

Functions Predicted for *N. equitans* Proteins

Key: The predicted protein function for each CDS is listed, with the archaeon containing the most similar homolog shown in brackets.

Referenced euryarchaea include:

Archaeoglobus fulgidus VC-16
Ferroplasma acidarmanus
Halobacterium sp. NRC-1
Methanocaldococcus jannaschii JAL-1
 "Methanococcus jannaschii"
Methanopyrus kandleri AV19
Methanoscincus acetivorans C2A
Methanothermobacter thermautotrophicus ΔH
 "Methanobacterium thermoautotrophicum"
Pyrococcus abyssi GE5
Pyrococcus furiosus DSM 3638
Pyrococcus horikoshii OT3
Thermoplasma acidophilum
Thermoplasma volcanium GSS1

Referenced crenarchaea include:

Aeropyrum pernix K1
Pyrobaculum aerophilum IM2
Sulfolobus solfataricus
Sulfolobus tokodaii

Amino acid biosynthesis

Aromatic amino acid family

NEQ192 Prephenate dehydrogenase/chorismate mutase/prephenate dehydratase [*A. fulgidus*]

Glutamate family

NEQ126 Glutamyl-tRNA^{Gln} amidotransferase, subunit D [*P. horikoshii*]
 NEQ245 Glutamyl-tRNA^{Gln} amidotransferase, subunit E [*S. tokodaii*] SPLIT, see NEQ396
 NEQ396 Glutamyl-tRNA^{Gln} amidotransferase, subunit E [*M. jannaschii*] SPLIT, see NEQ245
 NEQ185 Glutamyl-tRNA^{Gln}/aspartyl-tRNA^{Asn} amidotransferase, subunit B [*A. fulgidus*]
 NEQ360 Glutamyl-tRNA^{Gln}/aspartyl-tRNA^{Asn} amidotransferase, subunit A [*A. fulgidus*]
 NEQ513 Glutamyl-tRNA^{Gln}/aspartyl-tRNA^{Asn} amidotransferase, subunit C [*A. fulgidus*]

Coenzyme biosynthesis

NEQ367 Nicotinamide mononucleotide adenylyltransferase [*S. tokodaii*]

Cell envelope

Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides

NEQ012 Glycosyltransferase [*M. acetivorans*]
 NEQ025 Mannose-1-phosphate guanylyltransferase [*A. fulgidus*]
 NEQ061 UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosamine-phosphotransferase [*S. solfataricus*]
 NEQ155 Oligosaccharyl transferase [*P. furiosus*]
 NEQ172 Glycosyltransferase [*P. horikoshii*]
 NEQ195 Glycosyltransferase [*S. tokodaii*]

Surface structures

NEQ300 Hypothetical surface layer protein [*M. jannaschii*]

Cellular processes

Cell division

NEQ119 Septum site-determining protein [*P. furiosus*]
 NEQ133 Cell division protein FlsZ [*P. horikoshii*]
 NEQ473 Cell division protein FtsZ [*A. fulgidus*]
 NEQ475 Cell division control protein (CDC48; AAA family ATPase) [*P. furiosus*]

Detoxification

NEQ011 Superoxide reductase [*P. horikoshii*]
 NEQ191 Thioredoxin peroxidase [*M. jannaschii*]

DNA metabolism

Chromosome-associated proteins

NEQ288 Histone protein [*M. jannaschii*]
 NEQ348 Histone protein [*M. jannaschii*]
 NEQ363 DNA-binding protein [*P. horikoshii*]
 NEQ538 Histon deacetylase/aminohydrolase [*P. aerophilum*]

DNA replication, recombination and repair

NEQ282 DNA replication initiation protein (MCM family) [*M. thermoautotrophicum*]
 NEQ057 Cell division control protein 6 related [*S. tokodaii*]
 NEQ003 ATP-dependent RNA helicase [*P. abyssi*]; SPLIT See NEQ409.
 NEQ409 ATP-dependent RNA helicase [*P. furiosus*] SPLIT see NEQ003
 NEQ007 O⁶-Methylguanine DNA—protein -cysteine S-methyltransferase [*P. aerophilum*]
 NEQ045 DNA topoisomerase I [*P. horikoshii*]
 SPLIT see NEQ324.
 NEQ324 DNA topoisomerase I [*P. horikoshii*]
 SPLIT see NEQ045
 NEQ063 Ribonuclease HII [*P. aerophilum*]
 NEQ068 DNA-Directed DNA polymerase BI [*P. furiosus*] SPLIT see NEQ528.
 NEQ528 DNA-Directed DNA polymerase BI [*P. furiosus*] SPLIT see NEQ068
 NEQ077a Endonuclease IV [*P. abyssi*]
 NEQ088 Structure-specific flap endonuclease (FEN1) [*P. abyssi*]
 NEQ118 Single-stranded DNA-specific exonuclease, 5'-3' [*M. acetivorans*]
 NEQ126a Endonuclease III [*P. abyssi*] SPLIT see NEQ398
 NEQ398 Endonuclease III [*A. fulgidus*] SPLIT see NEQ126a
 NEQ144 DNA Topoisomerase VI, subunit B [*A. fulgidus*]
 NEQ542 DNA Topoisomerase VI, subunit A [*P. furiosus*]
 NEQ170 Replication factor C, small subunit [*A. fulgidus*]
 NEQ430 Replication factor C, large subunit [*M. jannaschii*]
 NEQ199 ssDNA Binding protein (RPA70/SSB family) [*M. jannaschii*]
 NEQ240 DNA-Directed DNA polymerase II, small subunit [*A. fulgidus*]
 NEQ420 DNA-Directed DNA polymerase II, large subunit [*P. furiosus*]
 NEQ256 DNA Double-strand break repair ATPase [*T. volcanium*]
 NEQ295 Sliding clamp protein for DNA replication (PCNA) [*P. abyssi*]
 NEQ536 Sliding clamp protein for DNA replication (PCNA) [*P. furiosus*]
 NEQ537 Sliding clamp protein for DNA replication (PCNA) [*P. abyssi*]
 NEQ318 Reverse gyrase [C-terminus] [*P. abyssi*] SPLIT see NEQ434

NEQ434 Reverse gyrase [N-terminus] [*P. horikoshii*] SPLIT see NEQ318
 NEQ341 DNA primase/topoisomerase [*P. furiosus*]
 NEQ395 DNA Primas [*T. acidophilum*]
 NEQ346a Endonuclease V [*F. acidarmanus*]
 NEQ368 DNA-(Apurinic or apyrimidinic site) lyase (endonuclease IV) [*M. jannaschii*]
 NEQ369 Helicase-related DNA repair protein (RAD25/XPB subfamily) [*S. solfataricus*]
 NEQ372 Uracil DNA glycosylase [*S. tokodaii*]
 NEQ383 DNA repair protein (Rad32/Mre11) [*P. horikoshii*]
 NEQ424 Holliday-junction resolvase [*M. thermoautotrophicum*]
 NEQ426 DNA Recombinase (RadA) [*P. furiosus*]
 NEQ509 DNA Ligase; ATP-dependent [*P. abyssi*]
 NEQ387 DNA Helicase/structure-specific endonuclease [*P. abyssi*]

Energy metabolism

ATP-proton motive force interconversion

NEQ103 A₁A₀ ATP synthase, subunit A [*M. kandleri*]
 NEQ263 A₁A₀ ATP synthase, subunit B [*M. jannaschii*]
 NEQ166 A₁A₀ ATP synthase, subunit D [*P. horikoshii*]
 NEQ217 A₁A₀ ATP synthase, proteolipid subunit K [*M. jannaschii*]
 NEQ410 A₁A₀ ATP synthase, subunit I [*P. furiosus*]

Amino acids and amines

NEQ077 Glutamate dehydrogenase [*T. volcanium*]
 NEQ190 Branched-chain amino acid aminotransferase [*P. aerophilum*]
 NEQ223 Agmatinase/arginase [*M. jannaschii*]

Electron transport

NEQ024 Hypothetical flavoprotein [*P. aerophilum*]
 NEQ049 Hypothetical [Fe-S] protein [*A. fulgidus*]
 NEQ051 Ferredoxin—NADP reductase [*P. furiosus*]
 NEQ084 IMP Dehydrogenase-related protein [*A. fulgidus*]
 NEQ306 Hypothetical NAD(P)-dependent oxidoreductase [*S. tokodaii*]
 NEQ321 Thioredoxin [*P. furiosus*]
 NEQ373 Ferredoxin protein [*P. horikoshii*]
 NEQ382 Hypothetical oxidoreductase (contains Fe-S cluster) [*P. furiosus*]
 NEQ491 Thioredoxin reductase [*S. solfataricus*]

Other

NEQ461 Inorganic pyrophosphatase [*S. tokodaii*]

Hypothetical proteins

NEQ006 Hypothetical protein
 NEQ010 Hypothetical protein
 NEQ018 Hypothetical protein
 NEQ020 Hypothetical protein
 NEQ026 Hypothetical protein
 NEQ027 Hypothetical protein
 NEQ028 Hypothetical protein
 NEQ029 Hypothetical protein
 NEQ032 Hypothetical protein
 NEQ033 Hypothetical protein
 NEQ034 Hypothetical protein
 NEQ035 Hypothetical protein
 NEQ036 Hypothetical protein

Functions Predicted for *N. equitans* Proteins

Protein folding and stabilization

- NEQ141 Thermosome (type II chaperonin) [*P. horikoshii*]
 NEQ344 Small heat shock protein (class I) [*M. acetivorans*]
 NEQ385 GimC Chaperonin, subunit α [*P. furiosus*]
 NEQ516 GimC Chaperonin, subunit β [*M. jannaschii*]

Protein modification and repair

- NEQ002 Peptidyl-prolyl *cis-trans* isomerase [*M. jannaschii*]
 NEQ047 Protein adenyllyltransferase [*A. pernix*]
 NEQ226 Hypothetical diphthamide synthesis protein [*F. acidarmanus*]
 NEQ399 Methionine aminopeptidase [*P. abyssi*]
 NEQ402 Deoxyhypusine synthase [*T. acidophilum*]
 NEQ422 Diphthine synthase [*P. furiosus*]
 NEQ459 Protein disulfide oxidoreductase [*P. furiosus*]

Protein synthesis

Ribosomal proteins: synthesis and modification

- NEQ508 SSU Ribosomal protein S2 [*P. horikoshii*]
 NEQ481 SSU Ribosomal protein S3P [*M. jannaschii*]
 NEQ375 SSU Ribosomal protein S3AE [*M. kandleri*]
 NEQ478 SSU Ribosomal protein S4E [*M. thermoautotrophicum*]
 NEQ247 SSU Ribosomal protein S4P [*P. horikoshii*]
 NEQ388 SSU Ribosomal protein S5 [*P. aerophilum*]
 NEQ105 SSU Ribosomal protein S6E [*M. kandleri*]
 NEQ319 Hypothetical SSU ribosomal protein H56 [*S. tokodaii*]
 NEQ242 SSU Ribosomal protein S7 [*M. kandleri*]
 NEQ469 SSU Ribosomal protein S8E [*A. fulgidus*]
 NEQ274 SSU Ribosomal protein S8P [*P. furiosus*]
 NEQ446 SSU Ribosomal protein S9 [*P. furiosus*]
 NEQ083 SSU Ribosomal protein S10AB [*S. solfataricus*]
 NEQ069 SSU Ribosomal protein S11 [*M. kandleri*]
 NEQ058 SSU ribosomal protein S12P [*P. furiosus*]
 NEQ467 SSU Ribosomal protein S13P [*M. kandleri*]
 NEQ227 SSU Ribosomal protein S14 [*S. solfataricus*]
 NEQ487 SSU Ribosomal protein S15P/S13E [*M. kandleri*]
 NEQ326 SSU Ribosomal protein S17P [*P. horikoshii*]
 NEQ320 SSU Ribosomal protein S17E [*P. horikoshii*]
 NEQ480 SSU Ribosomal protein S19P [*P. abyssi*]
 NEQ187 SSU Ribosomal protein S19E [*P. furiosus*]
 NEQ548 SSU Ribosomal protein S24E [*M. jannaschii*]
 NEQ219 SSU Ribosomal protein S27E [*M. kandleri*]
 NEQ176 SSU Ribosomal protein S27AE [*P. furiosus*]
 NEQ359 SSU Ribosomal protein S28E [*P. horikoshii*]
 NEQ546 LSU Ribosomal protein L1P [*P. abyssi*]
 NEQ361 LSU Ribosomal protein L2P [*P. abyssi*]
 NEQ433 LSU Ribosomal protein L3P [*M. thermoautotrophicum*]

- NEQ146 LSU Ribosomal protein L4 [*M. kandleri*]
 NEQ093 LSU Ribosomal protein L5P [*P. abyssi*]
 NEQ241 LSU Ribosomal protein L6P [*P. abyssi*]
 NEQ091 LSU Ribosomal protein L10E [*M. jannaschii*]
 NEQ101 LSU Ribosomal protein L11 [*M. kandleri*]
 NEQ201 LSU Ribosomal protein L12A [*P. abyssi*]
 NEQ207 LSU Ribosomal protein L13 [*M. kandleri*]
 NEQ178 LSU Ribosomal protein L14E [*M. jannaschii*]
 NEQ092 LSU Ribosomal protein L14P [*M. jannaschii*]
 NEQ317 LSU Ribosomal protein L15 [*P. aerophilum*]
 NEQ181 LSU Ribosomal protein L15E [*P. furiosus*]
 NEQ450 LSU Ribosomal protein L16P/L10E [*A. fulgidus*]
 NEQ075 LSU Ribosomal protein L18P [*M. jannaschii*]
 NEQ489 LSU Ribosomal protein L18E [*S. solfataricus*]
 NEQ379 LSU ribosomal protein L19E [*M. jannaschii*]
 NEQ346 LSU Ribosomal protein LX4A [*P. horikoshii*]
 NEQ397 LSU Ribosomal protein L21E [*P. furiosus*]
 NEQ204 LSU Ribosomal protein L22 [*M. kandleri*]
 NEQ065 LSU Ribosomal protein L23 [*S. tokodaii*]
 NEQ257 LSU Ribosomal protein L24P [*P. abyssi*]
 NEQ337 LSU Ribosomal protein L24E [*A. fulgidus*]
 NEQ262 LSU Ribosomal protein L29 [*M. jannaschii*]
 NEQ179 LSU Ribosomal protein L30E [*M. jannaschii*]
 NEQ311 LSU Ribosomal protein L30P [*M. jannaschii*]
 NEQ364 LSU Ribosomal protein L31E [*M. jannaschii*]
 NEQ530 LSU Ribosomal protein L32E [*P. abyssi*]
 NEQ297 LSU Ribosomal protein L34E [*M. jannaschii*]
 NEQ303 LSU Ribosomal protein L35AE [*P. abyssi*]
 NEQ038 LSU Ribosomal protein L37AE/L43A [*M. kandleri*]
 NEQ006a LSU Ribosomal protein L37E [*P. horikoshii*]
 NEQ427a LSU Ribosomal protein L39E [*P. abyssi*]
 NEQ505a LSU Ribosomal protein L40E [*P. furiosus*]
 NEQ183 LSU Ribosomal protein L44E; [*T. acidophilum*]

Translation factors

- NEQ235 Hypothetical ribosome assembly protein [*M. thermoautotrophicum*]
 NEQ264 Translation initiation factor (SUII family) [*P. furiosus*]
 NEQ130 Translation initiation factor eIF-1A [*P. furiosus*]
 NEQ405 Translation initiation factor eIF2- α [*M. kandleri*]
 NEQ323 Translation initiation factor eIF-2B [*P. horikoshii*]
 NEQ270 Translation initiation factor eIF-2 γ [*P. abyssi*]
 NEQ498 Translation initiation factor 2 related protein [*M. kandleri*]
 NEQ393 Translation initiation factor eIF-5A [*P. furiosus*]
 NEQ517 Translation initiation factor eIF-6 [*S. tokodaii*]
 NEQ082 Translation elongation factor EF-1 α [*P. furiosus*]
 NEQ220 Translation elongation factor EF-1 β [*M. kandleri*]
 NEQ543 Elongation factor 2 (eEF-2) [*P. furiosus*]

- NEQ052 Peptide chain release factor aRF, subunit 1 [*P. abyssi*]

tRNA aminoacylation

- NEQ547 Alanyl-tRNA synthetase [*M. acetivorans*] SPLIT see NEQ211
 NEQ211 Alanyl-tRNA synthetase [C-terminus] [*P. abyssi*] SPLIT see NEQ547
 NEQ208 Arginyl-tRNA synthetase (class 1) [*M. jannaschii*]
 NEQ535 Aspartyl-tRNA synthetase (class 2) [*A. pernix*]
 NEQ055 Cysteinyl-tRNA synthetase [*P. furiosus*]
 NEQ302 Glutamyl-tRNA synthetase (class 1) [*P. abyssi*]
 NEQ417 Glycyl-tRNA synthetase (class 2) [*P. abyssi*]
 NEQ102 Histidyl-tRNA synthetase (class 2) [*A. pernix*]
 NEQ230 Isoleucyl-tRNA synthetase (class 1a) [*P. furiosus*]
 NEQ239 Leucyl-tRNA synthetase (class 1a) [*M. jannaschii*]
 NEQ087 Lysyl-tRNA synthetase (class-1) [*Halobacterium* sp.]
 NEQ457 Methionyl-tRNA synthetase (class 1a) [*P. horikoshii*]
 NEQ505 Phenylalanyl-tRNA synthetase, α -subunit [*S. solfataricus*]
 NEQ479 Phenylalanyl-tRNA synthetase, β -chain [*P. furiosus*]
 NEQ210 Prolyl-tRNA synthetase (class 2) [*M. kandleri*]
 NEQ308 Seryl-tRNA synthetase (class 2) [*S. tokodaii*]
 NEQ177 Threonyl-tRNA synthetase (class 2) [*P. aerophilum*]
 NEQ115 Tryptophanyl-tRNA synthetase (class 1b) [*S. solfataricus*]
 NEQ389 Tyrosyl-tRNA synthetase (class 1b) [*P. furiosus*]
 NEQ252 Valyl-tRNA synthetase (class 1a) [*A. pernix*]

tRNA and rRNA modification and processing

- NEQ008 2-Methylthioadenosine synthase [*S. tokodaii*]
 NEQ037 Small nuclear ribonucleoprotein (snRNP) [*M. kandleri*]
 NEQ053 rRNA Methyltransferase [*P. abyssi*]
 NEQ108 tRNA(Guanine-26,N²-N⁷) methyltransferase [*S. tokodaii*]
 NEQ111 Ribonuclease PH [*A. fulgidus*]
 NEQ124 tRNA-Guanine transglycosylase [*P. furiosus*] SPLIT see NEQ305
 NEQ305 tRNA-Guanine transglycosylase [*M. acetivorans*] SPLIT See NEQ124
 NEQ125 Box C/D snoRNP RNA modification enzyme, fibrillarin subunit [*P. furiosus*]
 NEQ342 Box C/D snoRNP RNA modification enzyme, Nop5p subunit [*S. tokodaii*]
 NEQ152 tRNA Nucleotidyltransferase (CCA-adding enzyme) [*S. tokodaii*]
 NEQ165 LSU Ribosomal protein L11P methyltransferase [*P. furiosus*]
 NEQ205 tRNA Intron endonuclease [*M. jannaschii*]
 NEQ261 tRNA Intron endonuclease [*M. acetivorans*]
 NEQ502 2'-5' RNA Ligase [*M. jannaschii*]
 NEQ228 tRNA Methyltransferase [*P. furiosus*]
 NEQ238 N⁶-Adenine tRNA methyltransferase [*M. jannaschii*]
 NEQ248 Ribonuclease PH-related protein [*P. furiosus*]
 NEQ293 tRNA Pseudouridine synthase [*P. abyssi*]
 NEQ333 tRNA Pseudouridine synthase [*M. jannaschii*]
 NEQ337 tRNA 1-Methyladenosine methyltransferase [*M. jannaschii*]
 NEQ384 tRNA Methyltransferase [*S. solfataricus*]
 NEQ423 Thiamin biosynthesis/4-thiouridine synthesis protein [*A. fulgidus*]
 NEQ440 tRNA Methyltransferase [*M. thermoautotrophicum*]

Functions Predicted for *N. equitans* Proteins

NEQ454 tRNA Pseudouridine synthase [*P. furiosus*]
 NEQ522 tRNA Methyltransferase [*M. jannaschii*]

Purines, pyrimidines, nucleosides, and nucleotides

2'-Deoxyribonucleotide metabolism

NEQ316 dCTP deaminase/dUTP diphosphatase [*M. thermoautotrophicum*]
 NEQ329 dUTP diphosphatase [*M. acetivorans*]

Nucleotide and nucleoside interconversions

NEQ015 Thymidylate synthase; flavin-dependent [*S. tokodaii*]
 NEQ149 Adenylate kinase [*S. tokodaii*]
 NEQ307 Nucleoside diphosphate kinase [*P. aerophilum*]
 NEQ345 Anaerobic ribonucleoside-triphosphate reductase [*P. abyssi*]

Signal transduction

NEQ460 Serine/threonine protein kinase [*M. kandleri*]
 NEQ464 Serine/threonine protein kinase with N-terminal DNA-binding HTH domain [*M. kandleri*]

Transcription

DNA-dependent RNA polymerase

NEQ503 DNA-Directed RNA polymerase, subunit A' [*P. furiosus*]
 NEQ427 DNA-Directed RNA polymerase, subunit A'' [*P. abyssi*]
 NEQ156 DNA-Directed RNA polymerase, subunit B' [*P. abyssi*]
 NEQ173 DNA-Directed RNA polymerase, subunit B'' [*P. horikoshii*]
 NEQ452 DNA-Directed RNA polymerase, subunit D [*P. abyssi*]
 NEQ370 DNA-Directed RNA polymerase, subunit E' [*M. jannaschii*]
 NEQ231 DNA-Directed RNA polymerase, subunit E'' [*P. aerophilum*]
 NEQ411 DNA-Directed RNA polymerase, subunit F [*M. jannaschii*]
 NEQ507 DNA-Directed RNA polymerase, subunit H [*M. jannaschii*]
 NEQ205a DNA-Directed RNA polymerase, subunit K [*P. horikoshii*]
 NEQ182 DNA-Directed RNA polymerase, subunit L [*S. tokodaii*]
 NEQ377 DNA-Directed RNA polymerase, subunit M [*S. tokodaii*]
 NEQ338 DNA-Directed RNA polymerase, subunit N [*A. pernix*]
 NEQ399a DNA-Directed RNA polymerase, subunit P [*P. furiosus*]

Degradation of DNA or RNA

NEQ064 Binuclear zinc phosphodiesterase [*M. jannaschii*]
 NEQ097 Thermo-nuclease [*M. thermoautotrophicum*]

Transcription factors

NEQ039 Transcription initiation TATA-binding protein (TBP) [*M. jannaschii*]
 NEQ276 Transcription initiation factor IIB [*P. abyssi*]
 NEQ482 Transcription initiation protein E (TFE) [*M. thermoautotrophicum*]

NEQ073a Hypothetical zinc-finger protein [*P. aerophilum*]
 NEQ078a Hypothetical helix-turn-helix transcriptional regulator [*A. fulgidus*]
 NEQ541 Transcriptional regulator [*S. tokodaii*]
 NEQ229 Transcriptional regulator (AsnC family) [*M. jannaschii*]
 NEQ328 Transcriptional regulator (AsnC family) [*P. furiosus*]
 NEQ453 Transcriptional regulator (V4R and HTH domains) [*M. kandleri*]
 NEQ534 Transcriptional regulator [*P. horikoshii*]
 NEQ022 ATP-dependent RNA helicase [*P. horikoshii*]
 NEQ540 Transcription elongation factor (SPT5/NusG family) [*P. furiosus*]
 NEQ180 Transcription termination-antitermination factor [*M. acetivorans*]
 NEQ076 Hypothetical mRNA 3'-end processing factor [*P. furiosus*]
 NEQ143 Multiprotein bridging factor [*S. tokodaii*]

Transport and binding proteins

NEQ014 TDT (tellurite/dicarboxylate) family transporter [*P. abyssi*]
 NEQ073 ABC transporter, substrate-binding subunit
 NEQ074 ABC transporter, ATP-binding subunit [*P. furiosus*]
 NEQ090 Polysaccharide transporter [*A. fulgidus*]
 NEQ129 ABC transporter, permease subunit [*A. fulgidus*]
 NEQ175 glutamine ABC transporter, permease subunit [*M. jannaschii*]
 NEQ198 Mechanosensitive ion channel membrane protein [*M. jannaschii*]
 NEQ299 ABC transporter, ATP-binding subunit; contains [4Fe-4S] cluster [*P. horikoshii*]
 NEQ421 ABC transporter, ATP-binding subunit [*M. acetivorans*]
 NEQ486 Na⁺/Ca²⁺ antiporter (CaCA family) [*P. abyssi*]
 NEQ501 Metal ion transporter (MIT-family) [*P. horikoshii*]
 NEQ531 Mechanosensitive ion channel membrane protein [*M. jannaschii*]

Unknown function

NEQ013 Hypothetical "radical SAM" protein [*S. tokodaii*]
 NEQ031 RNA-binding protein [*S. tokodaii*]
 NEQ059 Hypothetical NTP-binding protein [*P. abyssi*]
 NEQ067 Hypothetical member of metallo-β-lactamase superfamily [*P. abyssi*]
 NEQ096 Hypothetical NTP-binding protein [*M. kandleri*] SPLIT see NEQ495
 NEQ495 Hypothetical NTP-binding protein [*P. horikoshii*] SPLIT see NEQ096
 NEQ112 Hypothetical GTPase (OBG/HflX superfamily) [*P. furiosus*]
 NEQ117 Hypothetical NTP-binding protein [*M. jannaschii*]
 NEQ122 Hypothetical member of metallo-β-lactamase superfamily [*P. furiosus*]
 NEQ127 Hypothetical O-carbamoyltransferase [*M. jannaschii*]
 NEQ148 Hypothetical "radical SAM" protein [*P. horikoshii*]
 NEQ157 Hypothetical GTPase (OBG/HflX superfamily) [*P. horikoshii*]
 NEQ159 Phosphatidylethanolamine-binding protein [*S. solfataricus*]
 NEQ174 Hypothetical GTP-binding protein [*P. horikoshii*]
 NEQ184 Hypothetical RNA-binding protein (contain S1 domain and KH domain) [*A. fulgidus*]
 NEQ198a Phosphoadenosine phosphosulfate reductase related protein [C-terminal domain] [*P. furiosus*]

NEQ206 Hypothetical protein with RNA-binding PUA domain [*P. aerophilum*]
 NEQ213 Histidine triad family protein [*M. acetivorans*]
 NEQ234 Magnesium chelatase, ChII subunit [*P. furiosus*]
 NEQ284a Hypothetical Zn-ribbon protein [*M. jannaschii*]
 NEQ294 Hypothetical ATP-binding protein [*P. horikoshii*]
 NEQ340 Hypothetical protein (HAD superfamily) [*T. volcanium*]
 NEQ355 Hypothetical Zn-ribbon protein [*A. fulgidus*]
 NEQ358 Hypothetical phosphoesterase protein [*P. abyssi*]
 NEQ366 Hypothetical GTP-binding protein [*P. horikoshii*]
 NEQ378 Hypothetical member of metallo-β-lactamase superfamily [*P. abyssi*]
 NEQ381 Hypothetical "radical SAM" protein [*P. abyssi*]
 NEQ401 ATP-binding protein (AAA+ class) [*M. kandleri*]
 NEQ406 Hypothetical nucleotide-binding
 NEQ432a Hypothetical Zn-ribbon protein [*P. horikoshii*]
 NEQ438 Hypothetical RNA-binding protein [*P. abyssi*] SPLIT see NEQ506
 NEQ506 Hypothetical RNA-binding protein [*S. solfataricus*] SPLIT see NEQ438
 NEQ456 Divalent metal cation-dependent hydrolase (TatD family) [*S. solfataricus*]
 NEQ463 Hypothetical GTPase [*S. solfataricus*]
 NEQ466 Hypothetical member of metallo-β-lactamase superfamily [*M. jannaschii*]
 NEQ472 Hypothetical phosphoesterase [*M. thermoautotrophicum*]
 NEQ489a Hypothetical Zn-ribbon protein [*M. acetivorans*]
 NEQ494 Hypothetical "radical SAM protein" [*S. tokodaii*]
 NEQ512 Hypothetical ATP-binding protein [*M. acetivorans*]
 NEQ519 Hypothetical zinc-binding nucleotidyl β-phosphatase (HIT family) [*M. jannaschii*]
 NEQ523 Hypothetical ATP diphosphatase (PP-loop family) [*P. horikoshii*]
 NEQ525 Phosphoadenosine phosphosulfate reductase related protein [*P. furiosus*]
 NEQ527 Hypothetical NTP-binding protein [*S. tokodaii*]