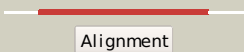

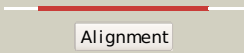



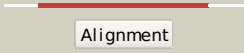



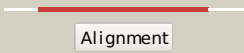

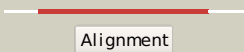

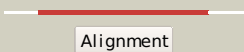

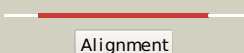



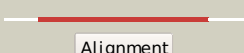












| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">d1y6va1</a> |  Alignment   |    | 100.0      | 100    | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> Alkaline phosphatase   |
| 2  | <a href="#">d1k7ha_</a> |  Alignment   |    | 100.0      | 36     | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> Alkaline phosphatase   |
| 3  | <a href="#">d1zeda1</a> |  Alignment   |    | 100.0      | 33     | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> Alkaline phosphatase   |
| 4  | <a href="#">c1ew2A_</a> |  Alignment   |   | 100.0      | 33     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphatase;<br><b>PDBTitle:</b> crystal structure of a human phosphatase  |
| 5  | <a href="#">c3e2dB_</a> |  Alignment |  | 100.0      | 33     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase;<br><b>PDBTitle:</b> the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase          |
| 6  | <a href="#">c2x98A_</a> |  Alignment |  | 100.0      | 33     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alkaline phosphatase;<br><b>PDBTitle:</b> h.salinarum alkaline phosphatase   |
| 7  | <a href="#">c2w0yB_</a> |  Alignment |  | 100.0      | 33     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase;<br><b>PDBTitle:</b> h.salinarum alkaline phosphatase   |
| 8  | <a href="#">c3a52A_</a> |  Alignment |  | 100.0      | 36     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cold-active alkaline phosphatase;<br><b>PDBTitle:</b> crystal structure of cold-active alkaine phosphatase from2 psychrophile shewanella sp. |
| 9  | <a href="#">c2iucB_</a> |  Alignment |  | 100.0      | 31     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase;<br><b>PDBTitle:</b> structure of alkaline phosphatase from the antarctic2 bacterium tab5                               |
| 10 | <a href="#">c3m8yC_</a> |  Alignment |  | 99.9       | 20     | <b>PDB header:</b> isomerase<br><b>Chain:</b> C: <b>PDB Molecule:</b> phosphopentomutase;<br><b>PDBTitle:</b> phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation                   |
| 11 | <a href="#">c2i09A_</a> |  Alignment |  | 99.9       | 18     | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphopentomutase;<br><b>PDBTitle:</b> crystal structure of putative phosphopentomutase from streptococcus2 mutans                          |

|    |                          |           |   |      |    |  |
|----|--------------------------|-----------|---|------|----|--|
| 12 | <a href="#">c3igzB_</a>  | Alignment |     | 99.7 | 20 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cofactor-independent phosphoglycerate mutase;<br><b>PDBTitle:</b> crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration                                   |
| 13 | <a href="#">c1o98A_</a>  | Alignment |    | 99.6 | 18 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent<br><b>PDBTitle:</b> 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate                     |
| 14 | <a href="#">d1o98a2</a>  | Alignment |    | 99.5 | 21 | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain  |
| 15 | <a href="#">d1hdha_</a>  | Alignment |    | 99.5 | 19 | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> Arylsulfatase  |
| 16 | <a href="#">c3ed4A_</a>  | Alignment |    | 99.5 | 22 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> arylsulfatase;<br><b>PDBTitle:</b> crystal structure of putative arylsulfatase from escherichia coli   |
| 17 | <a href="#">d1lauka_</a> | Alignment |    | 99.4 | 20 | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> Arylsulfatase  |
| 18 | <a href="#">c3q3qA_</a>  | Alignment |  | 99.4 | 21 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alkaline phosphatase;<br><b>PDBTitle:</b> crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1  |
| 19 | <a href="#">d1p49a_</a>  | Alignment |  | 99.4 | 20 | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> Arylsulfatase  |
| 20 | <a href="#">d2i09a1</a>  | Alignment |  | 99.3 | 19 | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> DeoB catalytic domain-like   |
| 21 | <a href="#">c3lxqB_</a>  | Alignment | not modelled  | 99.3 | 18 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein vp1736;<br><b>PDBTitle:</b> the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a |
| 22 | <a href="#">c2vqrA_</a>  | Alignment | not modelled  | 99.2 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative sulfatase;<br><b>PDBTitle:</b> crystal structure of a phosphonate monoester hydrolase2 from rhizobium leguminosarum: a new member of the3 alkaline phosphatase superfamily                |
| 23 | <a href="#">c2w8dB_</a>  | Alignment | not modelled  | 99.2 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> processed glycerol phosphate lipoteichoic acid synthase 2;<br><b>PDBTitle:</b> distinct and essential morphogenic functions for wall- and2 lipo-teichoic acids in bacillus subtilis              |
| 24 | <a href="#">c2qzuA_</a>  | Alignment | not modelled  | 99.2 | 14 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative sulfatase yidj;<br><b>PDBTitle:</b> crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123                   |
| 25 | <a href="#">c2w5tA_</a>  | Alignment | not modelled  | 99.2 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> processed glycerol phosphate lipoteichoic acid<br><b>PDBTitle:</b> structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltaS.                                      |
| 26 | <a href="#">d1fsua_</a>  | Alignment | not modelled  | 99.2 | 20 | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> Arylsulfatase  |
| 27 | <a href="#">c2xrgA_</a>  | Alignment | not modelled  | 99.2 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family<br><b>PDBTitle:</b> crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor                               |
|    |                          |           |   |      |    | <b>PDB header:</b> hydrolase   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
| 28 | <a href="#">c2xr9A_</a> | Alignment | not modelled | 99.2 | 22 | <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family<br><b>PDBTitle:</b> crystal structure of autotaxin (enpp2)   |
| 29 | <a href="#">c3b5qB_</a> | Alignment | not modelled | 99.1 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative sulfatase yidj;<br><b>PDBTitle:</b> crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution                                   |
| 30 | <a href="#">c2zktB_</a> | Alignment | not modelled | 98.9 | 20 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate<br><b>PDBTitle:</b> structure of ph0037 protein from pyrococcus horikoshii  |
| 31 | <a href="#">d1ei6a_</a> | Alignment | not modelled | 98.5 | 23 | <b>Fold:</b> Alkaline phosphatase-like<br><b>Superfamily:</b> Alkaline phosphatase-like<br><b>Family:</b> Phosphonoacetate hydrolase   |
| 32 | <a href="#">c3szzA_</a> | Alignment | not modelled | 98.5 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphonoacetate hydrolase;<br><b>PDBTitle:</b> crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate  |
| 33 | <a href="#">c2gsoB_</a> | Alignment | not modelled | 98.3 | 20 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase-nucleotide pyrophosphatase;<br><b>PDBTitle:</b> structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate  |
| 34 | <a href="#">c2d1gB_</a> | Alignment | not modelled | 96.8 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acid phosphatase;<br><b>PDBTitle:</b> structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate  |
| 35 | <a href="#">c3iddA_</a> | Alignment | not modelled | 82.6 | 25 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent<br><b>PDBTitle:</b> cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728   |
| 36 | <a href="#">d1b4ub_</a> | Alignment | not modelled | 72.9 | 23 | <b>Fold:</b> Phosphorylase/hydrolase-like<br><b>Superfamily:</b> LigB-like<br><b>Family:</b> LigB-like   |
| 37 | <a href="#">d2ihta3</a> | Alignment | not modelled | 36.9 | 16 | <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Family:</b> Pyruvate oxidase and decarboxylase PP module   |
| 38 | <a href="#">d1j8fa_</a> | Alignment | not modelled | 30.3 | 16 | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Sir2 family of transcriptional regulators  |
| 39 | <a href="#">d1frfs_</a> | Alignment | not modelled | 29.0 | 25 | <b>Fold:</b> HydA/Nqo6-like<br><b>Superfamily:</b> HydA/Nqo6-like<br><b>Family:</b> Nickel-iron hydrogenase, small subunit   |
| 40 | <a href="#">c2q1wC_</a> | Alignment | not modelled | 29.0 | 13 | <b>PDB header:</b> sugar binding protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative nucleotide sugar epimerase/dehydratase;<br><b>PDBTitle:</b> crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+                                    |
| 41 | <a href="#">c1q14A_</a> | Alignment | not modelled | 28.6 | 13 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hst2 protein;<br><b>PDBTitle:</b> structure and autoregulation of the yeast hst2 homolog of sir2   |
| 42 | <a href="#">c2pjuD_</a> | Alignment | not modelled | 23.9 | 16 | <b>PDB header:</b> transcription<br><b>Chain:</b> D: <b>PDB Molecule:</b> propionate catabolism operon regulatory protein;<br><b>PDBTitle:</b> crystal structure of propionate catabolism operon2 regulatory protein prpr  |
| 43 | <a href="#">c2pr7A_</a> | Alignment | not modelled | 21.4 | 32 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase/epoxide hydrolase family;<br><b>PDBTitle:</b> crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution |
| 44 | <a href="#">d2pjua1</a> | Alignment | not modelled | 20.5 | 16 | <b>Fold:</b> Chelatase-like<br><b>Superfamily:</b> PrpR receptor domain-like<br><b>Family:</b> PrpR receptor domain-like   |
| 45 | <a href="#">d1wuis1</a> | Alignment | not modelled | 20.4 | 29 | <b>Fold:</b> HydA/Nqo6-like<br><b>Superfamily:</b> HydA/Nqo6-like<br><b>Family:</b> Nickel-iron hydrogenase, small subunit   |
| 46 | <a href="#">c1h2aS_</a> | Alignment | not modelled | 20.4 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> S: <b>PDB Molecule:</b> hydrogenase;<br><b>PDBTitle:</b> single crystals of hydrogenase from desulfovibrio vulgaris   |
| 47 | <a href="#">c3bq9A_</a> | Alignment | not modelled | 20.2 | 12 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> predicted rossmann fold nucleotide-binding domain-<br><b>PDBTitle:</b> crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145              |
| 48 | <a href="#">d1e3da_</a> | Alignment | not modelled | 19.3 | 29 | <b>Fold:</b> HydA/Nqo6-like<br><b>Superfamily:</b> HydA/Nqo6-like<br><b>Family:</b> Nickel-iron hydrogenase, small subunit   |
| 49 | <a href="#">d1u7pa_</a> | Alignment | not modelled | 19.0 | 18 | <b>Fold:</b> HAD-like<br><b>Superfamily:</b> HAD-like<br><b>Family:</b> Magnesium-dependent phosphatase-1, Mdp1  |
| 50 | <a href="#">d1xjca_</a> | Alignment | not modelled | 18.5 | 15 | <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases<br><b>Family:</b> Nitrogenase iron protein-like  |
| 51 | <a href="#">d1q1aa_</a> | Alignment | not modelled | 18.2 | 16 | <b>Fold:</b> DHS-like NAD/FAD-binding domain<br><b>Superfamily:</b> DHS-like NAD/FAD-binding domain<br><b>Family:</b> Sir2 family of transcriptional regulators  |
| 52 | <a href="#">c3qlsC_</a> | Alignment | not modelled | 17.0 | 8  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> C: <b>PDB Molecule:</b> nad-dependent deacetylase sirtuin-3,<br><b>PDBTitle:</b> crystal structure of human sirt3  |
|    |                         |           |              |      |    | <b>Fold:</b> Adenine nucleotide alpha hydrolase-like   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 53 | <a href="#">d2a84a1</a> | Alignment | not modelled | 16.1 | 13 | <b>Superfamily:</b> Nucleotidyl transferase<br><b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)  |
| 54 | <a href="#">d1es9a</a>  | Alignment | not modelled | 16.0 | 21 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> SGNH hydrolase<br><b>Family:</b> Acetylhydrolase  |
| 55 | <a href="#">c3p94A</a>  | Alignment | not modelled | 15.7 | 17 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> gdsI-like lipase;<br><b>PDBTitle:</b> crystal structure of a gdsI-like lipase (bdi_0976) from2 parabacteroides distasonis atcc 8503 at 1.93 a resolution  |
| 56 | <a href="#">c3t9qB</a>  | Alignment | not modelled | 15.6 | 25 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> stage ii sporulation protein e;<br><b>PDBTitle:</b> structure of the phosphatase domain of the cell fate determinant2 spoIIE from bacillus subtilis (mn presoaked)  |
| 57 | <a href="#">d1j83a</a>  | Alignment | not modelled | 15.0 | 26 | <b>Fold:</b> Galactose-binding domain-like<br><b>Superfamily:</b> Galactose-binding domain-like<br><b>Family:</b> Family 17 carbohydrate binding module, CBM17  |
| 58 | <a href="#">c2wpaA</a>  | Alignment | not modelled | 15.0 | 34 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic [nifese] hydrogenase, small subunit;<br><b>PDBTitle:</b> structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough   |
| 59 | <a href="#">c3pu9A</a>  | Alignment | not modelled | 14.6 | 29 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein serine/threonine phosphatase;<br><b>PDBTitle:</b> crystal structure of serine/threonine phosphatase spharobacter2 thermophilus dsm 20745  |
| 60 | <a href="#">d1ghca</a>  | Alignment | not modelled | 14.5 | 33 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Linker histone H1/H5   |
| 61 | <a href="#">c3gvzB</a>  | Alignment | not modelled | 14.1 | 13 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein cv2077;<br><b>PDBTitle:</b> crystal structure of the protein cv2077 from2 chromobacterium violaceum. northeast structural genomics3 consortium target cvr62                           |
| 62 | <a href="#">d1uhma</a>  | Alignment | not modelled | 14.1 | 23 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Linker histone H1/H5   |
| 63 | <a href="#">d1ozha3</a> | Alignment | not modelled | 14.0 | 24 | <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Family:</b> Pyruvate oxidase and decarboxylase PP module  |
| 64 | <a href="#">c3ibsA</a>  | Alignment | not modelled | 14.0 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein batb;<br><b>PDBTitle:</b> crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron  |
| 65 | <a href="#">d1t9ba3</a> | Alignment | not modelled | 13.9 | 24 | <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Family:</b> Pyruvate oxidase and decarboxylase PP module  |
| 66 | <a href="#">d1qh8a</a>  | Alignment | not modelled | 13.6 | 6  | <b>Fold:</b> Chelatase-like<br><b>Superfamily:</b> "Helical backbone" metal receptor<br><b>Family:</b> Nitrogenase iron-molybdenum protein  |
| 67 | <a href="#">d1p4da</a>  | Alignment | not modelled | 13.4 | 23 | <b>Fold:</b> Origin of replication-binding domain, RBD-like<br><b>Superfamily:</b> Origin of replication-binding domain, RBD-like<br><b>Family:</b> Relaxase domain   |
| 68 | <a href="#">c3b3jA</a>  | Alignment | not modelled | 13.3 | 31 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> histone-arginine methyltransferase carm1;<br><b>PDBTitle:</b> the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered) |
| 69 | <a href="#">c3u1hA</a>  | Alignment | not modelled | 13.0 | 45 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 3-isopropyl malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of ipndh from the last common ancestor of bacillus   |
| 70 | <a href="#">c2q5cA</a>  | Alignment | not modelled | 12.8 | 11 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> ntrc family transcriptional regulator;<br><b>PDBTitle:</b> crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum  |
| 71 | <a href="#">c2kjaA</a>  | Alignment | not modelled | 12.8 | 38 | <b>PDB header:</b> ribosomal protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 30s ribosomal protein s6;<br><b>PDBTitle:</b> solution structure and backbone dynamics of the permutant2 p54-55   |
| 72 | <a href="#">d2d0oa2</a> | Alignment | not modelled | 12.7 | 29 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Actin-like ATPase domain<br><b>Family:</b> ATPase domain of dehydratase reactivase alpha subunit  |
| 73 | <a href="#">d1fxwf</a>  | Alignment | not modelled | 12.2 | 21 | <b>Fold:</b> Flavodoxin-like<br><b>Superfamily:</b> SGNH hydrolase<br><b>Family:</b> Acetylhydrolase  |
| 74 | <a href="#">c1z2iA</a>  | Alignment | not modelled | 12.2 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium  |
| 75 | <a href="#">d1qvia</a>  | Alignment | not modelled | 12.1 | 23 | <b>Fold:</b> HAD-like<br><b>Superfamily:</b> HAD-like<br><b>Family:</b> Hypothetical protein MW1667 (SA1546)  |
| 76 | <a href="#">d1usta</a>  | Alignment | not modelled | 12.0 | 23 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Linker histone H1/H5   |
| 77 | <a href="#">d1hsta</a>  | Alignment | not modelled | 12.0 | 37 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Linker histone H1/H5   |
| 78 | <a href="#">c3uoeb</a>  | Alignment | not modelled | 12.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase;<br><b>PDBTitle:</b> the crystal structure of dehydrogenase from sinorhizobium meliloti  |

|    |                          |           |              |      |    |   |
|----|--------------------------|-----------|--------------|------|----|---|
| 79 | <a href="#">dlek6a_</a>  | Alignment | not modelled | 11.9 | 25 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> Tyrosine-dependent oxidoreductases  |
| 80 | <a href="#">c3enkB_</a>  | Alignment | not modelled | 11.8 | 25 | <b>PDB header:</b> isomerase<br><b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 4-epimerase;<br><b>PDBTitle:</b> 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei  |
| 81 | <a href="#">c3cdiA_</a>  | Alignment | not modelled | 11.8 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polynucleotide phosphorylase;<br><b>PDBTitle:</b> crystal structure of e. coli pnpase   |
| 82 | <a href="#">dlw0da_</a>  | Alignment | not modelled | 11.7 | 25 | <b>Fold:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Superfamily:</b> Isocitrate/Isopropylmalate dehydrogenase-like<br><b>Family:</b> Dimeric isocitrate & isopropylmalate dehydrogenases   |
| 83 | <a href="#">dlcc1s_</a>  | Alignment | not modelled | 11.7 | 38 | <b>Fold:</b> HydA/Nqo6-like<br><b>Superfamily:</b> HydA/Nqo6-like<br><b>Family:</b> Nickel-iron hydrogenase, small subunit  |
| 84 | <a href="#">c3rgwS_</a>  | Alignment | not modelled | 11.4 | 29 | <b>PDB header:</b> oxidoreductase/oxidoreductase<br><b>Chain:</b> S: <b>PDB Molecule:</b> membrane-bound hydrogenase (nife) small subunit hoxk;<br><b>PDBTitle:</b> crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster |
| 85 | <a href="#">dl1xna_</a>  | Alignment | not modelled | 11.3 | 26 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> MTH1187/YkoF-like<br><b>Family:</b> MTH1187-like  |
| 86 | <a href="#">dl1dj0a_</a> | Alignment | not modelled | 11.2 | 10 | <b>Fold:</b> Pseudouridine synthase<br><b>Superfamily:</b> Pseudouridine synthase<br><b>Family:</b> Pseudouridine synthase I TruA   |
| 87 | <a href="#">c3bz6A_</a>  | Alignment | not modelled | 11.1 | 22 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> upf0502 protein pspto_2686;<br><b>PDBTitle:</b> crystal structure of a conserved protein of unknown function from2 pseudomonas syringae pv. tomato str. dc3000  |
| 88 | <a href="#">dlussa_</a>  | Alignment | not modelled | 11.0 | 30 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Linker histone H1/H5   |
| 89 | <a href="#">c1nl3B_</a>  | Alignment | not modelled | 10.8 | 14 | <b>PDB header:</b> protein transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> preprotein translocase seca 1 subunit;<br><b>PDBTitle:</b> crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form  |
| 90 | <a href="#">dl1yqaa1</a> | Alignment | not modelled | 10.6 | 30 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Linker histone H1/H5   |
| 91 | <a href="#">c1t9dB_</a>  | Alignment | not modelled | 10.3 | 24 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> acetolactate synthase, mitochondrial;<br><b>PDBTitle:</b> crystal structure of yeast acetohydroxyacid synthase in2 complex with a sulfonylurea herbicide, metsulfuron methyl  |
| 92 | <a href="#">dl1fra2</a>  | Alignment | not modelled | 10.2 | 18 | <b>Fold:</b> PIN domain-like<br><b>Superfamily:</b> PIN domain-like<br><b>Family:</b> 5' to 3' exonuclease catalytic domain   |
| 93 | <a href="#">dl1pvda3</a> | Alignment | not modelled | 10.1 | 62 | <b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding)<br><b>Family:</b> Pyruvate oxidase and decarboxylase PP module  |
| 94 | <a href="#">c2odaB_</a>  | Alignment | not modelled | 10.1 | 9  | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein pspto_2114;<br><b>PDBTitle:</b> crystal structure of pspto_2114  |
| 95 | <a href="#">c2iueA_</a>  | Alignment | not modelled | 9.6  | 14 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> pactolus i-domain;<br><b>PDBTitle:</b> pactolus i-domain: functional switching of the rossmann2 fold   |
| 96 | <a href="#">dl1nxua_</a> | Alignment | not modelled | 9.6  | 16 | <b>Fold:</b> L-sulfolactate dehydrogenase-like<br><b>Superfamily:</b> L-sulfolactate dehydrogenase-like<br><b>Family:</b> L-sulfolactate dehydrogenase-like   |
| 97 | <a href="#">dl1xrha_</a> | Alignment | not modelled | 9.6  | 16 | <b>Fold:</b> L-sulfolactate dehydrogenase-like<br><b>Superfamily:</b> L-sulfolactate dehydrogenase-like<br><b>Family:</b> L-sulfolactate dehydrogenase-like   |
| 98 | <a href="#">dl1e3ha5</a> | Alignment | not modelled | 9.3  | 10 | <b>Fold:</b> Ribonuclease PH domain 2-like<br><b>Superfamily:</b> Ribonuclease PH domain 2-like<br><b>Family:</b> Ribonuclease PH domain 2-like   |
| 99 | <a href="#">c3blxL_</a>  | Alignment | not modelled | 9.2  | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> L: <b>PDB Molecule:</b> isocitrate dehydrogenase [nad] subunit 2;<br><b>PDBTitle:</b> yeast isocitrate dehydrogenase (apo form)  |