# Phyre$^2$

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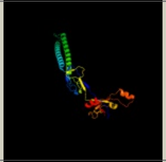
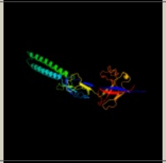
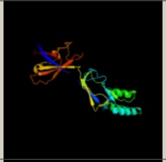
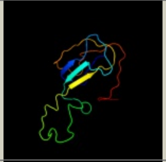
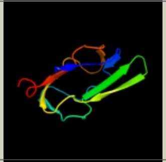
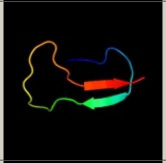
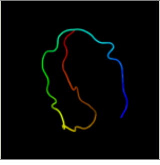
| Description | P75777 |
| Date | Wed Jan 25 15:21:02 GMT 2012 |
| Unique Job ID | 7b6a3872973be2ff |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3fppB_ | Alignment |  | 100.0 | 26 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca;<br>**PDBTitle:** crystal structure of e.coli maca |
| 2 | c2f1mA_ | Alignment |  | 99.9 | 27 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**acriflavine resistance protein a;<br>**PDBTitle:** conformational flexibility in the multidrug efflux system protein acra |
| 3 | c3lnnB_ | Alignment |  | 99.9 | 29 | **PDB header:**metal transport<br>**Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux<br>**PDBTitle:** crystal structure of zneb from cupriavidus metallidurans |
| 4 | c1t5eB_ | Alignment |  | 99.9 | 25 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**multidrug resistance protein mexa;<br>**PDBTitle:** the structure of mexa |
| 5 | d1vf7a_ | Alignment |  | 99.9 | 28 | **Fold:**HlyD-like secretion proteins<br>**Superfamily:**HlyD-like secretion proteins<br>**Family:**HlyD-like secretion proteins |
| 6 | c3h9iB_ | Alignment |  | 99.8 | 21 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**cation efflux system protein cusb;<br>**PDBTitle:** crystal structure of the membrane fusion protein cusb from escherichia2 coli |
| 7 | c2k33A_ | Alignment |  | 99.1 | 22 | **PDB header:**membrane protein, transport protein<br>**Chain:** A: **PDB Molecule:**acra;<br>**PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation |
| 8 | c2b8gA_ | Alignment |  | 97.4 | 29 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein;<br>**PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure) |
| 9 | c2ejgD_ | Alignment |  | 96.8 | 31 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase<br>**PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3 |
| 10 | d1dcza_ | Alignment |  | 96.8 | 34 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 11 | c2l5tA_ | Alignment |  | 96.5 | 26 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**lipoamide acyltransferase;<br>**PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum |

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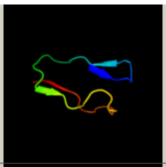
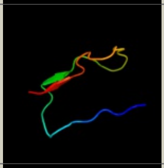
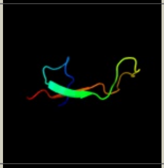
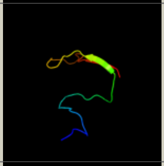
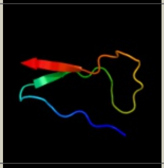
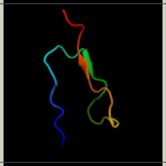
|---|---|---|---|---|---|---|
| 12 | d1bdoa_ | Alignment |  | 96.5 | 15 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 13 | c3n6rK_ | Alignment |  | 96.5 | 18 | **PDB header:**ligase<br>**Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit;<br>**PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc) |
| 14 | d1iyua_ | Alignment |  | 96.4 | 28 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 15 | c2dn8A_ | Alignment |  | 96.4 | 22 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2;<br>**PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase |
| 16 | d1o78a_ | Alignment |  | 96.3 | 30 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 17 | c2kccA_ | Alignment |  | 96.3 | 18 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2;<br>**PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2 |
| 18 | d1ghja_ | Alignment |  | 96.2 | 24 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 19 | c2ejmA_ | Alignment |  | 96.0 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha;<br>**PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase |
| 20 | d1k8ma_ | Alignment |  | 95.9 | 20 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 21 | d1qjoa_ | Alignment | not modelled | 95.9 | 24 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 22 | d1laba_ | Alignment | not modelled | 95.7 | 35 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 23 | d1glaf_ | Alignment | not modelled | 95.6 | 25 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Duplicated hybrid motif<br>**Family:**Glucose permease-like |
| 24 | d1gjxa_ | Alignment | not modelled | 95.4 | 26 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 25 | d2f3ga_ | Alignment | not modelled | 95.4 | 25 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Duplicated hybrid motif<br>**Family:**Glucose permease-like |
| 26 | d1gpra_ | Alignment | not modelled | 95.3 | 32 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Duplicated hybrid motif<br>**Family:**Glucose permease-like |
| 27 | d2gpra_ | Alignment | not modelled | 95.3 | 20 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Duplicated hybrid motif<br>**Family:**Glucose permease-like |
| 28 | c2q8iB_ | Alignment | not modelled | 94.7 | 21 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of<br>**PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol |
| | | | | | | **Fold:**Barrel-sandwich hybrid |

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|---|---|---|---|---|---|---|
| 29 | d1pmra_ | Alignment | not modelled | 94.5 | 24 | **Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 30 | c2qf7A_ | Alignment | not modelled | 94.5 | 22 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**pyruvate carboxylase protein;<br>**PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli |
| 31 | d1y8ob1 | Alignment | not modelled | 94.4 | 23 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 32 | d2pnrc1 | Alignment | not modelled | 94.2 | 22 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Single hybrid motif<br>**Family:**Biotinyl/lipoyl-carrier proteins and domains |
| 33 | c2dncA_ | Alignment | not modelled | 94.0 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component;<br>**PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase |
| 34 | c2dneA_ | Alignment | not modelled | 93.4 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase<br>**PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase |
| 35 | d2tpta3 | Alignment | not modelled | 93.3 | 22 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain<br>**Family:**Pyrimidine nucleoside phosphorylase C-terminal domain |
| 36 | c2jkuA_ | Alignment | not modelled | 93.1 | 30 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain,<br>**PDBTitle:** crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase |
| 37 | d1uoua3 | Alignment | not modelled | 93.0 | 43 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain<br>**Family:**Pyrimidine nucleoside phosphorylase C-terminal domain |
| 38 | d1brwa3 | Alignment | not modelled | 92.7 | 31 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain<br>**Family:**Pyrimidine nucleoside phosphorylase C-terminal domain |
| 39 | c2dsjA_ | Alignment | not modelled | 90.5 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase;<br>**PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8 |
| 40 | c1otpA_ | Alignment | not modelled | 89.9 | 22 | **PDB header:**phosphorylase<br>**Chain:** A: **PDB Molecule:**thymidine phosphorylase;<br>**PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase |
| 41 | c2gu1A_ | Alignment | not modelled | 89.9 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**zinc peptidase;<br>**PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae |
| 42 | c2j0fC_ | Alignment | not modelled | 89.8 | 43 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**thymidine phosphorylase;<br>**PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design |
| 43 | c3h5qA_ | Alignment | not modelled | 89.6 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase;<br>**PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus |
| 44 | c1brwB_ | Alignment | not modelled | 87.2 | 27 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase);<br>**PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation |
| 45 | c2aukA_ | Alignment | not modelled | 82.9 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain;<br>**PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert |
| 46 | c2hsiB_ | Alignment | not modelled | 82.9 | 26 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative peptidase m23;<br>**PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium |
| 47 | d2ix0a1 | Alignment | not modelled | 81.1 | 10 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 48 | c2qj8B_ | Alignment | not modelled | 80.9 | 26 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**mlr6093 protein;<br>**PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution |
| 49 | c3fmcC_ | Alignment | not modelled | 80.5 | 22 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase;<br>**PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution |
| 50 | c1h9sA_ | Alignment | not modelled | 79.9 | 25 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**molybdenum transport protein mode;<br>**PDBTitle:** molybdate bound complex of dimop domain of mode from e.coli |
| 51 | c3nyyA_ | Alignment | not modelled | 78.5 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative glycyl-glycine endopeptidase lytm;<br>**PDBTitle:** crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution |
| 52 | d1qwya_ | Alignment | not modelled | 78.1 | 30 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Duplicated hybrid motif<br>**Family:**Peptidoglycan hydrolase LytM |

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|---|---|---|---|---|---|---|
| 53 | c2xhaB_ | Alignment | not modelled | 75.5 | 21 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**transcription antitermination protein nusg;<br>**PDBTitle:** crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg) |
| 54 | d1qpoa2 | Alignment | not modelled | 75.4 | 21 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like<br>**Family:**NadC N-terminal domain-like |
| 55 | c1h9mB_ | Alignment | not modelled | 75.4 | 14 | **PDB header:**binding protein<br>**Chain:** B: **PDB Molecule:**molybdenum-binding-protein;<br>**PDBTitle:** two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound |
| 56 | d1ci3m2 | Alignment | not modelled | 73.8 | 44 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Rudiment single hybrid motif<br>**Family:**Cytochrome f, small domain |
| 57 | d1e2wa2 | Alignment | not modelled | 72.6 | 44 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Rudiment single hybrid motif<br>**Family:**Cytochrome f, small domain |
| 58 | c2xhcA_ | Alignment | not modelled | 72.3 | 20 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription antitermination protein nusg;<br>**PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg) |
| 59 | c3cdxB_ | Alignment | not modelled | 70.7 | 13 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase;<br>**PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides |
| 60 | c3na6A_ | Alignment | not modelled | 70.5 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase;<br>**PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution |
| 61 | c3e20A_ | Alignment | not modelled | 70.5 | 14 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor gtp-binding<br>**PDBTitle:** crystal structure of s.pombe erf1/erf3 complex |
| 62 | c2b44A_ | Alignment | not modelled | 67.8 | 30 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm;<br>**PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form |
| 63 | d1o4ua2 | Alignment | not modelled | 67.5 | 23 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like<br>**Family:**NadC N-terminal domain-like |
| 64 | d1qapa2 | Alignment | not modelled | 65.0 | 45 | **Fold:**alpha/beta-Hammerhead<br>**Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like<br>**Family:**NadC N-terminal domain-like |
| 65 | c2aujD_ | Alignment | not modelled | 64.5 | 39 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain;<br>**PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert |
| 66 | c3it5B_ | Alignment | not modelled | 63.6 | 24 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**protease lasa;<br>**PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa |
| 67 | d1fr3a_ | Alignment | not modelled | 63.4 | 17 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**Molybdate/tungstate binding protein MOP |
| 68 | d1h9ma2 | Alignment | not modelled | 59.4 | 14 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 69 | d2rdea2 | Alignment | not modelled | 58.7 | 9 | **Fold:**Split barrel-like<br>**Superfamily:**PilZ domain-like<br>**Family:**PilZ domain-associated domain |
| 70 | d1guta_ | Alignment | not modelled | 58.2 | 9 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**Molybdate/tungstate binding protein MOP |
| 71 | c3gnnA_ | Alignment | not modelled | 57.1 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase;<br>**PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei |
| 72 | d1h9ra1 | Alignment | not modelled | 56.7 | 21 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 73 | c1o4uA_ | Alignment | not modelled | 54.0 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase;<br>**PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution |
| 74 | d1h9ra2 | Alignment | not modelled | 53.4 | 27 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 75 | d1krha1 | Alignment | not modelled | 53.4 | 25 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 76 | c1e2vB_ | Alignment | not modelled | 53.0 | 44 | **PDB header:**electron transport proteins<br>**Chain:** B: **PDB Molecule:**cytochrome f;<br>**PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii |

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|---|---|---|---|---|---|---|
| 77 | c3e1yG_ | Alignment | not modelled | 53.0 | 15 | **PDB header:**translation<br>**Chain:** G: **PDB Molecule:**eukaryotic peptide chain release factor gtp-binding subunit<br>**PDBTitle:** crystal structure of human erf1/erf3 complex |
| 78 | c1ctmA_ | Alignment | not modelled | 52.5 | 50 | **PDB header:**electron transport(cytochrome)<br>**Chain:** A: **PDB Molecule:**cytochrome f;<br>**PDBTitle:** crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation |
| 79 | c2b7pA_ | Alignment | not modelled | 51.7 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase;<br>**PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori |
| 80 | c3d4rE_ | Alignment | not modelled | 51.5 | 21 | **PDB header:**unknown function<br>**Chain:** E: **PDB Molecule:**domain of unknown function from the pfam-b_34464 family;<br>**PDBTitle:** crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution |
| 81 | c2jxmB_ | Alignment | not modelled | 51.3 | 50 | **PDB header:**electron transport<br>**Chain:** B: **PDB Molecule:**cytochrome f;<br>**PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex |
| 82 | c1tu2B_ | Alignment | not modelled | 50.6 | 50 | **PDB header:**electron transport<br>**Chain:** B: **PDB Molecule:**apocytochrome f;<br>**PDBTitle:** the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures |
| 83 | c2jbmA_ | Alignment | not modelled | 49.7 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase;<br>**PDBTitle:** qprtase structure from human |
| 84 | c1q90A_ | Alignment | not modelled | 49.7 | 44 | **PDB header:**photosynthesis<br>**Chain:** A: **PDB Molecule:**apocytochrome f;<br>**PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii |
| 85 | c2l1tA_ | Alignment | not modelled | 49.7 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution structure of the n-terminal domain of np_954075.1 |
| 86 | c1qapA_ | Alignment | not modelled | 49.3 | 33 | **PDB header:**glycosyltransferase<br>**Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase;<br>**PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid |
| 87 | c3chxE_ | Alignment | not modelled | 49.1 | 25 | **PDB header:**membrane protein<br>**Chain:** E: **PDB Molecule:**pmob;<br>**PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo) |
| 88 | d1h9ma1 | Alignment | not modelled | 48.7 | 21 | **Fold:**OB-fold<br>**Superfamily:**MOP-like<br>**Family:**BiMOP, duplicated molybdate-binding domain |
| 89 | c3tqvA_ | Alignment | not modelled | 48.6 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase;<br>**PDBTitle:** structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis. |
| 90 | c3csqC_ | Alignment | not modelled | 48.3 | 33 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**morphogenesis protein 1;<br>**PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail |
| 91 | c3pajA_ | Alignment | not modelled | 47.6 | 27 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating;<br>**PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961 |
| 92 | d1tu2b2 | Alignment | not modelled | 47.5 | 50 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Rudiment single hybrid motif<br>**Family:**Cytochrome f, small domain |
| 93 | c2e75C_ | Alignment | not modelled | 47.1 | 56 | **PDB header:**photosynthesis<br>**Chain:** C: **PDB Molecule:**apocytochrome f;<br>**PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus |
| 94 | c3kygB_ | Alignment | not modelled | 44.8 | 7 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein vca0042;<br>**PDBTitle:** crystal structure of vca0042 (l135r) complexed with c-di-gmp |
| 95 | c1qpoA_ | Alignment | not modelled | 44.5 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase;<br>**PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis |
| 96 | c3l0gD_ | Alignment | not modelled | 43.3 | 9 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase;<br>**PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution |
| 97 | d1whla_ | Alignment | not modelled | 43.0 | 13 | **Fold:**SH3-like barrel<br>**Superfamily:**Cap-Gly domain<br>**Family:**Cap-Gly domain |
| 98 | d1hcza2 | Alignment | not modelled | 42.0 | 50 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Rudiment single hybrid motif<br>**Family:**Cytochrome f, small domain |
| 99 | c1x1oC_ | Alignment | not modelled | 41.9 | 17 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase;<br>**PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8 |
| | | | | | | **Fold:**SH3-like barrel |

| | | | | | | |
|---|---|---|---|---|---|---|
| 100 | d1tova_ | Alignment | not modelled | 41.7 | 10 | **Superfamily:**Cap-Gly domain<br>**Family:**Cap-Gly domain |
| 101 | c2b5oA_ | Alignment | not modelled | 41.3 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ferredoxin--nadp reductase;<br>**PDBTitle:** ferredoxin-nadp reductase |
| 102 | d1ixda_ | Alignment | not modelled | 40.4 | 17 | **Fold:**SH3-like barrel<br>**Superfamily:**Cap-Gly domain<br>**Family:**Cap-Gly domain |
| 103 | c1qgyA_ | Alignment | not modelled | 40.1 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ferredoxin--nadp+ reductase;<br>**PDBTitle:** ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e) |
| 104 | c2jz2A_ | Alignment | not modelled | 39.6 | 22 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**ssl0352 protein;<br>**PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42 |
| 105 | d2cp2a1 | Alignment | not modelled | 39.4 | 18 | **Fold:**SH3-like barrel<br>**Superfamily:**Cap-Gly domain<br>**Family:**Cap-Gly domain |
| 106 | c3dlmA_ | Alignment | not modelled | 39.0 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setdb1;<br>**PDBTitle:** crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1 |
| 107 | d1whma_ | Alignment | not modelled | 38.4 | 9 | **Fold:**SH3-like barrel<br>**Superfamily:**Cap-Gly domain<br>**Family:**Cap-Gly domain |
| 108 | d2je6i2 | Alignment | not modelled | 36.8 | 16 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Ribosomal L27 protein-like<br>**Family:**ECR1 N-terminal domain-like |
| 109 | d2ahob2 | Alignment | not modelled | 36.6 | 15 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 110 | c2rdeB_ | Alignment | not modelled | 36.0 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein vca0042;<br>**PDBTitle:** crystal structure of vca0042 complexed with c-di-gmp |
| 111 | d1efca2 | Alignment | not modelled | 35.5 | 8 | **Fold:**Elongation factor/aminomethyltransferase common domain<br>**Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain<br>**Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain |
| 112 | d1ep3b1 | Alignment | not modelled | 35.0 | 14 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 113 | d1smxa_ | Alignment | not modelled | 33.8 | 23 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 114 | c1tqqC_ | Alignment | not modelled | 33.1 | 13 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**outer membrane protein tolc;<br>**PDBTitle:** structure of tolc in complex with hexamminecobalt |
| 115 | d2bmwa1 | Alignment | not modelled | 32.8 | 13 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 116 | d2c78a2 | Alignment | not modelled | 32.6 | 5 | **Fold:**Elongation factor/aminomethyltransferase common domain<br>**Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain<br>**Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain |
| 117 | d1qfja1 | Alignment | not modelled | 32.5 | 27 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 118 | c3e0eA_ | Alignment | not modelled | 32.2 | 16 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**replication protein a;<br>**PDBTitle:** crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b |
| 119 | d1whga_ | Alignment | not modelled | 32.0 | 8 | **Fold:**SH3-like barrel<br>**Superfamily:**Cap-Gly domain<br>**Family:**Cap-Gly domain |
| 120 | d1wp1a_ | Alignment | not modelled | 31.5 | 14 | **Fold:**Outer membrane efflux proteins (OEP)<br>**Superfamily:**Outer membrane efflux proteins (OEP)<br>**Family:**Outer membrane efflux proteins (OEP) |