Table S1. List of the 162 genes found out of the 198 target protein profiles grouped into nine categories and 44 subcategories.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Protein Name | Gene | Protein profile | Category | Subcategory |
| Protocatechuate 3,4-dioxygenase | *pcaH* | TIGR02422 | Carbon metabolism | Aromatics degradation |
| Tetrahydrofolate dehydrogenase/cyclohydrolase | *folD* | PF00763 | Carbon metabolism | C1 metabolism |
| methylenetetrahydrofolate reductase | *metF* | TIGR00676 | Carbon metabolism | C1 metabolism |
| Fructose-1,6-bisphosphatase | *fbp* | PF01950 | Carbon metabolism | Carbohydrate metabolism |
| Oxidoreductase FAD-binding domain | *fpr* | PF00970 | Carbon metabolism | Carbohydrate metabolism |
| glyceraldehyde-3-phosphate dehydrogenase, type I | *gap2* | TIGR01534 | Carbon metabolism | Carbohydrate metabolism |
| glyoxylate carboligase | *gcl* | TIGR01504 | Carbon metabolism | Carbohydrate metabolism |
| Glycosyl hydrolase family 1 | *gh1* | PF00232 | Carbon metabolism | Carbohydrate metabolism |
| glucose-1-phosphate adenylyltransferase | *glgC* | TIGR02091 | Carbon metabolism | Carbohydrate metabolism |
| glucose-1-phosphate adenylyltransferase A subunit | *glpA* | TIGR03377 & TIGR03378 | Carbon metabolism | Carbohydrate metabolism |
| glucose-1-phosphate adenylyltransferase C subunit | *glpC* | TIGR03379 | Carbon metabolism | Carbohydrate metabolism |
| Glycerophosphoryl diester phosphodiesterase | *glpQ* | PF03009 | Carbon metabolism | Carbohydrate metabolism |
| glycerol-3-phosphate transporter | *glpT* | TIGR00712 | Carbon metabolism | Carbohydrate metabolism |
| methylmalonate-semialdehyde dehydrogenase (acylating) | *IolA* | TIGR01722 | Carbon metabolism | Carbohydrate metabolism |
| Phosphoglucose isomerase | *pgi* | PF00342 | Carbon metabolism | Carbohydrate metabolism |
| polyphosphate kinase | *ppk* | TIGR03705 | Carbon metabolism | Carbohydrate metabolism |
| pyruvate kinase | *pyk* | TIGR01064 | Carbon metabolism | Carbohydrate metabolism |
| glucose-6-phosphate dehydrogenase | *zwf* | TIGR00871 | Carbon metabolism | Carbohydrate metabolism |
| Phosphoribulokinase / Uridine kinase family | *prkB* | PF00485 | Carbon metabolism | Carbon fixation |
| NADH-ubiquinone/plastoquinone oxidoreductase chain 4L | *nd* | PF00420 | Carbon metabolism | Energy metabolism |
| polyhydroxyalkanoate depolymerase, intracellular | *phaZ* | TIGR01849 | Carbon metabolism | Energy metabolism |
| formaldehyde-activating enzyme | *fae* | TIGR03126 | Carbon metabolism | Methane metabolism |
| formylmethanofuran--tetrahydromethanopterin N-formyltransferase | *ftf* | TIGR03119 | Carbon metabolism | Methane metabolism |
| Formylmethanofuran-tetrahydromethanopterin formyltransferase | *ftr* | PF01913 | Carbon metabolism | Methane metabolism |
| Cyclohydrolase | *mch* | PF02289 | Carbon metabolism | Methane metabolism |
| Methylene-tetrahydromethanopterin dehydrogenase, N-terminal | *mtdB* | PF09176 | Carbon metabolism | Methane metabolism |
| Phosphoenolpyruvate carboxylase | *ppc* | PF00311 | Carbon metabolism | Methane metabolism |
| Fumarase C C-terminus | *fumC* | PF10415 & PF00206 | Carbon metabolism | TCA cycle |
| isocitrate dehydrogenase, NADP-dependent | *icd* | TIGR00183 | Carbon metabolism | TCA cycle |
| isocitrate dehydrogenase, NAD-dependent | *idh* | TIGR00175 | Carbon metabolism | TCA cycle |
| succinate dehydrogenase or fumarate reductase, flavoprotein subunit | *sdhA* | TIGR01811 | Carbon metabolism | TCA cycle |
| succinate dehydrogenase and fumarate reductase iron-sulfur protein | *sdhB* | TIGR00384 | Carbon metabolism | TCA cycle |
| Carbonic anhydrase, (Carbonate dehydratase) | *can* | PF00484 | Carbon metabolism | Uncategorized |
| Iron-utilization periplasmic protein | *fbpA* | PF01547 | Iron metabolism | Ferric uptake |
| Fe(3+)-transport system permease protein FbpB 2 | *fbpB* | PF00528 | Iron metabolism | Ferric uptake |
| iron(III) transport system substrate\_binding protein | *fhuD* | PF01497 | Iron metabolism | Ferric uptake |
| high\_affinity iron transporter | *efeU* | PF03239 | Iron metabolism | Ferrous uptake |
| Ferrous iron transport protein A | *feoA* | PF04023 | Iron metabolism | Ferrous uptake |
| Ferrous iron transport protein B | *feoB* | TIGR00437 | Iron metabolism | Ferrous uptake |
| ferrous\_iron efflux pump FieF | *fieF* | PF01545 | Iron metabolism | Ferrous uptake |
| Manganese/zinc/iron transport system substrate-binding protein | *ZnuA* | PF01297 | Iron metabolism | Ferrous uptake |
| bacterioferritin | *bfr* | TIGR00754 | Iron metabolism | Iron storage |
| Ferritin | *ftnA* | PF00210 | Iron metabolism | Iron storage |
| Ferric uptake regulator family | *furB* | PF01475 | Iron metabolism | Iron uptake regulators |
| Iron-dependent Transcriptional regulator | *ideR* | PF02082 | Iron metabolism | Iron uptake regulators |
| HTH-type transcriptional regulator MntR | *mntR* | PF02742 | Iron metabolism | Iron uptake regulators |
| MotA/TolQ/ExbB proton channel | *exbB* | PF01618 | Iron metabolism | Siderophore metabolism |
| Biopolymer transport protein ExbD | *exbD* | PF02472 | Iron metabolism | Siderophore metabolism |
| TonB-dependent siderophore receptor | *fecA* | TIGR01783 | Iron metabolism | Siderophore metabolism |
| TonB-dependent heme/hemoglobin receptor family protein | *hmuR* | TIGR01785 | Iron metabolism | Siderophore metabolism |
| periplasmic protein TonB | *tonB* | PF03544 | Iron metabolism | Siderophore metabolism |
| Glutamate N-acetyltransferase | *argJ* | TIGR00120 | Nitrogen metabolism | Amino acid metabolism |
| 3-dehydroquinate synthase-II | *aroB* | PF01959 | Nitrogen metabolism | Amino acid metabolism |
| Carbamoyl-phosphate synthase | *carA* | TIGR01368 | Nitrogen metabolism | Amino acid metabolism |
| Cystathionine beta-synthase | *cbs* | TIGR01137 | Nitrogen metabolism | Amino acid metabolism |
| Cystathionine beta-synthase | *cth* | TIGR01324 | Nitrogen metabolism | Amino acid metabolism |
| Glutamine synthetase | *glnA* | TIGR00653 | Nitrogen metabolism | Amino acid metabolism |
| Nitrogen regulatory protein P-II | *glnB* | PF00543 | Nitrogen metabolism | Amino acid metabolism |
| Bifunctional uridylyltransferase | *glnD* | PF08335 | Nitrogen metabolism | Amino acid metabolism |
| Bifunctional glutamine synthetase | *glnE* | PF03710 | Nitrogen metabolism | Amino acid metabolism |
| Glutamate synthase | *gltS* | PF01645 | Nitrogen metabolism | Amino acid metabolism |
| Glutamate synthase | *gtl1* | TIGR01317 | Nitrogen metabolism | Amino acid metabolism |
| Ketol-acid reductoisomerase | *ilvC* | PF01450 | Nitrogen metabolism | Amino acid metabolism |
| Cysteine-S-conjugate beta-lyase | *metC* | TIGR01324 | Nitrogen metabolism | Amino acid metabolism |
| Ornithine--oxo-acid transaminase | *orn* | TIGR01885 | Nitrogen metabolism | Amino acid metabolism |
| Proline racemase | *prdF* | PF05544 | Nitrogen metabolism | Amino acid metabolism |
|  | *amt1* | TIGR00836 | Nitrogen metabolism | Ammonium uptake |
| Ammonium transporter | *amt2* | PF00909 | Nitrogen metabolism | Ammonium uptake |
| Carbamoyl-phosphate synthase | *cps1* | PF00988 | Nitrogen metabolism | Ammonium uptake |
| Carbonic anhydrase | *cah* | PF00484 & PF00194 | Nitrogen metabolism | Carbon concentration |
| Cyanate lyase | *cynS* | PF02560 | Nitrogen metabolism | Cyanate metabolism |
| Nitrate reductase cytochrome | *napB* | PF03892 | Nitrogen metabolism | Denitrification |
| Periplasmic nitrate reductase | *napC* | TIGR02161 | Nitrogen metabolism | Denitrification |
| Nitrate reductase | *narJ* | PF02613 | Nitrogen metabolism | Denitrification |
| Nitrite reductase | *nirK* | TIGR02376 | Nitrogen metabolism | Denitrification |
| Nitrate reductase | *nirt* | PF02665 | Nitrogen metabolism | Denitrification |
| Nitrate reductase | *nirt* | PF14710 | Nitrogen metabolism | Denitrification |
| Nitrate reductase | *nirt* | PF14711 | Nitrogen metabolism | Denitrification |
| Nitric oxide reductase | *norB* | cOG3256 | Nitrogen metabolism | Denitrification |
| Nitrate reductase | *napA* | TIGR01706 | Nitrogen metabolism | Nitrate assimilation |
| Periplasmic nitrate reductase | *napD* | PF03927 | Nitrogen metabolism | Nitrate assimilation |
| Periplasmic nitrate reductase | *napE* | PF06796 | Nitrogen metabolism | Nitrate assimilation |
| Nitrate reductase | *narH* | TIGR01660 | Nitrogen metabolism | Nitrate assimilation |
| Ammonia monooxygenase | *amoA* | PF12942 | Nitrogen metabolism | Nitrification |
| Ammonia monooxygenase | *amoA* | PF02461 | Nitrogen metabolism | Nitrification |
| Nitrate reductase cofactor | *narJ* | TIGR00684 | Nitrogen metabolism | Nitrite assimilation |
| Nitrite reductase | *nirB* | PF01077 | Nitrogen metabolism | Nitrite assimilation |
| Nitrite transporter | *nirC* | TIGR00886 | Nitrogen metabolism | Nitrite assimilation |
| Nitrogen fixation protein | *nifA* | TIGR01817 | Nitrogen metabolism | Nitrogen fixation |
| Nitrogen fixation protein | *nifB* | TIGR01290 | Nitrogen metabolism | Nitrogen fixation |
| Nitrogenase iron protein | *nifD* | TIGR01282 | Nitrogen metabolism | Nitrogen fixation |
| Nitrogenase iron protein | *nifH* | TIGR01287 | Nitrogen metabolism | Nitrogen fixation |
| Nitrogenase iron protein | *nifK* | TIGR01286 | Nitrogen metabolism | Nitrogen fixation |
| Nitrogenase iron protein | *nifN* | TIGR01285 | Nitrogen metabolism | Nitrogen fixation |
| Nitrogen fixation protein | *nifX* | TIGR02663 | Nitrogen metabolism | Nitrogen fixation |
| Global nitrogen regulator | *ntcA* | TIGR03697 | Nitrogen metabolism | Nitrogen regulator |
| Urease | *ureA* | TIGR00193 | Nitrogen metabolism | Urea utilization |
| Urease | *ureB* | TIGR00192 | Nitrogen metabolism | Urea utilization |
| Urea ABC transporter | *urtA* | TIGR03407 | Nitrogen metabolism | Urea utilization |
| Urea ABC transporter | *urtB* | TIGR03409 | Nitrogen metabolism | Urea utilization |
| Alkaline phosphatase | *phoA* | PF00245 | Phosphorus metabolism | Phosphatases |
| Alkaline phosphatase | *phoD* | PF19050 & PF16655 & PF09423 | Phosphorus metabolism | Phosphatases |
| Inorganic pyrophosphatase | *ppa* | PF00719 | Phosphorus metabolism | Phosphatases |
| Ribose 1,5-bisphosphokinase | *phnN* | TIGR02322 | Phosphorus metabolism | Phosphate metabolism |
| Phosphate regulon | *phoB* | TIGR02154 | Phosphorus metabolism | Phosphate metabolism |
| Phosphate regulon | *phoR* | TIGR02966 | Phosphorus metabolism | Phosphate metabolism |
| Phosphate transport system | *phoU* | TIGR02135 | Phosphorus metabolism | Phosphate metabolism |
| Inorganic phosphate transporter | *pit* | PF01384 | Phosphorus metabolism | Phosphate metabolism |
| Phosphate permease | *pstA* | TIGR00974 | Phosphorus metabolism | Phosphate metabolism |
| Phosphate import ATP-binding protein/UDP-glucose/iron transport system ATP-binding protein | *pstB* | TIGR00972 | Phosphorus metabolism | Phosphate metabolism |
| Phosphate permease | *pstC* | TIGR02138 | Phosphorus metabolism | Phosphate metabolism |
| Phosphate-binding protein | *pstS* | TIGR02136 | Phosphorus metabolism | Phosphate metabolism |
| Phosphonate transport system | *phnD* | PF12974 | Phosphorus metabolism | Phosphonate metabolism |
| Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase | *phnG* | PF06754 | Phosphorus metabolism | Phosphonate metabolism |
| Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase | *phnH* | PF05845 | Phosphorus metabolism | Phosphonate metabolism |
| Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase | *phnI* | PF05861 | Phosphorus metabolism | Phosphonate metabolism |
| Alpha-D-ribose 1-methylphosphonate 5-phosphate | *phnJ* | PF06007 | Phosphorus metabolism | Phosphonate metabolism |
| Phosphonate transport system | *phnK* | TIGR02323 | Phosphorus metabolism | Phosphonate metabolism |
| Phosphoribosyl 1,2-cyclic phosphate phosphodiesterase | *phnP* | TIGR03307 | Phosphorus metabolism | Phosphonate metabolism |
| 2-aminoethylphosphonate aminotransferase | *phnW* | TIGR03301 & TIGR02326 | Phosphorus metabolism | Phosphonate metabolism |
| Phosphonoacetaldehyde hydrolase | *phnX* | TIGR01422 | Phosphorus metabolism | Phosphonate metabolism |
| chlorophyllide reductase iron protein subunit X | *bchX* | TIGR02016 | Phototrophy | Bacteriochlorophyll |
| photosynthetic reaction center L subunit | *pufL* | TIGR01157 | Phototrophy | Bacteriochlorophyll |
| Reaction center protein M chain (Photosynthetic reaction center M subunit) | *pufM* | TIGR01115 | Phototrophy | Bacteriochlorophyll |
| Bacteriorhodopsin-like protein | *bop* | PF01036 | Phototrophy | Bacteriorhodopsin |
|  | *cbbX* | TIGR02880 | Phototrophy | Carbon fixation |
| Ribulose bisphosphate carboxylase large chain | *rbcL* | PF00016 | Phototrophy | Carbon fixation |
| Ribulose bisphosphate carboxylase small chain | *rbcs* | PF00101 | Phototrophy | Carbon fixation |
|  | *cphXY* | TIGR01964 | Phototrophy | CO2 uptake |
| NAD(P)H dehydrogenase, subunit NdhF3 family | *ndhF* | TIGR01960 | Phototrophy | CO2 uptake |
| phycocyanin, alpha subunit | *cpcA* | TIGR01338 | Phototrophy | Photosynthesis |
|  | *cpcB* | TIGR01339 | Phototrophy | Photosynthesis |
| Chromophore lyase CpcT/CpeT 2, | *cpcT* | PF06206 | Phototrophy | Photosynthesis |
| Phycoerythrin alpha-2 chain, chloroplastic | *cpeA* | PF02972 | Phototrophy | Photosynthesis |
| Phycoerythrin beta chain | *cpeB* | PF00502 | Phototrophy | Photosynthesis |
| Phycoerythrin-associated linker protein | *cpeC* | PF00427 | Phototrophy | Photosynthesis |
| Phycoerythrin-associated linker protein | *cpeD* | PF01383 | Phototrophy | Photosynthesis |
| Photosystem I P700 chlorophyll a apoprotein A1, EC 1.97.1.12 (PSI-A) (PsaA) | *psaA* | PF00223 | Phototrophy | Photosynthesis |
| photosystem I core protein PsaB | *psaB* | TIGR01336 | Phototrophy | Photosynthesis |
| photosystem II q(b) protein | *psbA* | TIGR01151 | Phototrophy | Photosynthesis |
| photosystem II chlorophyll-binding protein CP47 | *psbB* | TIGR03039 | Phototrophy | Photosynthesis |
| photosystem II D2 protein (photosystem q(a) protein) | *psbD* | TIGR01152 | Phototrophy | Photosynthesis |
| Signal transducing histidine kinase, homodimeric domain | *cheA* | PF02895 | Response to stimuli | Chemotaxis |
| CheB methylesterase | *cheB* | PF01339 | Response to stimuli | Chemotaxis |
| CheR methyltransferase, SAM binding domain | *cheR* | PF01739 | Response to stimuli | Chemotaxis |
| CheW-like domain | *cheW* | PF01584 | Response to stimuli | Chemotaxis |
| tonB-system energizer ExbB | *exbB/motA* | TIGR02797 | Response to stimuli | Motility |
| Archaebacterial flagellin | *flaB* | PF01917 | Response to stimuli | Motility |
| archaeal flagellar protein FlaJ, Type II secretion system (T2SS) | *flaJ* | PF00482 | Response to stimuli | Motility |
| flagellar M-ring protein FliF | *fliC* | PF00669 | Response to stimuli | Motility |
| flagellar motor switch protein FliG | *fliG* | TIGR00207 | Response to stimuli | Motility |
| Flagellar assembly protein FliH | *fliH* | PF02108 | Response to stimuli | Motility |
| flagellar motor switch protein FliM | *fliM* | TIGR01397 | Response to stimuli | Motility |
| Flagellar biosynthesis protein, FliO | *fliO* | PF04347 | Response to stimuli | Motility |
| flagellar biosynthetic protein FliR | *fliR* | TIGR01400 | Response to stimuli | Motility |
| flagellar protein FliS | *fliS* | TIGR00208 | Response to stimuli | Motility |
| flagellar motor stator protein MotA | *motA* | TIGR03818 | Response to stimuli | Motility |
| Membrane MotB of proton-channel complex MotA/MotB | *motB* | PF13677 | Response to stimuli | Motility |
| twitching motility protein | *pilT* | TIGR01420 | Response to stimuli | Motility |
| Autoinducer synthase | *luxI* | PF00765 | Response to stimuli | Quorum-sensing |
| LuxQ, periplasmic | *luxQ* | PF09308 | Response to stimuli | Quorum-sensing |
| Bacterial regulatory proteins, luxR family | *luxR* | PF00196 | Response to stimuli | Quorum-sensing |
| S-Ribosylhomocysteinase (LuxS) | *luxS* | PF02664 | Response to stimuli | Quorum-sensing |
| Chaperonin GroL | *groEL* | TIGR02348 | Response to stress | Chaperonins |
| Chaperonin GroES | *groES* | PF00166 | Response to stress | Chaperonins |
| glutaredoxin 1 | *grxA* | TIGR02183 | Response to stress | Chaperonins |
| glutaredoxin 2 | *grxB* | TIGR02182 | Response to stress | Chaperonins |
| glutaredoxin 3 | *grxC* | TIGR02181 | Response to stress | Chaperonins |
| arsenical-resistance protein | *acr* | TIGR00832 | Response to stress | Detoxification |
| ArsC family | *arsC* | PF03960 | Response to stress | Detoxification |
| chromate efflux transporter | *ChrA* | TIGR00937 | Response to stress | Detoxification |
| heavy metal efflux pump, CzcA family | *CzcA* | TIGR00914 | Response to stress | Detoxification |
| Catalase | *catB* | PF00199 | Response to stress | Oxidative stress |
| Iron/manganese superoxide dismutases | *MnSod* | PF00081 | Response to stress | Oxidative stress |
| Peroxidase | *per* | PF00141 | Response to stress | Oxidative stress |
| Peroxiredoxins | *prx* | PF00578 | Response to stress | Oxidative stress |
| Iron/manganese superoxide dismutases, C-terminal domain | *sodA* | PF02777 | Response to stress | Oxidative stress |
| Copper/zinc superoxide dismutase (SODC) | *sodC* | PF00080 | Response to stress | Oxidative stress |
| Nickel-containing superoxide dismutase | *sodN* | PF09055 | Response to stress | Oxidative stress |
| Dimethylsulfonioproprionate demethylase DmdA | *dmdA1* | PF01571 | Sulfur metabolism | DMSP assimilation |
| Dimethylsulfonioproprionate demethylase DmdA | *dmdA2* | COG0404 | Sulfur metabolism | DMSP assimilation |
| Dimethylsulfonioproprionate demethylase DmdA | *dmdA3* | PF08669 | Sulfur metabolism | DMSP assimilation |
| ATP-sulfurylase | *cysC* | PF01583 | Sulfur metabolism | Sulfate assimilation |
| sulfate adenylyltransferase, small subunit | *cysD* | TIGR02039 | Sulfur metabolism | Sulfate assimilation |
| sulfite reductase (NADPH) hemoprotein, beta-component | *cysI* | TIGR02041 | Sulfur metabolism | Sulfate assimilation |
| cysteine synthase A | *CysKB* | TIGR01139 | Sulfur metabolism | Sulfate assimilation |
| sulfate adenylyltransferase, large subunit | *cysN* | TIGR02034 | Sulfur metabolism | Sulfate assimilation |
| Sulfatase | *Sulf* | PF00884 | Sulfur metabolism | Sulfate assimilation |
| adenylylsulfate reductase, alpha subunit | *aprA* | TIGR02061 | Sulfur metabolism | Sulfite assimilation |
| adenylylsulfate reductase, beta subunit | *aprB* | TIGR02060 | Sulfur metabolism | Sulfite assimilation |
| Sulfite reductase, dissimilatory-type subunit alpha | *dsrA* | TIGR02064 | Sulfur metabolism | Sulfite assimilation |
| sulfite reductase [NADPH] flavoprotein, alpha-component | *cysJ* | TIGR01931 | Sulfur metabolism | Sulfite reduction |
| sulfur oxidation c-type cytochrome SoxA | *soxA* | TIGR04484 | Sulfur metabolism | Thiosulfate oxidation |
| thiosulfohydrolase SoxB | *soxB* | TIGR04486 | Sulfur metabolism | Thiosulfate oxidation |
| phosphomethylpyrimidine synthase | *thiC* | TIGR00190 | Vitamins | B1 |
| thiamine-phosphate kinase | *thiL* | TIGR01379 | Vitamins | B1 |
| Sirohydrochlorin cobaltochelatase CbiX-like | *cbiX* | PF01903 | Vitamins | B12 |
| precorrin-3B synthase | *cobG* | TIGR02435 | Vitamins | B12 |
| cobaltochelatase, CobN subunit | *cobN* | TIGR02257 | Vitamins | B12 |
| cobaltochelatase, CobT subunit | *cobT* | TIGR01651 | Vitamins | B12 |