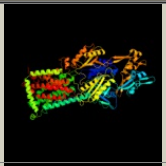
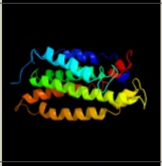
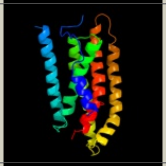
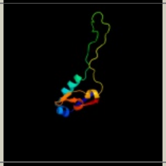
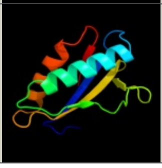
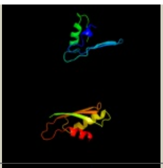
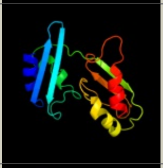
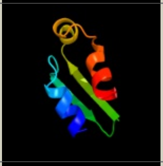
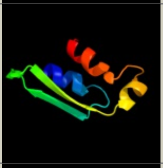
# Phyre²

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P24177 |
| Date | Wed Jan 25 15:20:44 GMT 2012 |
| Unique Job ID | 8137cd87d7d9248b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1oy8A_ | Alignment |  | 100.0 | 66 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**acriflavine resistance protein b;<br>**PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump |
| 2 | c3k07A_ | Alignment |  | 100.0 | 21 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**cation efflux system protein cusa;<br>**PDBTitle:** crystal structure of cusa |
| 3 | c3aqpB_ | Alignment |  | 100.0 | 16 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein;<br>**PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus |
| 4 | d1iwga8 | Alignment |  | 100.0 | 68 | **Fold:**Multidrug efflux transporter AcrB transmembrane domain<br>**Superfamily:**Multidrug efflux transporter AcrB transmembrane domain<br>**Family:**Multidrug efflux transporter AcrB transmembrane domain |
| 5 | d1iwga7 | Alignment |  | 100.0 | 79 | **Fold:**Multidrug efflux transporter AcrB transmembrane domain<br>**Superfamily:**Multidrug efflux transporter AcrB transmembrane domain<br>**Family:**Multidrug efflux transporter AcrB transmembrane domain |
| 6 | d1iwga1 | Alignment |  | 99.8 | 61 | **Fold:**Ferredoxin-like<br>**Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains<br>**Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |
| 7 | d1iwga5 | Alignment |  | 99.5 | 59 | **Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains<br>**Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains<br>**Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains |
| 8 | d1iwga2 | Alignment |  | 99.5 | 35 | **Fold:**Ferredoxin-like<br>**Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains<br>**Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |
| 9 | d1iwga6 | Alignment |  | 99.1 | 75 | **Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains<br>**Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains<br>**Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains |
| 10 | d1iwga3 | Alignment |  | 98.9 | 49 | **Fold:**Ferredoxin-like<br>**Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains<br>**Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |
| 11 | d1iwga4 | Alignment |  | 98.3 | 64 | **Fold:**Ferredoxin-like<br>**Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains<br>**Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c2ropA_ | Alignment |  | 95.9 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**copper-transporting atpase 2;<br>**PDBTitle:** solution structure of domains 3 and 4 of human atp7b |
| 13 | c2ew9A_ | Alignment |  | 95.7 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**copper-transporting atpase 2;<br>**PDBTitle:** solution structure of apowln5-6 |
| 14 | c2rmlA_ | Alignment |  | 93.7 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**copper-transporting p-type atpase copa;<br>**PDBTitle:** solution structure of the n-terminal soluble domains of2 bacillus subtilis copa |
| 15 | d1s6ua_ | Alignment |  | 90.7 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 16 | d2aw0a_ | Alignment |  | 90.4 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 17 | d1cpza_ | Alignment |  | 90.4 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 18 | d2qifa1 | Alignment |  | 89.8 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 19 | c3dxsX_ | Alignment |  | 89.2 | 26 | **PDB header:**hydrolase<br>**Chain:** X: **PDB Molecule:**copper-transporting atpase ran1;<br>**PDBTitle:** crystal structure of a copper binding domain from hma7, a p-2 type atpase |
| 20 | d1kvja_ | Alignment |  | 89.0 | 30 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 21 | c2l3mA_ | Alignment | not modelled | 89.0 | 24 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**copper-ion-binding protein;<br>**PDBTitle:** solution structure of the putative copper-ion-binding protein from2 bacillus anthracis str. ames |
| 22 | d1q8la_ | Alignment | not modelled | 88.4 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 23 | c1yjrA_ | Alignment | not modelled | 87.7 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**copper-transporting atpase 1;<br>**PDBTitle:** solution structure of the apo form of the sixth soluble2 domain a69p mutant of menkes protein |
| 24 | c2ga7A_ | Alignment | not modelled | 87.3 | 28 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**copper-transporting atpase 1;<br>**PDBTitle:** solution structure of the copper(i) form of the third metal-2 binding domain of atp7a protein (menkes disease protein) |
| 25 | d1p6ta2 | Alignment | not modelled | 87.3 | 17 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 26 | c2ldiA_ | Alignment | not modelled | 87.2 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**zinc-transporting atpase;<br>**PDBTitle:** nmr solution structure of ziaan sub mutant |
| 27 | c2kkhA_ | Alignment | not modelled | 86.0 | 15 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**putative heavy metal transporter;<br>**PDBTitle:** structure of the zinc binding domain of the atpase hma4 |
| 28 | c1yg0A_ | Alignment | not modelled | 85.5 | 22 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**cop associated protein;<br>**PDBTitle:** solution structure of apo-copp from helicobacter pylori |
| 29 | c2kt2A | Alignment | not modelled | 85.2 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**mercuric reductase; |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | Alignment | | | | **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase |
| 30 | d1p6ta1 | Alignment | not modelled | 85.2 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 31 | d1osda_ | Alignment | not modelled | 84.7 | 22 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 32 | c2yvxD_ | Alignment | not modelled | 84.2 | 15 | **PDB header:**transport protein<br>**Chain:** D: **PDB Molecule:**mg2+ transporter mgte;<br>**PDBTitle:** crystal structure of magnesium transporter mgte |
| 33 | d1afia_ | Alignment | not modelled | 84.1 | 20 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 34 | c2ofhX_ | Alignment | not modelled | 81.7 | 20 | **PDB header:**hydrolase, membrane protein<br>**Chain:** X: **PDB Molecule:**zinc-transporting atpase;<br>**PDBTitle:** solution structure of the n-terminal domain of the zinc(ii) atpase2 ziaa in its apo form |
| 35 | c1y3kA_ | Alignment | not modelled | 80.4 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**copper-transporting atpase 1;<br>**PDBTitle:** solution structure of the apo form of the fifth domain of2 menkes protein |
| 36 | d2ggpb1 | Alignment | not modelled | 77.3 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 37 | d1mwza_ | Alignment | not modelled | 75.7 | 14 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 38 | d1qupa2 | Alignment | not modelled | 75.6 | 14 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 39 | c2gcfA_ | Alignment | not modelled | 74.8 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cation-transporting atpase pacs;<br>**PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form |
| 40 | c2k2pA_ | Alignment | not modelled | 74.0 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein atu1203;<br>**PDBTitle:** solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183 |
| 41 | c1jk9D_ | Alignment | not modelled | 73.8 | 16 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase;<br>**PDBTitle:** heterodimer between h48f-ysod1 and yccs |
| 42 | c3j09A_ | Alignment | not modelled | 73.5 | 17 | **PDB header:**hydrolase, metal transport<br>**Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a;<br>**PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa |
| 43 | d1sb6a_ | Alignment | not modelled | 70.9 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 44 | c2aj1A_ | Alignment | not modelled | 70.4 | 9 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable cadmium-transporting atpase;<br>**PDBTitle:** solution structure of apocada |
| 45 | c2rogA_ | Alignment | not modelled | 69.8 | 16 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**heavy metal binding protein;<br>**PDBTitle:** solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells |
| 46 | c1qupA_ | Alignment | not modelled | 64.6 | 14 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone;<br>**PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase |
| 47 | c2crlA_ | Alignment | not modelled | 64.3 | 16 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**copper chaperone for superoxide dismutase;<br>**PDBTitle:** the apo form of hma domain of copper chaperone for2 superoxide dismutase |
| 48 | d1cc8a_ | Alignment | not modelled | 57.1 | 12 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 49 | c1yj7A_ | Alignment | not modelled | 53.8 | 19 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**escj;<br>**PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj |
| 50 | d2nwwa1 | Alignment | not modelled | 53.0 | 7 | **Fold:**Proton glutamate symport protein<br>**Superfamily:**Proton glutamate symport protein<br>**Family:**Proton glutamate symport protein |
| 51 | c2kyzA_ | Alignment | not modelled | 47.9 | 15 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**heavy metal binding protein;<br>**PDBTitle:** nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima |
| 52 | d1pw4a_ | Alignment | not modelled | 43.9 | 7 | **Fold:**MFS general substrate transporter<br>**Superfamily:**MFS general substrate transporter<br>**Family:**Glycerol-3-phosphate transporter |
| 53 | d2yvxa3 | Alignment | not modelled | 42.5 | 16 | **Fold:**MgtE membrane domain-like<br>**Superfamily:**MgtE membrane domain-like<br>**Family:**MgtE membrane domain-like |
| 54 | d2cu6a1 | Alignment | not modelled | 42.3 | 18 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Fe-S cluster assembly (FSCA) domain-like<br>**Family:**PaaD-like |
| | | | | | | **Fold:**Alpha-lytic protease prodomain-like |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 55 | d1uwda_ | Alignment | not modelled | 39.7 | 18 | **Superfamily:**Fe-S cluster assembly (FSCA) domain-like<br>**Family:**PaaD-like |
| 56 | c2yy3B_ | Alignment | not modelled | 38.5 | 6 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**elongation factor 1-beta;<br>**PDBTitle:** crystal structure of translation elongation factor ef-1 beta from2 pyrococcus horikoshii |
| 57 | d2vv5a2 | Alignment | not modelled | 34.0 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**Mechanosensitive channel protein MscS (YggB), C-terminal domain<br>**Family:**Mechanosensitive channel protein MscS (YggB), C-terminal domain |
| 58 | c1ciiA_ | Alignment | not modelled | 31.3 | 15 | **PDB header:**transmembrane protein<br>**Chain:** A: **PDB Molecule:**colicin ia;<br>**PDBTitle:** colicin ia |
| 59 | c3fryB_ | Alignment | not modelled | 24.3 | 10 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**probable copper-exporting p-type atpase a;<br>**PDBTitle:** crystal structure of the copa c-terminal metal binding domain |
| 60 | c3lnoA_ | Alignment | not modelled | 23.7 | 19 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of domain of unknown function duf59 from2 bacillus anthracis |
| 61 | c2f1fA_ | Alignment | not modelled | 22.2 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit;<br>**PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli |
| 62 | c2bbjB_ | Alignment | not modelled | 21.2 | 11 | **PDB header:**metal transport/membrane protein<br>**Chain:** B: **PDB Molecule:**divalent cation transport-related protein;<br>**PDBTitle:** crystal structure of the cora mg2+ transporter |
| 63 | d2cfxa2 | Alignment | not modelled | 18.3 | 7 | **Fold:**Ferredoxin-like<br>**Superfamily:**Dimeric alpha+beta barrel<br>**Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain |
| 64 | c1w8xP_ | Alignment | not modelled | 16.9 | 24 | **PDB header:**virus<br>**Chain:** P: **PDB Molecule:**protein p16;<br>**PDBTitle:** structural analysis of prd1 |
| 65 | d1fe0a_ | Alignment | not modelled | 16.8 | 14 | **Fold:**Ferredoxin-like<br>**Superfamily:**HMA, heavy metal-associated domain<br>**Family:**HMA, heavy metal-associated domain |
| 66 | d1f7ua3 | Alignment | not modelled | 16.6 | 10 | **Fold:**RRF/tRNA synthetase additional domain-like<br>**Superfamily:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain<br>**Family:**Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain |
| 67 | c2k9yA_ | Alignment | not modelled | 15.3 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ephrin type-a receptor 2;<br>**PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 68 | c2k9yB_ | Alignment | not modelled | 15.3 | 17 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**ephrin type-a receptor 2;<br>**PDBTitle:** epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 69 | d1nvmb2 | Alignment | not modelled | 14.9 | 13 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |
| 70 | d2cyya2 | Alignment | not modelled | 14.4 | 9 | **Fold:**Ferredoxin-like<br>**Superfamily:**Dimeric alpha+beta barrel<br>**Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain |
| 71 | c3qlbA_ | Alignment | not modelled | 14.1 | 8 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**enantio-pyochelin receptor;<br>**PDBTitle:** enantiopyochelin outer membrane tonb-dependent transporter from2 pseudomonas fluorescens bound to the ferri-enantiopyochelin |
| 72 | d2iuba2 | Alignment | not modelled | 14.1 | 30 | **Fold:**Transmembrane helix hairpin<br>**Superfamily:**Magnesium transport protein CorA, transmembrane region<br>**Family:**Magnesium transport protein CorA, transmembrane region |
| 73 | d2phcb2 | Alignment | not modelled | 14.0 | 13 | **Fold:**DCoH-like<br>**Superfamily:**PH0987 N-terminal domain-like<br>**Family:**PH0987 N-terminal domain-like |
| 74 | d1xhja_ | Alignment | not modelled | 13.9 | 10 | **Fold:**Alpha-lytic protease prodomain-like<br>**Superfamily:**Fe-S cluster assembly (FSCA) domain-like<br>**Family:**NifU C-terminal domain-like |
| 75 | c2hdiA_ | Alignment | not modelled | 13.7 | 28 | **PDB header:**protein transport,antimicrobial protein<br>**Chain:** A: **PDB Molecule:**colicin i receptor;<br>**PDBTitle:** crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia. |
| 76 | c3lkxB_ | Alignment | not modelled | 13.5 | 23 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**nascent polypeptide-associated complex subunit alpha;<br>**PDBTitle:** human nac dimerization domain |
| 77 | c3bdeA_ | Alignment | not modelled | 13.5 | 0 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**mll5499 protein;<br>**PDBTitle:** crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from mesorhizobium loti maff303099 at 1.79 a resolution |
| 78 | c3ibwA_ | Alignment | not modelled | 13.3 | 29 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**gtp pyrophosphokinase;<br>**PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a |
| 79 | d1jb0i_ | Alignment | not modelled | 13.3 | 19 | **Fold:**Single transmembrane helix<br>**Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI<br>**Family:**Subunit VIII of photosystem I reaction centre, PsaI |
|  |  |  |  |  |  | **PDB header:**bacteriocin |

| | | | | | | |
|---|---|---|---|---|---|---|
| 80 | c1a87A_ | Alignment | not modelled | 13.3 | 15 | **Chain:** A: **PDB Molecule:**colicin n;<br>**PDBTitle:** colicin n |
| 81 | d1a87a_ | Alignment | not modelled | 13.3 | 15 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Colicin<br>**Family:**Colicin |
| 82 | c2e1aD_ | Alignment | not modelled | 13.3 | 14 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc;<br>**PDBTitle:** crystal structure of ffrp-dm1 |
| 83 | d1qmga1 | Alignment | not modelled | 13.2 | 25 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI) |
| 84 | c2mltB_ | Alignment | not modelled | 13.1 | 14 | **PDB header:**toxin (hemolytic polypeptide)<br>**Chain:** B: **PDB Molecule:**melittin;<br>**PDBTitle:** melittin |
| 85 | c2mltA_ | Alignment | not modelled | 13.1 | 14 | **PDB header:**toxin (hemolytic polypeptide)<br>**Chain:** A: **PDB Molecule:**melittin;<br>**PDBTitle:** melittin |
| 86 | c2zbcH_ | Alignment | not modelled | 12.7 | 16 | **PDB header:**transcription<br>**Chain:** H: **PDB Molecule:**83aa long hypothetical transcriptional regulator asnc;<br>**PDBTitle:** crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7. |
| 87 | c2kssA_ | Alignment | not modelled | 12.5 | 24 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**carotenogenesis protein cars;<br>**PDBTitle:** nmr structure of myxococcus xanthus antirepressor cars1 |
| 88 | d2cg4a2 | Alignment | not modelled | 12.5 | 16 | **Fold:**Ferredoxin-like<br>**Superfamily:**Dimeric alpha+beta barrel<br>**Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain |
| 89 | c2zztA_ | Alignment | not modelled | 12.4 | 9 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein |
| 90 | d1ciia1 | Alignment | not modelled | 12.3 | 13 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Colicin<br>**Family:**Colicin |
| 91 | c2pc6C_ | Alignment | not modelled | 12.2 | 14 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit);<br>**PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea |
| 92 | c2z51A_ | Alignment | not modelled | 12.1 | 13 | **PDB header:**metal transport<br>**Chain:** A: **PDB Molecule:**nifu-like protein 2, chloroplast;<br>**PDBTitle:** crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis |
| 93 | c2kncA_ | Alignment | not modelled | 12.0 | 14 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha-iib;<br>**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 94 | c3g7sA_ | Alignment | not modelled | 11.4 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1);<br>**PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus |
| 95 | c2dvkA_ | Alignment | not modelled | 11.4 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0130 protein ape0816;<br>**PDBTitle:** crystal structure of hypothetical protein from aeropyrum pernix |
| 96 | c2it3B_ | Alignment | not modelled | 11.0 | 21 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**upf0130 protein ph1069;<br>**PDBTitle:** structure of ph1069 protein from pyrococcus horikoshii |
| 97 | c3c6fD_ | Alignment | not modelled | 10.9 | 4 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**yetf protein;<br>**PDBTitle:** crystal structure of protein bsu07140 from bacillus subtilis |
| 98 | d2gufa1 | Alignment | not modelled | 10.6 | 28 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Ligand-gated protein channel |
| 99 | c3aqoD_ | Alignment | not modelled | 10.6 | 16 | **PDB header:**membrane protein<br>**Chain:** D: **PDB Molecule:**probable secdf protein-export membrane protein;<br>**PDBTitle:** structure and function of a membrane component secdf that enhances2 protein export |