe-S assembly | *sufB* | YP\_004151059.1 | 35 | **0.08** |
| Theam\_0447 | Putative Superoxide reductase (Desulfoferrodoxin ferrous iron-binding region) | *sor* | YP\_004151060.1 | 13 | **0.15** |
| Theam\_0449 | Ppx/GppA phosphatase | *gppA* | YP\_004151062.1 | 34 | **0.04** |
| Theam\_0450 | nucleotide sugar dehydrogenase UDP glucose type | *udg* | YP\_004151063.1 | 49 | **0.06** |
| Theam\_0452 | 2,5-diamino-6-hydroxy-4-(5-phosphoribosylamino)pyrimidine 1-reductase | *ribD* | YP\_004151065.1 | 24 | **0.13** |
| Theam\_0456 | regulatory protein ArsR | *arsR* | YP\_004151069.1 | 12 | **0.08** |
| Theam\_0459 | ketol-acid reductoisomerase | *ilvC* | YP\_004151072.1 | 37 | **0.71** |
| Theam\_0460 | acetolactate synthase, small subunit | *acolacS* | YP\_004151073.1 | 20 | **0.05** |
| Theam\_0461 | acetolactate synthase, large subunit, biosynthetic type | *acolacL* | YP\_004151074.1 | 64 | **0.18** |
| Theam\_0464 | KpsF/GutQ family protein | *kpsF* | YP\_004151077.1 | 29 | **0.03** |
| Theam\_0467 | [Glutamate--ammonia-ligase] adenylyltransferase | *glnE* | YP\_004151080.1 | 102 | **0.05** |
| Theam\_0470 | ribosomal protein L34 | *rpmH* | YP\_004151083.1 | 7 | **0.03** |
| Theam\_0473 | membrane protein insertase, YidC/Oxa1 family | *yidC* | YP\_004151086.1 | 55 | **0.01** |
| Theam\_0478 | NADH dehydrogenase (quinone) Ni-Fe subunit III | *echE* | YP\_004151091.1 | 41 | **0.02** |
| Theam\_0480 | NADH ubiquinone oxidoreductase kDa subunit | *echC* | YP\_004151093.1 | 20 | **0.02** |
| Theam\_0481 | respiratory-chain NADH dehydrogenase subunit 1 | *echB* | YP\_004151094.1 | 31 | **0.01** |
| Theam\_0483 | cyclic nucleotide-binding |  | YP\_004151096.1 | 19 | **0.01** |
| Theam\_0484 | nickel-dependent hydrogenase large subunit | *hydA* | YP\_004151097.1 | 47 | **0.01** |
| Theam\_0485 | NADH ubiquinone oxidoreductase 20 kDa subunit | *fqhD* | YP\_004151098.1 | 28 | **0.01** |
| Theam\_0487 | cytochrome-c3 hydrogenase alpha chain | *hydB* | YP\_004151100.1 | 41 | **0.02** |
| Theam\_0488 | pantetheine-phosphate adenylyltransferase | *coaD* | YP\_004151101.1 | 19 | **0.04** |
| Theam\_0489 | Aldehyde Dehydrogenase | *ald* | YP\_004151102.1 | 52 | **0.28** |
| Theam\_0490 | metallophosphoesterase |  | YP\_004151103.1 | 26 | **0.01** |
| Theam\_0491 | tRNA synthetase class II (D K and N) |  | YP\_004151104.1 | 35 | **0.03** |
| Theam\_0492 | 3-octaprenyl-4-hydroxybenzoate carboxy-lyase | *ubiX* | YP\_004151105.1 | 21 | **0.08** |
| Theam\_0493 | acetylglutamate kinase | *argB* | YP\_004151106.1 | 32 | **0.12** |
| Theam\_0494 | cytochrome bd ubiquinol oxidase subunit I | *cydA* | YP\_004151107.1 | 52 | **0.01** |
| Theam\_0495 | cytochrome d ubiquinol oxidase, subunit II | *cydB* | YP\_004151108.1 | 44 | **0.01** |
| Theam\_0500 | RNA chaperone Hfq | *hfq* | YP\_004151113.1 | 9 | **0.05** |
| Theam\_0502 | glutamyl-tRNA synthetase | *gltXb* | YP\_004151115.1 | 56 | **0.08** |
| Theam\_0505 | Uroporphyrinogen III synthase HEM4 |  | YP\_004151118.1 | 27 | **0.01** |
| Theam\_0506 | porphobilinogen deaminase | *hemC* | YP\_004151119.1 | 35 | **0.14** |
| Theam\_0507 | glutamyl-tRNA reductase | *hemA* | YP\_004151120.1 | 47 | **0.00** |
| Theam\_0509 | 3-dehydroquinate dehydratase, type I | *aroD* | YP\_004151122.1 | 28 | **0.14** |
| Theam\_0510 | protein of unknown function DUF190 |  | YP\_004151123.1 | 13 | **0.02** |
| Theam\_0511 | type IV-A pilus assembly ATPase PilB | *pilB* | YP\_004151124.1 | 64 | **0.01** |
| Theam\_0512 | hypothetical protein |  | YP\_004151125.1 | 24 | **0.14** |
| Theam\_0514 | 3-phosphoshikimate 1-carboxyvinyltransferase | *aroA* | YP\_004151127.1 | 47 | **0.08** |
| Theam\_0520 | Porphobilinogen synthase | *hemC* | YP\_004151133.1 | 37 | **0.87** |
| Theam\_0521 | hypothetical protein |  | YP\_004151134.1 | 13 | **0.30** |
| Theam\_0522 | beta-lactamase domain-containing protein |  | YP\_004151135.1 | 31 | **0.07** |
| Theam\_0526 | acetylornithine and succinylornithine aminotransferase | *argD* | YP\_004151139.1 | 43 | **0.11** |
| Theam\_0534 | dihydroxy-acid dehydratase | *ilvD* | YP\_004151147.1 | 59 | **0.17** |
| Theam\_0537 | peptidase M22 glycoprotease | *pM22* | YP\_004151150.1 | 21 | **0.02** |
| Theam\_0542 | hypothetical protein |  | YP\_004151155.1 | 6 | **0.05** |
| Theam\_0544 | hypothetical protein |  | YP\_004151157.1 | 74 | **0.01** |
| Theam\_0548 | acetate/CoA ligase - Acetyl-CoA Synthase | *acsA* | YP\_004151161.1 | 71 | **0.14** |
| Theam\_0549 | excinuclease ABC, B subunit | *uvrb* | YP\_004151162.1 | 77 | **0.00** |
| Theam\_0551 | Tetratricopeptide TPR\_1 repeat-containing protein |  | YP\_004151164.1 | 104 | **0.02** |
| Theam\_0552 | protein of unknown function DUF507 |  | YP\_004151165.1 | 23 | **0.01** |
| Theam\_0553 | hypothetical protein |  | YP\_004151166.1 | 42 | **0.01** |
| Theam\_0566 | Radical SAM domain protein |  | YP\_004151179.1 | 25 | **0.02** |
| Theam\_0569 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase | *Dxr* | YP\_004151182.1 | 41 | **0.04** |
| Theam\_0570 | histidyl-tRNA synthetase | *hisS1* | YP\_004151183.1 | 47 | **0.04** |
| Theam\_0571 | phosphoribosyltransferase |  | YP\_004151184.1 | 24 | **0.11** |
| Theam\_0574 | hypothetical protein |  | YP\_004151187.1 | 32 | **0.04** |
| Theam\_0575 | glycosyl transferase family 2 |  | YP\_004151188.1 | 111 | **0.01** |
| Theam\_0576 | Methyltransferase type 12 |  | YP\_004151189.1 | 30 | **0.01** |
| Theam\_0577 | glucose-1-phosphate thymidylyltransferase | *rmlA* | YP\_004151190.1 | 33 | **0.05** |
| Theam\_0578 | dTDP-4-dehydrorhamnose 3,5-epimerase | *rmlC* | YP\_004151191.1 | 21 | **0.06** |
| Theam\_0579 | dTDP-glucose 4,6-dehydratase | *rmlB* | YP\_004151192.1 | 37 | **0.01** |
| Theam\_0581 | histone deacetylase superfamily |  | YP\_004151194.1 | 33 | **0.03** |
| Theam\_0582 | ribonuclease R | *3xrn* | YP\_004151195.1 | 82 | **0.07** |
| Theam\_0586 | enolase | *eno* | YP\_004151199.1 | 47 | **1.09** |
| Theam\_0589 | succinyldiaminopimelate transaminase |  | YP\_004151202.1 | 44 | **0.02** |
| Theam\_0590 | hypothetical protein |  | YP\_004151203.1 | 28 | **0.14** |
| Theam\_0591 | alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen |  | YP\_004151204.1 | 18 | **0.04** |
| Theam\_0592 | ribosomal protein S20 | *S20* | YP\_004151205.1 | 11 | **0.20** |
| Theam\_0593 | thiamine-phosphate pyrophosphorylase | *thiE* | YP\_004151206.1 | 24 | **0.03** |
| Theam\_0599 | glycosyl transferase family 9 |  | YP\_004151212.1 | 33 | **0.00** |
| Theam\_0601 | nucleotide sugar dehydrogenase |  | YP\_004151214.1 | 49 | **0.04** |
| Theam\_0602 | malate dehydrogenase, NAD-dependent | *mdh* | YP\_004151215.1 | 34 | **0.41** |
| Theam\_0603 | Fumarate hydratase, Fe-S type, tartrate/fumarate subfamily, alpha subunit | *fumA* | YP\_004151216.1 | 31 | **0.27** |
| Theam\_0605 | 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase | *ispG* | YP\_004151218.1 | 38 | **0.03** |
| Theam\_0607 | diguanylate cyclase | *ggdef* | YP\_004151220.1 | 42 | **0.04** |
| Theam\_0609 | homocysteine S-methyltransferase | *metH* | YP\_004151222.1 | 90 | **0.04** |
| Theam\_0610 | adenine phosphoribosyltransferase | *apt* | YP\_004151223.1 | 20 | **1.25** |
| Theam\_0611 | 3-oxoacyl-[acyl-carrier-protein] synthase 2 |  | YP\_004151224.1 | 44 | **0.12** |
| Theam\_0612 | ribonuclease III |  | YP\_004151225.1 | 27 | **0.02** |
| Theam\_0613 | maf protein | *maf* | YP\_004151226.1 | 21 | **0.18** |
| Theam\_0614 | hypothetical protein |  | YP\_004151227.1 | 27 | **0.04** |
| Theam\_0616 | 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase |  | YP\_004151229.1 | 18 | **0.01** |
| Theam\_0617 | beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ | *fabZ* | YP\_004151230.1 | 17 | **0.28** |
| Theam\_0618 | acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase | *lpxA* | YP\_004151231.1 | 28 | **0.09** |
| Theam\_0620 | Nucleoside-triphosphatase |  | YP\_004151233.1 | 20 | **0.02** |
| Theam\_0621 | Hsp33 protein |  | YP\_004151234.1 | 37 | **0.24** |
| Theam\_0622 | peptidase zinc-dependent |  | YP\_004151235.1 | 19 | **0.06** |
| Theam\_0624 | Purine-nucleoside phosphorylase |  | YP\_004151237.1 | 29 | **0.03** |
| Theam\_0625 | hypothetical protein |  | YP\_004151238.1 | 63 | **0.00** |
| Theam\_0626 | ammonium transporter |  | YP\_004151239.1 | 12 | **0.10** |
| Theam\_0629 | glutamine synthetase, type I | *glnA* | YP\_004151242.1 | 53 | **0.95** |
| Theam\_0631 | diaminopimelate decarboxylase | *lysA* | YP\_004151243.1 | 46 | **0.05** |
| Theam\_0633 | Prephenate dehydrogenase |  | YP\_004151245.1 | 32 | **0.10** |
| Theam\_0634 | class II aldolase/adducin family protein |  | YP\_004151246.1 | 21 | **0.04** |
| Theam\_0635 | histidine kinase HAMP region domain protein |  | YP\_004151247.1 | 37 | **0.02** |
| Theam\_0636 | hypothetical protein |  | YP\_004151248.1 | 33 | **0.02** |
| Theam\_0638 | protein of unknown function DUF178 |  | YP\_004151249.1 | 32 | **0.01** |
| Theam\_0640 | rfaE bifunctional protein | *rfaE* | YP\_004151251.1 | 36 | **0.04** |
| Theam\_0642 | isoleucyl-tRNA synthetase | *ileS* | YP\_004151253.1 | 108 | **0.08** |
| Theam\_0644 | Rhodanese domain protein |  | YP\_004151255.1 | 15 | **0.02** |
| Theam\_0645 | phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent | *pgm* | YP\_004151256.1 | 58 | **0.03** |
| Theam\_0646 | tRNA pseudouridine synthase A | *hisT\_truA* | YP\_004151257.1 | 30 | **0.01** |
| Theam\_0648 | glutamate--cysteine ligase GCS2 |  | YP\_004151259.1 | 40 | **0.02** |
| Theam\_0649 | gamma-glutamyltransferase |  | YP\_004151260.1 | 54 | **0.04** |
| Theam\_0651 | protein-P-II uridylyltransferase | *glnD* | YP\_004151262.1 | 102 | **0.01** |
| Theam\_0654 | UDP-glucose 4-epimerase | *galE* | YP\_004151265.1 | 36 | **0.02** |
| Theam\_0655 | triosephosphate isomerase | *tim* | YP\_004151266.1 | 27 | **0.10** |
| Theam\_0656 | ATP-dependent Clp protease, ATP-binding subunit ClpX | *clpX* | YP\_004151267.1 | 46 | **0.07** |
| Theam\_0657 | N-(5'phosphoribosyl)anthranilate isomerase (PRAI) |  | YP\_004151268.1 | 23 | **0.10** |
| Theam\_0658 | Ferritin Dps family protein |  | YP\_004151269.1 | 19 | **0.09** |
| Theam\_0661 | aspartyl-tRNA synthetase | *aspSb* | YP\_004151271.1 | 68 | **0.11** |
| Theam\_0663 | 3'(2'),5'-bisphosphate nucleotidase | *cysQ* | YP\_004151273.1 | 29 | **0.07** |
| Theam\_0666 | sulfate adenylyltransferase | *aps* | YP\_004151276.1 | 44 | **0.03** |
| Theam\_0671 | glycosyl transferase group 1 |  | YP\_004151281.1 | 40 | **0.00** |
| Theam\_0677 | RNA polymerase-binding protein DksA |  | YP\_004151286.1 | 15 | **0.02** |
| Theam\_0678 | aminotransferase class I and II |  | YP\_004151287.1 | 44 | **0.17** |
| Theam\_0683 | EAL domain protein |  | YP\_004151292.1 | 75 | **0.03** |
| Theam\_0686 | NAD-dependent glycerol-3-phosphate dehydrogenase domain protein |  | YP\_004151295.1 | 35 | **0.03** |
| Theam\_0688 | phosphate transport system regulatory protein PhoU | *phoU* | YP\_004151297.1 | 27 | **0.21** |
| Theam\_0691 | NADPH-dependent FMN reductase | *fmnr* | YP\_004151300.1 | 21 | **0.03** |
| Theam\_0692 | ribosome-associated GTPase EngA | *engA* | YP\_004151301.1 | 55 | **0.03** |
| Theam\_0693 | hypothetical protein |  | YP\_004151302.1 | 24 | **0.04** |
| Theam\_0694 | hypothetical protein |  | YP\_004151303.1 | 21 | **0.04** |
| Theam\_0701 | lysine 2,3-aminomutase YodO family protein | *yodO* | YP\_004151310.1 | 43 | **0.04** |
| Theam\_0703 | pseudogene |  |  | 18 | **0.05** |
| Theam\_0704 | histidinol-phosphate aminotransferase | *hisC* | YP\_004151312.1 | 42 | **0.09** |
| Theam\_0709 | 3-methyl-2-oxobutanoate hydroxymethyltransferase | *panB* | YP\_004151317.1 | 29 | **0.07** |
| Theam\_0710 | ribosome small subunit-dependent GTPase A | *rsgA* | YP\_004151318.1 | 34 | **0.03** |
| Theam\_0712 | ketose-bisphosphate aldolase class-II |  | YP\_004151320.1 | 53 | **0.22** |
| Theam\_0714 | L-aspartate oxidase | *nadB* | YP\_004151322.1 | 57 | **0.01** |
| Theam\_0718 | CTP synthase | *PyrG* | YP\_004151326.1 | 60 | **0.04** |
| Theam\_0719 | 3-deoxy-D-manno-octulosonate cytidylyltransferase | *kdsB* | YP\_004151327.1 | 27 | **0.02** |
| Theam\_0720 | phosphoribosylformylglycinamidine synthase I | *fgams* | YP\_004151328.1 | 25 | **0.14** |
| Theam\_0721 | phosphoribosylformylglycinamidine synthase, purS | *purS* | YP\_004151329.1 | 10 | **0.16** |
| Theam\_0725 | RNA polymerase sigma factor RpoD | *rpoD* | YP\_004151333.1 | 66 | **0.01** |
| Theam\_0727 | Peroxiredoxin |  | YP\_004151335.1 | 22 | **0.76** |
| Theam\_0730 | Fumarate hydratase, Fe-S type, tartrate/fumarate subfamily, beta subunit | *fumB* | YP\_004151338.1 | 21 | **0.25** |
| Theam\_0734 | NADH dehydrogenase I, D subunit | *nuoD* | YP\_004151342.1 | 45 | **0.02** |
| Theam\_0736 | NADH-quinone oxidoreductase, F subunit | *nuoF* | YP\_004151344.1 | 46 | **0.00** |
| Theam\_0737 | NADH:ubiquinone oxidoreductase, subunit G, iron-sulphur binding | *nuoG* | YP\_004151345.1 | 80 | **0.06** |
| Theam\_0738 | putative transcriptional regulator, Crp/Fnr family |  | YP\_004151346.1 | 18 | **0.04** |
| Theam\_0746 | L-seryl-tRNA selenium transferase | *selA* | YP\_004151354.1 | 52 | **0.01** |
| Theam\_0747 | TonB-dependent receptor |  | YP\_004151355.1 | 76 | **0.00** |
| Theam\_0751 | Peptidoglycan-binding lysin domain |  | YP\_004151359.1 | 27 | **0.14** |
| Theam\_0752 | hypothetical protein |  | YP\_004151360.1 | 13 | **0.10** |
| Theam\_0753 | acriflavin resistance protein |  | YP\_004151361.1 | 121 | **0.03** |
| Theam\_0754 | efflux transporter, RND family, MFP subunit | *mfp* | YP\_004151362.1 | 42 | **0.05** |
| Theam\_0755 | glutamine amidotransferase class-I | *gmps* | YP\_004151363.1 | 26 | **0.07** |
| Theam\_0756 | peptidase U62 modulator of DNA gyrase | *tldD* | YP\_004151364.1 | 50 | **0.09** |
| Theam\_0757 | NAD+ synthetase | *nadE* | YP\_004151365.1 | 31 | **0.11** |
| Theam\_0758 | Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase |  | YP\_004151366.1 | 32 | **0.09** |
| Theam\_0763 | PhoH family protein |  | YP\_004151371.1 | 36 | **0.08** |
| Theam\_0765 | SMC domain protein |  | YP\_004151373.1 | 105 | **0.00** |
| Theam\_0768 | Radical SAM domain protein |  | YP\_004151376.1 | 35 | **0.02** |
| Theam\_0770 | phosphoesterase RecJ domain protein |  | YP\_004151378.1 | 37 | **0.10** |
| Theam\_0772 | peptidase U62 modulator of DNA gyrase | *tldD* | YP\_004151380.1 | 48 | **0.11** |
| Theam\_0773 | thymidylate synthase, flavin-dependent |  | YP\_004151381.1 | 23 | **0.04** |
| Theam\_0778 | NHL repeat containing protein |  | YP\_004151386.1 | 29 | **0.04** |
| Theam\_0779 | hypothetical protein |  | YP\_004151387.1 | 27 | **0.01** |
| Theam\_0784 | hypothetical protein |  | YP\_004151392.1 | 50 | **0.00** |
| Theam\_0785 | molybdenum cofactor synthesis domain protein |  | YP\_004151393.1 | 43 | **0.01** |
| Theam\_0786 | molybdopterin binding domain |  | YP\_004151394.1 | 38 | **0.02** |
| Theam\_0790 | mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase |  | YP\_004151398.1 | 53 | **0.03** |
| Theam\_0797 | nucleotide sugar dehydrogenase |  | YP\_004151405.1 | 50 | **0.03** |
| Theam\_0800 | DNA polymerase I | *dna2* | YP\_004151408.1 | 94 | **0.01** |
| Theam\_0804 | putative lipoprotein |  | YP\_004151412.1 | 16 | **0.03** |
| Theam\_0812 | DNA helicase |  | YP\_004151420.1 | 83 | **0.02** |
| Theam\_0814 | hypothetical protein |  | YP\_004151422.1 | 31 | **0.01** |
| Theam\_0815 | Nucleoside-diphosphate kinase |  | YP\_004151423.1 | 16 | **0.20** |
| Theam\_0820 | protein-export membrane protein SecD | *secD* | YP\_004151428.1 | 61 | **0.00** |
| Theam\_0824 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | *murA* | YP\_004151432.1 | 47 | **0.00** |
| Theam\_0825 | ATP phosphoribosyltransferase | *hisG* | YP\_004151433.1 | 24 | **0.06** |
| Theam\_0826 | formyltetrahydrofolate deformylase | *PurU* | YP\_004151434.1 | 33 | **0.04** |
| Theam\_0827 | glucosamine/fructose-6-phosphate aminotransferase, isomerizing | *glmS* | YP\_004151435.1 | 68 | **0.05** |
| Theam\_0828 | tRNA modification GTPase TrmE |  | YP\_004151436.1 | 52 | **0.04** |
| Theam\_0830 | protein of unknown function DUF583 |  | YP\_004151438.1 | 13 | **0.20** |
| Theam\_0836 | HAD-superfamily hydrolase, subfamily IIA |  | YP\_004151444.1 | 29 | **0.12** |
| Theam\_0838 | GTP-binding protein YchF | *ychF* | YP\_004151446.1 | 41 | **0.02** |
| Theam\_0843 | response regulator receiver | *cheY* | YP\_004151451.1 | 15 | **0.08** |
| Theam\_0844 | response regulator receiver | *cheV* | YP\_004151452.1 | 36 | **0.03** |
| Theam\_0845 | chemotaxis sensory transducer | *mcp* | YP\_004151453.1 | 72 | **0.09** |
| Theam\_0846 | CheW domain protein | *cheW* | YP\_004151454.1 | 19 | **0.02** |
| Theam\_0847 | ATP-binding region ATPase domain protein - histidine kinase | *cheA* | YP\_004151455.1 | 74 | **0.03** |
| Theam\_0848 | putative myosin-2 heavy chain, non muscle  | *cheZ* | YP\_004151456.1 | 20 | **0.07** |
| Theam\_0849 | cell division protein FtsZ | *ftsZ* | YP\_004151457.1 | 39 | **0.04** |
| Theam\_0852 | D-alanine/D-alanine ligase |  | YP\_004151460.1 | 32 | **0.01** |
| Theam\_0854 | UDP-N-acetylmuramyl-tripeptide synthetase | *murE* | YP\_004151462.1 | 53 | **0.00** |
| Theam\_0855 | hypothetical protein |  | YP\_004151463.1 | 11 | **0.04** |
| Theam\_0856 | hypothetical protein |  | YP\_004151464.1 | 10 | **0.02** |
| Theam\_0862 | outer membrane efflux protein |  | YP\_004151470.1 | 48 | **0.01** |
| Theam\_0873 | DNA ligase, NAD-dependent | *dnlj* | YP\_004151481.1 | 82 | **0.05** |
| Theam\_0876 | molybdenum cofactor biosynthesis protein C | *moa* | YP\_004151484.1 | 33 | **0.36** |
| Theam\_0877 | hypothetical protein |  | YP\_004151485.1 | 21 | **0.02** |
| Theam\_0878 | molybdopterin biosynthesis MoaE protein | *moaE* | YP\_004151486.1 | 13 | **0.01** |
| Theam\_0884 | signal recognition particle-docking protein FtsY | *ftsY* | YP\_004151492.1 | 54 | **0.02** |
| Theam\_0885 | anthranilate phosphoribosyltransferase | *trpD* | YP\_004151493.1 | 38 | **0.04** |
| Theam\_0887 | metalloendopeptidase, glycoprotease family | *gcp* | YP\_004151495.1 | 35 | **0.03** |
| Theam\_0889 | transglutaminase domain-containing protein |  | YP\_004151497.1 | 72 | **0.00** |
| Theam\_0890 | phosphoglucosamine mutase | *glmM* | YP\_004151498.1 | 49 | **0.07** |
| Theam\_0893 | dihydropteroate synthase | *dhps* | YP\_004151501.1 | 44 | **0.01** |
| Theam\_0894 | Polynucleotide adenylyltransferase region |  | YP\_004151502.1 | 98 | **0.01** |
| Theam\_0896 | general secretion pathway protein D | *gspD* | YP\_004151504.1 | 71 | **0.04** |
| Theam\_0903 | type II and III secretion system protein | *gspC* | YP\_004151511.1 | 72 | **0.02** |
| Theam\_0906 | reverse gyrase | *rgy* | YP\_004151514.1 | 137 | **0.04** |
| Theam\_0907 | iron-containing alcohol dehydrogenase |  | YP\_004151515.1 | 41 | **0.09** |
| Theam\_0909 | transcription antitermination factor NusB | *nusB* | YP\_004151517.1 | 16 | **0.03** |
| Theam\_0910 | 6,7-dimethyl-8-ribityllumazine synthase | *ribH* | YP\_004151518.1 | 17 | **0.27** |
| Theam\_0911 | enoyl-(acyl-carrier-protein) reductase II | *fabK* | YP\_004151519.1 | 34 | **0.07** |
| Theam\_0912 | 3-oxoacyl-(acyl-carrier-protein) synthase III | *fabH* | YP\_004151520.1 | 34 | **0.05** |
| Theam\_0913 | fatty acid/phospholipid synthesis protein PlsX | *plsX* | YP\_004151521.1 | 36 | **0.00** |
| Theam\_0919 | methylenetetrahydrofolate reductase F | *metF* | YP\_004151527.1 | 32 | **0.04** |
| Theam\_0920 | undecaprenyl diphosphate synthase | *uppS* | YP\_004151528.1 | 27 | **0.05** |
| Theam\_0922 | hydrogenase expression/formation protein HypE | *hypE* | YP\_004151530.1 | 35 | **0.11** |
| Theam\_0924 | hydrogenase expression/formation protein HypD | *hypD* | YP\_004151532.1 | 39 | **0.06** |
| Theam\_0936 | hypothetical protein |  | YP\_004151544.1 | 38 | **0.05** |
| Theam\_0938 | Orn/DAP/Arg decarboxylase 2 |  | YP\_004151546.1 | 51 | **0.02** |
| Theam\_0940 | hypothetical protein |  | YP\_004151548.1 | 34 | **0.10** |
| Theam\_0942 | phosphoribosylamine/glycine ligase | *purD* | YP\_004151550.1 | 46 | **0.08** |
| Theam\_0948 | histidine triad (HIT) protein |  | YP\_004151556.1 | 19 | **0.18** |
| Theam\_0953 | Domain of unkown function DUF1786 putative pyruvate format-lyase activating enzyme |  | YP\_004151561.1 | 37 | **0.01** |
| Theam\_0954 | cell division protein FtsZ | *ftsZ* | YP\_004151562.1 | 39 | **0.03** |
| Theam\_0955 | Nicotinamidase | *pncA* | YP\_004151563.1 | 21 | **0.10** |
| Theam\_0956 | hypothetical protein |  | YP\_004151564.1 | 33 | **0.22** |
| Theam\_0962 | peptidase M16 domain protein |  | YP\_004151570.1 | 46 | **0.02** |
| Theam\_0963 | hypothetical protein |  | YP\_004151571.1 | 48 | **0.00** |
| Theam\_0964 | ADP-ribosylation/Crystallin J1 |  | YP\_004151572.1 | 35 | **0.03** |
| Theam\_0965 | hypothetical protein |  | YP\_004151573.1 | 126 | **0.01** |
| Theam\_0969 | fumarate |  | YP\_004151577.1 | 42 | **0.01** |
| Theam\_0970 | Radical SAM domain protein |  | YP\_004151578.1 | 42 | **0.01** |
| Theam\_0972 | phosphoenolpyruvate synthase water dikinase | *ppsA* | YP\_004151580.1 | 91 | **0.08** |
| Theam\_0973 | D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding |  | YP\_004151581.1 | 38 | **0.04** |
| Theam\_0974 | phosphoglucose isomerase | *pgi* | YP\_004151582.1 | 45 | **0.03** |
| Theam\_0984 | malonyl CoA-acyl carrier protein transacylase | *fabD* | YP\_004151592.1 | 34 | **0.21** |
| Theam\_0985 | ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent |  | YP\_004151593.1 | 63 | **0.01** |
| Theam\_0990 | twitching motility protein | *pilT* | YP\_004151598.1 | 40 | **0.03** |
| Theam\_0998 | Glutamate synthase (NADPH) | *gltA* | YP\_004151606.1 | 55 | **0.17** |
| Theam\_1000 | NAD – Nitrite reductase (FAD-dependent pyridine nucleotide-disulphide oxidoreductase) | *nirA* | YP\_004151608.1 | 47 | **0.20** |
| Theam\_1001 | glutamine amidotransferase class-II |  | YP\_004151609.1 | 42 | **0.12** |
| Theam\_1002 | glutamate synthase alpha subunit domain protein | *glt* | YP\_004151610.1 | 29 | **0.24** |
| Theam\_1003 | tryptophan synthase, beta subunit | *trpB* | YP\_004151611.1 | 44 | **0.10** |
| Theam\_1005 | tyrosyl-tRNA synthetase | *tyrS* | YP\_004151613.1 | 47 | **0.07** |
| Theam\_1008 | lysyl-tRNA synthetase | *lysSb* | YP\_004151616.1 | 61 | **0.11** |
| Theam\_1011 | Mammalian cell entry related domain protein |  | YP\_004151619.1 | 58 | **0.00** |
| Theam\_1013 | ??fumarate reductase/succinate dehydrogenase flavoprotein domain protein | *fum?* | YP\_004151621.1 | 20 | **0.26** |
| Theam\_1017 | adenylosuccinate lyase | *purB* | YP\_004151625.1 | 51 | **0.25** |
| Theam\_1020 | molybdopterin oxidoreductase fdhA hydrogenase family | *fdhA* | YP\_004151628.1 | 76 | **0.04** |
| Theam\_1021 | ATP-citrate (pro-S-)-lyase subunit alpha | *aclA* | YP\_004151629.1 | 68 | **2.03** |
| Theam\_1022 | ATP-citrate (pro-S-)-lyase subunit beta | *aclB* | YP\_004151630.1 | 49 | **0.64** |
| Theam\_1023 | isocitrate dehydrogenase/2-oxoglutarate carboxylase , NADP-dependent | *idh2* | YP\_004151631.1 | 83 | **1.24** |
| Theam\_1024 | aconitate hydratase | *acnB* | YP\_004151632.1 | 71 | **0.59** |
| Theam\_1027 | methyl-accepting chemotaxis protein |  | YP\_004151635.1 | 38 | **0.04** |
| Theam\_1028 | hypothetical protein |  | YP\_004151636.1 | 42 | **0.12** |
| Theam\_1029 | hypothetical protein |  | YP\_004151637.1 | 75 | **0.63** |
| Theam\_1035 | phosphopantothenoylcysteine decarboxylase/phosphopantothenate/cysteine ligase | *coaBC\_dfp* | YP\_004151643.1 | 42 | **0.01** |
| Theam\_1036 | RNA methyltransferase, TrmH family, group 3 |  | YP\_004151644.1 | 26 | **0.02** |
| Theam\_1041 | carbohydrate kinase, YjeF related protein |  | YP\_004151649.1 | 57 | **0.10** |
| Theam\_1042 | peptide deformylase |  | YP\_004151650.1 | 20 | **0.07** |
| Theam\_1043 | Xylose isomerase domain-containing protein TIM barrel |  | YP\_004151651.1 | 28 | **0.02** |
| Theam\_1045 | Phosphoribosyl-AMP cyclohydrolase |  | YP\_004151653.1 | 13 | **0.11** |
| Theam\_1053 | tRNA 2-selenouridine synthase |  | YP\_004151661.1 | 40 | **0.01** |
| Theam\_1055 | pyruvate fromate-lyase activating enzyme |  | YP\_004151663.1 | 38 | **0.03** |
| Theam\_1056 | PEBP family protein |  | YP\_004151664.1 | 17 | **0.01** |
| Theam\_1062 | heat shock protein Hsp20 |  | YP\_004151670.1 | 20 | **0.04** |
| Theam\_1063 | PHP domain protein |  | YP\_004151671.1 | 65 | **0.02** |
| Theam\_1065 | hypothetical protein |  | YP\_004151673.1 | 41 | **0.02** |
| Theam\_1067 | 3-dehydroquinate synthase | *aroB* | YP\_004151675.1 | 37 | **0.32** |
| Theam\_1069 | ADP-L-glycero-D-manno-heptose-6-epimerase |  | YP\_004151677.1 | 36 | **0.14** |
| Theam\_1070 | regulatory protein MerR | *merR* | YP\_004151678.1 | 14 | **0.01** |
| Theam\_1071 | ATPase AAA-2 domain protein | *clp?* | YP\_004151679.1 | 95 | **0.12** |
| Theam\_1075 | Methionine adenosyltransferase | *samS* | YP\_004151683.1 | 44 | **0.29** |
| Theam\_1076 | hypothetical protein |  | YP\_004151684.1 | 71 | **0.01** |
| Theam\_1078 | hypothetical protein |  | YP\_004151686.1 | 30 | **0.02** |
| Theam\_1081 | preprotein translocase, SecA subunit | *secA* | YP\_004151689.1 | 100 | **0.06** |
| Theam\_1083 | protease Do |  | YP\_004151691.1 | 52 | **0.05** |
| Theam\_1087 | MotA/TolQ/ExbB proton channel | *motA* | YP\_004151695.1 | 27 | **0.01** |
| Theam\_1088 | D-lactate dehydrogenase (cytochrome) |  | YP\_004151696.1 | 49 | **0.03** |
| Theam\_1090 | polysaccharide export protein |  | YP\_004151698.1 | 107 | **0.01** |
| Theam\_1095 | branched-chain amino acid aminotransferase | *ilvE\_I* | YP\_004151703.1 | 34 | **0.32** |
| Theam\_1098 | general secretion pathway protein G | *gspG* | YP\_004151706.1 | 16 | **0.02** |
| Theam\_1100 | hypothetical protein |  | YP\_004151708.1 | 14 | **0.27** |
| Theam\_1106 | uroporphyrinogen decarboxylase | *hemE* | YP\_004151713.1 | 39 | **0.14** |
| Theam\_1107 | exodeoxyribonuclease III Xth | *xth* | YP\_004151714.1 | 30 | **0.01** |
| Theam\_1109 | protein-L-isoaspartate(D-aspartate) O-methyltransferase |  | YP\_004151716.1 | 30 | **0.03** |
| Theam\_1111 | protein of unknown function DUF28 |  | YP\_004151718.1 | 27 | **0.01** |
| Theam\_1113 | hydrolase, TatD family |  | YP\_004151720.1 | 53 | **0.02** |
| Theam\_1115 | arginyl-tRNA synthetase | *argS* | YP\_004151722.1 | 62 | **0.09** |
| Theam\_1116 | [NiFe] hydrogenase maturation protein HypF | *hypF* | YP\_004151723.1 | 83 | **0.01** |
| Theam\_1121 | hydrogenase (NiFe) small subunit HydA | *hynA* | YP\_004151728.1 | 39 | **0.03** |
| Theam\_1122 | nickel-dependent hydrogenase large subunit | *hynB* | YP\_004151729.1 | 65 | **0.27** |
| Theam\_1123 | Ni/Fe-hydrogenase, b-type cytochrome subunit | *hynC* | YP\_004151730.1 | 26 | **0.01** |
| Theam\_1124 | hydrogenase 2 maturation protease | *hupD* | YP\_004151731.1 | 20 | **0.02** |
| Theam\_1128 | hydrogenase accessory protein HypB | *hypB* | YP\_004151735.1 | 28 | **0.24** |
| Theam\_1130 | outer membrane efflux protein |  | YP\_004151737.1 | 51 | **0.00** |
| Theam\_1133 | flavodoxin/nitric oxide synthase not related to nitrogen metabolism |  | YP\_004151740.1 | 45 | **0.09** |
| Theam\_1138 | glutamyl-tRNA(Gln) amidotransferase, B subunit | *gatB* | YP\_004151743.1 | 55 | **0.20** |
| Theam\_1141 | DNA gyrase, A subunit | *gyrA* | YP\_004151746.1 | 91 | **0.08** |
| Theam\_1142 | seryl-tRNA synthetase | *serS* | YP\_004151747.1 | 49 | **0.09** |
| Theam\_1150 | transcriptional regulator domain-containing protein |  | YP\_004151755.1 | 25 | **0.01** |
| Theam\_1154 | 3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, YrbI family |  | YP\_004151759.1 | 17 | **0.02** |
| Theam\_1156 | Cytochrome-c peroxidase | *ccpA* | YP\_004151761.1 | 45 | **0.02** |
| Theam\_1157 | dethiobiotin synthase | *bioD* | YP\_004151762.1 | 22 | **0.07** |
| Theam\_1162 | flagellin domain protein - flagellin structural protein | *FliC* | YP\_004151767.1 | 32 | **1.66** |
| Theam\_1165 | glycosyl transferase family 2 |  | YP\_004151770.1 | 47 | **0.06** |
| Theam\_1166 | riboflavin biosynthesis protein RibD | *ribD* | YP\_004151771.1 | 40 | **0.00** |
| Theam\_1168 | tryptophanyl-tRNA synthetase | *trpS* | YP\_004151773.1 | 41 | **0.10** |
| Theam\_1173 | phosphoribosylaminoimidazole-succinocarboxamide synthase | *purC* | YP\_004151778.1 | 28 | **0.34** |
| Theam\_1174 | amidophosphoribosyltransferase | *purF* | YP\_004151779.1 | 51 | **0.04** |
| Theam\_1177 | threonyl-tRNA synthetase | *thrS* | YP\_004151782.1 | 76 | **0.05** |
| Theam\_1178 | translation initiation factor IF-3 | *infC* | YP\_004151783.1 | 17 | **0.03** |
| Theam\_1180 | ribosomal protein L20 | *rplT* | YP\_004151785.1 | 14 | **0.13** |
| Theam\_1181 | hypothetical protein |  | YP\_004151786.1 | 41 | **0.13** |
| Theam\_1183 | 6-pyruvoyl tetrahydropterin synthase and hypothetical protein |  | YP\_004151788.1 | 24 | **0.18** |
| Theam\_1184 | methyltransferase | *metR* | YP\_004151789.1 | 22 | **0.08** |
| Theam\_1188 | DNA gyrase, B subunit | *gyrB* | YP\_004151793.1 | 91 | **0.03** |
| Theam\_1189 | cytidylate kinase | *cmk* | YP\_004151794.1 | 24 | **0.06** |
| Theam\_1190 | nicotinate phosphoribosyltransferase |  | YP\_004151795.1 | 49 | **0.04** |
| Theam\_1191 | DNA-(apurinic or apyrimidinic site) lyase |  | YP\_004151796.1 | 25 | **0.01** |
| Theam\_1192 | 2-dehydro-3-deoxyphosphooctonate aldolase | *kdo* | YP\_004151797.1 | 30 | **0.07** |
| Theam\_1195 | deoxyribose-phosphate aldolase | *deoC* | YP\_004151800.1 | 24 | **0.03** |
| Theam\_1197 | GTP-binding protein Era | *era* | YP\_004151802.1 | 35 | **0.03** |
| Theam\_1201 | hypothetical protein |  | YP\_004151806.1 | 9 | **0.15** |
| Theam\_1203 | phenylalanyl-tRNA synthetase, alpha subunit | *pheS* | YP\_004151808.1 | 39 | **0.10** |
| Theam\_1204 | phenylalanyl-tRNA synthetase, beta subunit | *pheTb* | YP\_004151809.1 | 89 | **0.18** |
| Theam\_1206 | 5-formyltetrahydrofolate cyclo-ligase | *folA* | YP\_004151811.1 | 21 | **0.02** |
| Theam\_1207 | YmdA/YtgF protein | *hdig* | YP\_004151812.1 | 63 | **0.02** |
| Theam\_1208 | selenocysteine-specific translation elongation factor | *selB* | YP\_004151813.1 | 71 | **0.00** |
| Theam\_1211 | phosphoribosylglycinamide formyltransferase 2 | *purT* | YP\_004151816.1 | 44 | **0.12** |
| Theam\_1213 | Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase |  | YP\_004151818.1 | 28 | **0.03** |
| Theam\_1215 | pyrroline-5-carboxylate reductase | *proC* | YP\_004151820.1 | 29 | **0.10** |
| Theam\_1217 | Phosphomethylpyrimidine kinase |  | YP\_004151822.1 | 26 | **0.01** |
| Theam\_1218 | sugar-phosphate isomerase, RpiB/LacA/LacB family | *rpiB* | YP\_004151823.1 | 17 | **0.07** |
| Theam\_1219 | Glycine hydroxymethyltransferase |  | YP\_004151824.1 | 46 | **0.20** |
| Theam\_1221 | chaperonin GroEL |  | YP\_004151826.1 | 59 | **1.37** |
| Theam\_1222 | Chaperonin Cpn10 |  | YP\_004151827.1 | 11 | **1.03** |
| Theam\_1223 | transglutaminase domain-containing protein |  | YP\_004151828.1 | 35 | **0.03** |
| Theam\_1225 | phosphate-selective porin O and P |  | YP\_004151830.1 | 44 | **0.13** |
| Theam\_1226 | Hydrogenase Mo catalitic subunit - molydopterin dinucleotide-binding region | *hycB2* | YP\_004151831.1 | 131 | **0.12** |
| Theam\_1227 | hypothetical protein |  | YP\_004151832.1 | 27 | **0.01** |
| Theam\_1228 | CBS domain containing protein |  | YP\_004151833.1 | 15 | **0.10** |
| Theam\_1234 | ATPase-like, ParA/MinD |  | YP\_004151839.1 | 32 | **0.18** |
| Theam\_1235 | inositol monophosphatase |  | YP\_004151840.1 | 28 | **0.13** |
| Theam\_1238 | histidine kinase |  | YP\_004151843.1 | 34 | **0.01** |
| Theam\_1240 | thioesterase superfamily protein |  | YP\_004151845.1 | 14 | **0.05** |
| Theam\_1241 | hypothetical protein |  | YP\_004151846.1 | 23 | **0.01** |
| Theam\_1242 | peptide chain release factor 1 | *prfA* | YP\_004151847.1 | 41 | **0.04** |
| Theam\_1244 | Radical SAM domain protein |  | YP\_004151849.1 | 43 | **0.03** |
| Theam\_1246 | 2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase |  | YP\_004151851.1 | 30 | **0.15** |
| Theam\_1247 | methionyl-tRNA synthetase | *metG* | YP\_004151852.1 | 61 | **0.09** |
| Theam\_1249 | S-Adenosyl homocisteine hydrolase (adenosylhomocysteinase) | *sahH* | YP\_004151854.1 | 47 | **0.16** |
| Theam\_1250 | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase | *lpxD* | YP\_004151855.1 | 36 | **0.03** |
| Theam\_1251 | outer membrane chaperone Skp (OmpH) |  | YP\_004151856.1 | 20 | **0.01** |
| Theam\_1252 | outer membrane protein assembly complex, YaeT protein |  | YP\_004151857.1 | 87 | **0.02** |
| Theam\_1254 | glyceraldehyde 3-phosphate dehydrogenase, type I | *gapdh* | YP\_004151859.1 | 36 | **0.68** |
| Theam\_1256 | nicotinate-nucleotide pyrophosphorylase | *nadC* | YP\_004151861.1 | 32 | **0.04** |
| Theam\_1259 | dephospho-CoA kinase |  | YP\_004151864.1 | 21 | **0.02** |
| Theam\_1260 | metallophosphoesterase |  | YP\_004151865.1 | 30 | **0.04** |
| Theam\_1261 | Methylenetetrahydrofolate dehydrogenase (NADP(+)) | *folD* | YP\_004151866.1 | 31 | **0.22** |
| Theam\_1265 | AMP-dependent synthetase and ligase |  | YP\_004151869.1 | 61 | **0.01** |
| Theam\_1266 | diaminopimelate epimerase | *DapF* | YP\_004151870.1 | 30 | **0.01** |
| Theam\_1267 | phage SPO1 DNA polymerase-related protein | *spo1* | YP\_004151871.1 | 27 | **0.07** |
| Theam\_1270 | CoB--CoM heterodisulfide reductase / Fumarate reductase ascciated protein A? | *hdrA* | YP\_004151874.1 | 32 | **0.09** |
| Theam\_1271 | fumarate reductase iron-sulfur protein | *frdB1* | YP\_004151875.1 | 43 | **0.11** |
| Theam\_1272 | fumarate reductase, flavoprotein subunit | *frdB* | YP\_004151876.1 | 62 | **0.18** |
| Theam\_1273 | fumarate reductase, flavoprotein subunit | *frdA1* | YP\_004151877.1 | 63 | **0.07** |
| Theam\_1274 | fumarate reductase iron-sulfur protein | *frdA* | YP\_004151878.1 | 36 | **0.03** |
| Theam\_1275 | CoB--CoM heterodisulfide reductase / Fumarate reductase ascciated protein B? | *hdrB* | YP\_004151879.1 | 32 | **0.05** |
| Theam\_1276 | outer membrane efflux protein |  | YP\_004151880.1 | 50 | **0.02** |
| Theam\_1279 | pyruvate kinase | *pvtK* | YP\_004151883.1 | 51 | **0.01** |
| Theam\_1282 | phosphoglucomutase/phosphomannomutase alpha/beta/alpha domain I |  | YP\_004151886.1 | 52 | **0.20** |
| Theam\_1283 | Circadian clock protein KaiC central region |  | YP\_004151887.1 | 33 | **0.11** |
| Theam\_1284 | P450 cytochrome, putative |  | YP\_004151888.1 | 16 | **0.07** |
| Theam\_1293 | Silent information regulator protein Sir2 |  | YP\_004151897.1 | 30 | **0.02** |
| Theam\_1296 | putative metal-dependent hydrolase |  | YP\_004151900.1 | 26 | **0.06** |
| Theam\_1297 | signal recognition particle protein | *ffh* | YP\_004151901.1 | 50 | **0.01** |
| Theam\_1298 | ribosomal protein S16 | *S16* | YP\_004151902.1 | 9 | **0.10** |
| Theam\_1299 | hypothetical protein |  | YP\_004151903.1 | 9 | **0.20** |
| Theam\_1300 | hypothetical protein |  | YP\_004151904.1 | 22 | **0.11** |
| Theam\_1301 | transaldolase | *talC* | YP\_004151905.1 | 24 | **0.50** |
| Theam\_1303 | hypothetical protein |  | YP\_004151907.1 | 24 | **0.06** |
| Theam\_1307 | protein of unknown function DUF77 |  | YP\_004151911.1 | 12 | **0.02** |
| Theam\_1309 | pantoate/beta-alanine ligase |  | YP\_004151913.1 | 32 | **0.02** |
| Theam\_1311 | hypothetical protein |  | YP\_004151915.1 | 13 | **0.05** |
| Theam\_1312 | glutamate 5-kinase | *proB* | YP\_004151916.1 | 38 | **0.01** |
| Theam\_1313 | GTP-binding protein Obg/CgtA |  | YP\_004151917.1 | 38 | **0.03** |
| Theam\_1317 | hypothetical protein |  | YP\_004151921.1 | 13 | **0.03** |
| Theam\_1320 | Ppx/GppA phosphatase |  | YP\_004151924.1 | 33 | **0.02** |
| Theam\_1321 | Pyrococcus NSR homolog / FAD-dependent pyridine nucleotide-disulphide oxidoreductase CoB-CoM related | *nsr* | YP\_004151925.1 | 47 | **0.11** |
| Theam\_1323 |  fructose-1,6-bisphosphatase I | *fbp* | YP\_004151927.1 | 34 | **0.20** |
| Theam\_1324 | radical SAM enzyme, Cfr family |  | YP\_004151928.1 | 39 | **0.02** |
| Theam\_1327 | histidinol dehydrogenase | *hisD* | YP\_004151931.1 | 49 | **0.07** |
| Theam\_1328 | aspartate carbamoyltransferase | *atc* | YP\_004151932.1 | 34 | **0.18** |
| Theam\_1330 | dihydroorotase, multifunctional complex type | *pyrC* | YP\_004151934.1 | 46 | **0.05** |
| Theam\_1331 | periplasmic serine protease |  | YP\_004151935.1 | 33 | **0.01** |
| Theam\_1334 | 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase | *ispD* | YP\_004151938.1 | 26 | **0.08** |
| Theam\_1337 | carbon-monoxide dehydrogenase, catalytic subunit | *codh* | YP\_004151941.1 | 70 | **0.41** |
| Theam\_1338 | Dinitrogenase iron-molybdenum cofactor biosynthesis protein | *nif* | YP\_004151942.1 | 14 | **0.09** |
| Theam\_1342 | Phosphoglycerate mutase | *pgm* | YP\_004151946.1 | 24 | **0.09** |
| Theam\_1343 | glutamate synthase (NADPH), homotetrameric | *gltA* | YP\_004151947.1 | 53 | **0.56** |
| Theam\_1344 | Protein of unknown function DUF2168 |  | YP\_004151948.1 | 21 | **0.06** |
| Theam\_1351 | hypothetical protein |  | YP\_004151955.1 | 20 | **0.01** |
| Theam\_1352 | fimbrial protein pilin |  | YP\_004151956.1 | 20 | **0.33** |
| Theam\_1354 | RNA-metabolising metallo-beta-lactamase |  | YP\_004151958.1 | 52 | **0.01** |
| Theam\_1356 | leucyl-tRNA synthetase | *leuS* | YP\_004151960.1 | 105 | **0.19** |
| Theam\_1357 | hypothetical protein |  | YP\_004151961.1 | 20 | **0.06** |
| Theam\_1359 | selenium metabolism protein YedF |  | YP\_004151963.1 | 22 | **0.02** |
| Theam\_1363 | Tetratricopeptide TPR\_1 repeat-containing protein |  | YP\_004151967.1 | 30 | **0.01** |
| Theam\_1364 | GTP cyclohydrolase I | *folE* | YP\_004151968.1 | 21 | **0.49** |
| Theam\_1366 | hypoxanthine phosphoribosyltransferase | *hgprt* | YP\_004151970.1 | 19 | **0.02** |
| Theam\_1368 | argininosuccinate synthase | *argG* | YP\_004151972.1 | 45 | **0.36** |
| Theam\_1369 | trigger factor | *tig* | YP\_004151973.1 | 49 | **0.13** |
| Theam\_1372 | phosphoribosylformylglycinamidine synthase II | *fgams* | YP\_004151976.1 | 82 | **0.24** |
| Theam\_1373 | Domain of unknown function DUF1931 |  | YP\_004151977.1 | 17 | **0.37** |
| Theam\_1375 | Protein of unknown function DUF2148 |  | YP\_004151979.1 | 19 | **0.13** |
| Theam\_1378 | 2-oxoglutarate ferredoxin oxidoreductase subunit alpha | *oorA1* | YP\_004151982.1 | 60 | **0.03** |
| Theam\_1379 | 2-oxoglutarate ferredoxin oxidoreductase subunit beta | *oorB1* | YP\_004151983.1 | 30 | **0.02** |
| Theam\_1385 | flagellar hook-associated protein FlgK | *flgH* | YP\_004151989.1 | 49 | **0.01** |
| Theam\_1387 | type IV pilus assembly PilZ |  | YP\_004151991.1 | 26 | **0.04** |
| Theam\_1390 | MglA protein |  | YP\_004151994.1 | 22 | **0.15** |
| Theam\_1391 | Roadblock/LC7 family protein |  | YP\_004151995.1 | 18 | **0.08** |
| Theam\_1392 | pyruvate synthetase / thiamine pyrophosphate TPP-binding domain-containing protein | *porB* | YP\_004151996.1 | 36 | **0.43** |
| Theam\_1393 | pyruvate synthetase flavodoxin/ferredoxin oxidoreductase domain protein | *porA* | YP\_004151997.1 | 45 | **0.46** |
| Theam\_1394 | pyruvate synthetase ferredoxin/flavodoxin oxidoreductase, delta subunit | *porD* | YP\_004151998.1 | 11 | **0.16** |
| Theam\_1395 | pyruvate synthetase /ketoisovalerate oxidoreductase, gamma subunit | *porG* | YP\_004151999.1 | 21 | **0.51** |
| Theam\_1400 | SurA domain |  | YP\_004152004.1 | 49 | **0.00** |
| Theam\_1401 | YicC-like domain-containing protein |  | YP\_004152005.1 | 33 | **0.17** |
| Theam\_1402 | guanylate kinase |  | YP\_004152006.1 | 26 | **0.03** |
| Theam\_1403 | DNA-directed RNA polymerase, omega subunit | *rpoZ* | YP\_004152007.1 | 8 | **0.10** |
| Theam\_1404 | Dihydroorotate dehydrogenase, electron transfer subunit, iron-sulphur cluster binding domain |  | YP\_004152008.1 | 28 | **0.06** |
| Theam\_1408 | succinyl-CoA synthetase, beta subunit | *sucD* | YP\_004152012.1 | 42 | **0.58** |
| Theam\_1409 | succinyl-CoA synthetase, alpha subunit | *sucC* | YP\_004152013.1 | 32 | **0.80** |
| Theam\_1411 | 2-oxoglutarate synthetase ferredoxin subunit alpha | *oorA* | YP\_004152015.1 | 42 | **0.64** |
| Theam\_1412 | 2-oxoglutarate synthetase ferredoxin subunit beta | *oorB* | YP\_004152016.1 | 32 | **0.48** |
| Theam\_1413 | 2-oxoglutarate synthetase ferredoxin gamma subunit | *oorC* | YP\_004152017.1 | 22 | **0.47** |
| Theam\_1418 | adenosylmethionine-8-amino-7-oxononanoate aminotransferase | *bioA* | YP\_004152022.1 | 50 | **0.04** |
| Theam\_1419 | hypothetical protein |  | YP\_004152023.1 | 18 | **0.22** |
| Theam\_1420 | UspA domain-containing protein |  | YP\_004152024.1 | 17 | **0.12** |
| Theam\_1421 | protein of unknown function DUF814 |  | YP\_004152025.1 | 37 | **0.01** |
| Theam\_1422 | ribosomal subunit interface protein | *yfiA* | YP\_004152026.1 | 21 | **0.11** |
| Theam\_1423 | protein of unknown function DUF820 |  | YP\_004152027.1 | 21 | **0.04** |
| Theam\_1424 | GTP-binding protein LepA | *lepA* | YP\_004152028.1 | 67 | **0.01** |
| Theam\_1428 | hypothetical protein |  | YP\_004152031.1 | 151 | **0.03** |
| Theam\_1429 | helicase domain protein |  | YP\_004152032.1 | 123 | **0.01** |
| Theam\_1430 | Inorganic diphosphatase | *ppa* | YP\_004152033.1 | 20 | **0.22** |
| Theam\_1435 | PHP domain protein |  | YP\_004152038.1 | 24 | **0.03** |
| Theam\_1446 | fagellar hook-basal body protein- hook structural protein | *flgE* | YP\_004152049.1 | 57 | **0.07** |
| Theam\_1470 | Citrate transporter |  | YP\_004152072.1 | 49 | **0.00** |
| Theam\_1472 | ribosome biogenesis GTP-binding protein YsxC |  | YP\_004152074.1 | 22 | **0.02** |
| Theam\_1473 | Redoxin domain protein |  | YP\_004152075.1 | 22 | **0.10** |
| Theam\_1474 | thioredoxin reductase | *trxr* | YP\_004152076.1 | 33 | **0.13** |
| Theam\_1475 | thioredoxin | *trx* | YP\_004152077.1 | 12 | **0.39** |
| Theam\_1476 | regulatory protein ArsR |  | YP\_004152078.1 | 11 | **0.04** |
| Theam\_1477 | protein of unknown function DUF52 |  | YP\_004152079.1 | 29 | **0.11** |
| Theam\_1479 | Myo-inositol-1-phosphate synthase |  | YP\_004152081.1 | 40 | **0.20** |
| Theam\_1480 | hypothetical protein |  | YP\_004152082.1 | 15 | **0.01** |
| Theam\_1481 | tol-pal system protein YbgF |  | YP\_004152083.1 | 26 | **0.05** |
| Theam\_1482 | 2-nitropropane dioxygenase NPD | *npd* | YP\_004152084.1 | 39 | **0.01** |
| Theam\_1484 | peptidase M16 domain protein |  | YP\_004152086.1 | 45 | **0.02** |
| Theam\_1486 | phosphoribosylformylglycinamidine cyclo-ligase | *purM* | YP\_004152088.1 | 37 | **0.13** |
| Theam\_1487 | metal dependent phophohydrolase | *hdig* | YP\_004152089.1 | 37 | **0.00** |
| Theam\_1493 | NADH dehydrogenase subunit I | *nuoI* | YP\_004152095.1 | 22 | **0.03** |
| Theam\_1495 | NADH dehydrogenase (quinone) | *nuoD* | YP\_004152097.1 | 43 | **0.03** |
| Theam\_1497 | NADH-quinone oxidoreductase, B subunit | *nuoB* | YP\_004152099.1 | 18 | **0.04** |
| Theam\_1499 | phosphate ABC transporter, ATPase subunit | *pstB* | YP\_004152101.1 | 29 | **0.04** |
| Theam\_1502 | DNA polymerase III, alpha subunit | *polc* | YP\_004152104.1 | 131 | **0.00** |
| Theam\_1503 | acetyl-CoA carboxylase, carboxyl transferase, alpha subunit | *accA* | YP\_004152105.1 | 36 | **0.02** |
| Theam\_1505 | DEAD/DEAH box helicase domain protein |  | YP\_004152107.1 | 47 | **0.05** |
| Theam\_1510 | D-3-phosphoglycerate dehydrogenase | *pgdh* | YP\_004152112.1 | 59 | **0.40** |
| Theam\_1512 | Holliday junction DNA helicase RuvA | *ruvA* | YP\_004152114.1 | 21 | **0.02** |
| Theam\_1517 | translation initiation factor, aIF-2BI family | *alF* | YP\_004152119.1 | 39 | **0.12** |
| Theam\_1518 | UspA domain-containing protein |  | YP\_004152120.1 | 18 | **0.19** |
| Theam\_1519 | MazG family protein | *mazG* | YP\_004152121.1 | 31 | **0.03** |
| Theam\_1520 | cysteinyl-tRNA synthetase | *cysS* | YP\_004152122.1 | 55 | **0.09** |
| Theam\_1526 | Nickel transport complex, NikM subunit, transmembrane |  | YP\_004152128.1 | 29 | **0.12** |
| Theam\_1527 | Carbohydrate-selective porin OprB |  | YP\_004152129.1 | 47 | **0.07** |
| Theam\_1539 | pyruvate carboxylase, biotin carboxylase | *pycA* | YP\_004152140.1 | 53 | **0.09** |
| Theam\_1540 | pyruvate carboxylase alpha subunit | *pycB* | YP\_004152141.1 | 69 | **0.28** |
| Theam\_1544 | chorismate synthase | *aroC* | YP\_004152145.1 | 42 | **0.04** |
| Theam\_1545 | ribosomal protein L19 | *rplS* | YP\_004152146.1 | 14 | **0.89** |
| Theam\_1548 | translation initiation factor IF-2 |  | YP\_004152148.1 | 99 | **0.07** |
| Theam\_1550 | 1-phosphofructokinase |  | YP\_004152150.1 | 34 | **0.04** |
| Theam\_1552 | ribonucleotide reductase |  | YP\_004152152.1 | 41 | **0.16** |
| Theam\_1554 | ribonucleoside-diphosphate reductase, alpha subunit |  | YP\_004152154.1 | 87 | **0.17** |
| Theam\_1555 | Redoxin domain protein |  | YP\_004152155.1 | 18 | **0.11** |
| Theam\_1559 | beta-lactamase domain protein |  | YP\_004152159.1 | 29 | **0.01** |
| Theam\_1560 | chemotaxis sensory transducer |  | YP\_004152160.1 | 28 | **0.01** |
| Theam\_1561 | 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase | *metE* | YP\_004152161.1 | 82 | **0.69** |
| Theam\_1563 | pseudogene |  |  | 79 | **0.01** |
| Theam\_1564 | ErfK/YbiS/YcfS/YnhG family protein |  | YP\_004152163.1 | 41 | **0.01** |
| Theam\_1566 | thioesterase superfamily protein |  | YP\_004152165.1 | 21 | **0.67** |
| Theam\_1567 | carbamoyl-phosphate synthase, large subunit | *cpsL* | YP\_004152166.1 | 119 | **0.33** |
| Theam\_1568 | Adenylate kinase |  | YP\_004152167.1 | 19 | **0.01** |
| Theam\_1569 | sun protein | *rsmB* | YP\_004152168.1 | 50 | **0.02** |
| Theam\_1570 | Metal-dependent hydrolase HDOD |  | YP\_004152169.1 | 24 | **0.04** |
| Theam\_1571 | Metal-dependent hydrolase HDOD |  | YP\_004152170.1 | 25 | **0.06** |
| Theam\_1576 | Carbonate dehydratase |  | YP\_004152175.1 | 28 | **0.08** |
| Theam\_1578 | DNA-directed RNA polymerase, beta' subunit | *rpoB1* | YP\_004152177.1 | 167 | **0.34** |
| Theam\_1579 | DNA-directed RNA polymerase, beta subunit | *rpoB* | YP\_004152178.1 | 163 | **0.38** |
| Theam\_1580 | ribosomal protein L7/L12 | *L12* | YP\_004152179.1 | 13 | **0.38** |
| Theam\_1581 | ribosomal protein L10 |  | YP\_004152180.1 | 20 | **0.47** |
| Theam\_1582 | ribosomal protein L1 | *rplA* | YP\_004152181.1 | 26 | **0.37** |
| Theam\_1583 | ribosomal protein L11 | *L11* | YP\_004152182.1 | 15 | **0.11** |
| Theam\_1584 | transcription termination/antitermination factor NusG | *nusG* | YP\_004152183.1 | 28 | **0.04** |
| Theam\_1587 | translation elongation factor Tu |  | YP\_004152186.1 | 44 | **2.19** |
| Theam\_1588 | hypothetical protein |  | YP\_004152187.1 | 52 | **0.83** |
| Theam\_1590 | 16S rRNA processing protein RimM |  | YP\_004152188.1 | 22 | **0.01** |
| Theam\_1591 | tRNA (guanine-N1)-methyltransferase | *trmD* | YP\_004152189.1 | 29 | **0.02** |
| Theam\_1596 | chorismate mutase |  | YP\_004152194.1 | 40 | **0.02** |
| Theam\_1598 | Imidazoleglycerol-phosphate dehydratase |  | YP\_004152196.1 | 22 | **0.03** |
| Theam\_1600 | glutamate-1-semialdehyde-2,1-aminomutase | *hemL* | YP\_004152198.1 | 47 | **0.21** |
| Theam\_1605 | ATP synthase F0, A subunit | *atpa* | YP\_004152203.1 | 26 | **0.01** |
| Theam\_1611 | OmpA/MotB domain protein |  | YP\_004152209.1 | 26 | **0.01** |
| Theam\_1612 | gamma-glutamyl phosphate reductase | *proA* | YP\_004152210.1 | 47 | **0.22** |
| Theam\_1626 | hypothetical protein |  | YP\_004152223.1 | 34 | **0.02** |
| Theam\_1627 | pyruvate:water dikinase | *pvtk* | YP\_004152224.1 | 100 | **0.85** |
| Theam\_1628 | glycyl-tRNA synthetase, beta subunit | *glyS* | YP\_004152225.1 | 77 | **0.11** |
| Theam\_1629 | glycyl-tRNA synthetase, alpha subunit | *glyQ* | YP\_004152226.1 | 33 | **0.11** |
| Theam\_1632 | exsB protein | *exsB* | YP\_004152229.1 | 26 | **0.03** |
| Theam\_1645 | hypothetical protein |  | YP\_004152242.1 | 17 | **0.06** |
| Theam\_1647 | glutamyl-tRNA(Gln) amidotransferase, A subunit | *gatA* | YP\_004152244.1 | 53 | **0.41** |
| Theam\_1648 | glutamyl-tRNA(Gln) amidotransferase, C subunit | *gatC* | YP\_004152245.1 | 11 | **0.02** |
| Theam\_1656 | H+transporting two-sector ATPase B/B' subunit | *atpB'* | YP\_004152253.1 | 17 | **0.14** |
| Theam\_1657 | ATP synthase F0, B subunit | *atpB* | YP\_004152254.1 | 18 | **0.08** |
| Theam\_1658 | ATP synthase F1, delta subunit | *atpD* | YP\_004152255.1 | 20 | **0.05** |
| Theam\_1659 | ATP synthase F1, alpha subunit | *atpA* | YP\_004152256.1 | 55 | **0.16** |
| Theam\_1660 | ATP synthase F1, gamma subunit | *atpC* | YP\_004152257.1 | 32 | **0.10** |
| Theam\_1661 | ATP synthase F1, beta subunit | *atpD* | YP\_004152258.1 | 54 | **0.19** |
| Theam\_1662 | ATP synthase F1, epsilon subunit | *atpE* | YP\_004152259.1 | 16 | **0.12** |
| Theam\_1667 | protein of unknown function DUF62 |  | YP\_004152264.1 | 29 | **0.01** |
| Theam\_1668 | glucose inhibited division protein A | *gidA* | YP\_004152265.1 | 72 | **0.06** |
| Theam\_1669 | methyltransferase GidB | *gidB* | YP\_004152266.1 | 24 | **0.02** |
| Theam\_1672 | homoserine kinase | *thrB* | YP\_004152269.1 | 33 | **0.16** |
| Theam\_1676 | valyl-tRNA synthetase | *valS* | YP\_004152273.1 | 102 | **0.19** |
| Theam\_1677 | CMP/dCMP deaminase zinc-binding |  | YP\_004152274.1 | 17 | **0.01** |
| Theam\_1678 | recA protein | *recA* | YP\_004152275.1 | 38 | **0.02** |
| Theam\_1679 | twitching motility protein | *pilT* | YP\_004152276.1 | 41 | **0.03** |
| Theam\_1682 | alanyl-tRNA synthetase | *alaS* | YP\_004152279.1 | 99 | **0.18** |
| Theam\_1684 | hypothetical protein |  | YP\_004152281.1 | 150 | **0.02** |
| Theam\_1685 | hypothetical protein |  | YP\_004152282.1 | 50 | **0.00** |
| Theam\_1686 | PfkB domain protein |  | YP\_004152283.1 | 36 | **0.02** |
| Theam\_1688 | transcription termination factor NusA | *NusA* | YP\_004152285.1 | 43 | **0.08** |
| Theam\_1689 | protein of unknown function DUF150 |  | YP\_004152286.1 | 18 | **0.04** |
| Theam\_1691 | RNA binding S1 domain protein |  | YP\_004152288.1 | 39 | **0.01** |
| Theam\_1696 | S-adenosyl-methyltransferase MraW | *mraW* | YP\_004152293.1 | 34 | **0.02** |
| Theam\_1697 | ornithine carbamoyltransferase | *otc* | YP\_004152294.1 | 35 | **0.14** |
| Theam\_1712 | stationary-phase survival protein SurE | *surE* | YP\_004152309.1 | 28 | **0.03** |
| Theam\_1725 | Indole-3-glycerol-phosphate synthase |  | YP\_004152322.1 | 29 | **0.08** |
| Theam\_1726 | UDP-N-acetylglucosamine pyrophosphorylase | *glmU* | YP\_004152323.1 | 51 | **0.10** |
| Theam\_1727 | NUDIX hydrolase |  | YP\_004152324.1 | 17 | **0.07** |
| Theam\_1728 | hypothetical protein |  | YP\_004152325.1 | 32 | **0.01** |
| Theam\_1729 | S-adenosylmethionine/tRNA-ribosyltransferase-isomerase | *queA* | YP\_004152326.1 | 39 | **0.03** |
| Theam\_1735 | hypothetical protein |  | ADU97691.1 | 43 | **0.03** |
| Theam\_1738 | hypothetical protein |  | ADU97694.1 | 19 | **0.06** |
| Theam\_1739 | hypothetical protein |  | ADU97695.1 | 23 | **0.03** |
| Theam\_1742 | hypothetical protein |  | ADU97698.1 | 35 | **0.01** |
| Theam\_1744 | hypothetical protein |  | ADU97700.1 | 22 | **0.01** |
| Theam\_1768 | hypothetical protein |  | ADU97724.1 | 30 | **0.01** |
| Theam\_1771 | ATPase associated with various cellular activities AAA\_5 |  | ADU97727.1 | 31 | **0.04** |
| Theam\_1774 | trichohyalin |  | ADU97730.1 | 21 | **0.05** |
| Theam\_1778 | hypothetical protein |  | ADU97734.1 | 12 | **0.12** |
| Theam\_1790 | hypothetical protein |  | ADU97746.1 | 63 | **0.01** |
| Theam\_1795 | peptidase C11 clostripain |  | ADU97751.1 | 76 | **0.01** |
| Theam\_1797 | hypothetical protein |  | ADU97753.1 | 45 | **0.06** |
| Theam\_1799 | type II secretion system protein E | *gspE* | ADU97755.1 | 46 | **0.22** |
| Theam\_1801 | hypothetical protein |  | ADU97757.1 | 19 | **0.05** |
| Theam\_1803 | hypothetical protein |  | ADU97759.1 | 19 | **0.07** |
| Theam\_1804 | type II secretion system protein E | *gspE* | ADU97760.1 | 60 | **0.01** |
| Theam\_1805 | hypothetical protein |  | ADU97761.1 | 28 | **0.01** |
| Theam\_1818 | hypothetical protein |  | ADU97774.1 | 18 | **0.06** |

Accession numbers refer to the *T. ammonificans* proteins in NCBI. NSAF% are normalized spectral abundance factors, i.e. relative abundances for each protein in % of all proteins in the sample. NSAF% are average values (n=3).