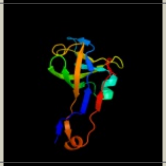
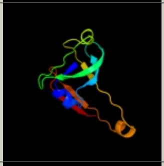
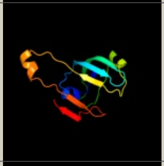
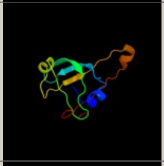
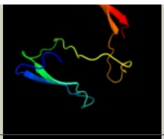
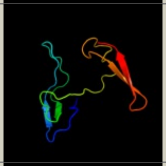
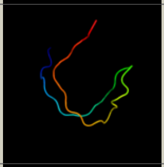
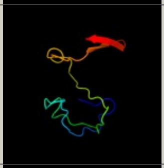
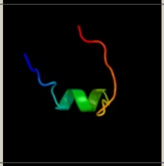
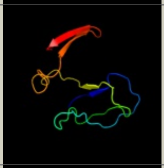
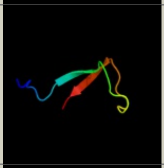
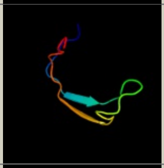
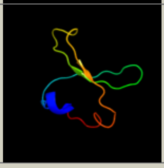
# Phyre2

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A790 |
| Date | Thu Jan 5 11:05:05 GMT 2012 |
| Unique Job ID | 1acab8f074ab7d83 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1pt1B_ | Alignment |  | 100.0 | 99 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase;<br>**PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine |
| 2 | c2c45F_ | Alignment |  | 100.0 | 50 | **PDB header:**lyase<br>**Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase precursor;<br>**PDBTitle:** native precursor of pyruvoyl dependent aspartate2 decarboxylase |
| 3 | d1ppya_ | Alignment |  | 100.0 | 100 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Pyruvoyl dependent aspartate decarboxylase, ADC |
| 4 | c3ougA_ | Alignment |  | 100.0 | 32 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase;<br>**PDBTitle:** crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis |
| 5 | c1vc3B_ | Alignment |  | 100.0 | 45 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**l-aspartate-alpha-decarboxylase heavy chain;<br>**PDBTitle:** crystal structure of l-aspartate-alpha-decarboxylase |
| 6 | c3plxB_ | Alignment |  | 100.0 | 42 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase;<br>**PDBTitle:** the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168 |
| 7 | c1pyuD_ | Alignment |  | 100.0 | 100 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**aspartate 1-decarboxylase alfa chain;<br>**PDBTitle:** processed aspartate decarboxylase mutant with ser25 mutated to cys |
| 8 | c1uheA_ | Alignment |  | 100.0 | 34 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase alpha chain;<br>**PDBTitle:** crystal structure of aspartate decarboxylase, isoaspargine complex |
| 9 | c2pjhB_ | Alignment |  | 96.5 | 12 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**transitional endoplasmic reticulum atpase;<br>**PDBTitle:** strctural model of the p97 n domain- npl4 ubd complex |
| 10 | c1cz5A_ | Alignment |  | 93.1 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**vcp-like atpase;<br>**PDBTitle:** nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma) |
| 11 | d1cz5a1 | Alignment |  | 82.2 | 14 | **Fold:**Double psi beta-barrel<br>**Superfamily:**ADC-like<br>**Family:**Cdc48 N-terminal domain-like |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c3mt1B_ | Alignment |  | 74.9 | 15 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**putative carboxynorspermidine decarboxylase protein;<br>**PDBTitle:** crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti |
| 13 | c1tufA_ | Alignment |  | 70.7 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase;<br>**PDBTitle:** crystal structure of diaminopimelate decarboxylase from m.2 jannaschi |
| 14 | c3krtC_ | Alignment |  | 65.5 | 13 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**crotonyl coa reductase;<br>**PDBTitle:** crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2) |
| 15 | c2yxxA_ | Alignment |  | 63.9 | 10 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase;<br>**PDBTitle:** crystal structure analysis of diaminopimelate decarboxylate (lysa) |
| 16 | c2glwA_ | Alignment |  | 60.5 | 33 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**92aa long hypothetical protein;<br>**PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii |
| 17 | c2o0tB_ | Alignment |  | 57.8 | 12 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**diaminopimelate decarboxylase;<br>**PDBTitle:** the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation |
| 18 | c4a10A_ | Alignment |  | 57.2 | 23 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**octenoyl-coa reductase/carboxylase;<br>**PDBTitle:** apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp. |
| 19 | c2ejvA_ | Alignment |  | 55.4 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**l-threonine 3-dehydrogenase;<br>**PDBTitle:** crystal structure of threonine 3-dehydrogenase complexed with nad+ |
| 20 | d1qw1a1 | Alignment |  | 53.2 | 16 | **Fold:**SH3-like barrel<br>**Superfamily:**C-terminal domain of transcriptional repressors<br>**Family:**FeoA-like |
| 21 | c1h2bA_ | Alignment | not modelled | 50.6 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**alcohol dehydrogenase;<br>**PDBTitle:** crystal structure of the alcohol dehydrogenase from the2 hyperthermophilic archaeon aeropyrum pernix at 1.65a3 resolution |
| 22 | d1ylea1 | Alignment | not modelled | 50.5 | 21 | **Fold:**Acyl-CoA N-acyltransferases (Nat)<br>**Superfamily:**Acyl-CoA N-acyltransferases (Nat)<br>**Family:**AstA-like |
| 23 | c1kevB_ | Alignment | not modelled | 50.2 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nadp-dependent alcohol dehydrogenase;<br>**PDBTitle:** structure of nadp-dependent alcohol dehydrogenase |
| 24 | c2eihA_ | Alignment | not modelled | 50.1 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**alcohol dehydrogenase;<br>**PDBTitle:** crystal structure of nad-dependent alcohol dehydrogenase |
| 25 | c2ouiB_ | Alignment | not modelled | 47.8 | 26 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nadp-dependent alcohol dehydrogenase;<br>**PDBTitle:** d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica |
| 26 | c2p3eA_ | Alignment | not modelled | 46.9 | 15 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase;<br>**PDBTitle:** crystal structure of aq1208 from aquifex aeolicus |
| 27 | c2xaaC_ | Alignment | not modelled | 45.5 | 17 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**secondary alcohol dehydrogenase;<br>**PDBTitle:** alcohol dehydrogenase adh-'a' from rhodococcus ruber dsm2 44541 at ph 8.5 in complex with nad and butane-1,4-diol |
| 28 | c2dfvB_ | Alignment | not modelled | 43.1 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**probable l-threonine 3-dehydrogenase;<br>**PDBTitle:** hyperthermophilic threonine dehydrogenase from pyrococcus horikoshii |
| 29 | c2vwrA_ | Alignment | not modelled | 42.6 | 19 | **PDB header:**protein-binding<br>**Chain:** A: **PDB Molecule:**ligand of numb protein x 2;<br>**PDBTitle:** crystal structure of the second pdz domain of numb- |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
|  |  |  |  |  |  | binding2 protein 2 |
| 30 | d1wrua1 | Alignment | not modelled | 42.4 | 21 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**Baseplate protein-like |
| 31 | c1e3jA_ | Alignment | not modelled | 42.2 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadp(h)-dependent ketose reductase;<br>**PDBTitle:** ketose reductase (sorbitol dehydrogenase) from silverleaf2 whitefly |
| 32 | c1r37B_ | Alignment | not modelled | 41.6 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nad-dependent alcohol dehydrogenase;<br>**PDBTitle:** alcohol dehydrogenase from sulfolobus solfataricus2 complexed with nad(h) and 2-ethoxyethanol |
| 33 | c1piwA_ | Alignment | not modelled | 41.2 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**hypothetical zinc-type alcohol dehydrogenase-<br>**PDBTitle:** apo and holo structures of an nadp(h)-dependent cinnamyl2 alcohol dehydrogenase from saccharomyces cerevisiae |
| 34 | c1lluD_ | Alignment | not modelled | 40.7 | 24 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**alcohol dehydrogenase;<br>**PDBTitle:** the ternary complex of pseudomonas aeruginosa alcohol2 dehydrogenase with its coenzyme and weak substrate |
| 35 | c2j66A_ | Alignment | not modelled | 39.4 | 10 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**btrk;<br>**PDBTitle:** structural characterisation of btrk decarboxylase from2 butirosin biosynthesis |
| 36 | c1pl6A_ | Alignment | not modelled | 36.6 | 17 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**sorbitol dehydrogenase;<br>**PDBTitle:** human sdh/nadh/inhibitor complex |
| 37 | c1p0fA_ | Alignment | not modelled | 36.0 | 28 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**nadp-dependent alcohol dehydrogenase;<br>**PDBTitle:** crystal structure of the binary complex: nadp(h)-dependent vertebrate2 alcohol dehydrogenase (adh8) with the cofactor nadp |
| 38 | c3n29A_ | Alignment | not modelled | 34.7 | 13 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carboxynorspermidine decarboxylase;<br>**PDBTitle:** crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni |
| 39 | d3cdda1 | Alignment | not modelled | 34.6 | 24 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**Baseplate protein-like |
| 40 | c1kolA_ | Alignment | not modelled | 33.7 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**formaldehyde dehydrogenase;<br>**PDBTitle:** crystal structure of formaldehyde dehydrogenase |
| 41 | d1uufa1 | Alignment | not modelled | 33.6 | 14 | **Fold:**GroES-like<br>**Superfamily:**GroES-like<br>**Family:**Alcohol dehydrogenase-like, N-terminal domain |
| 42 | d1hkva1 | Alignment | not modelled | 33.5 | 9 | **Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like<br>**Superfamily:**Alanine racemase C-terminal domain-like<br>**Family:**Eukaryotic ODC-like |
| 43 | c1yqxB_ | Alignment | not modelled | 33.4 | 18 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**sinapyl alcohol dehydrogenase;<br>**PDBTitle:** sinapyl alcohol dehydrogenase at 2.5 angstrom resolution |
| 44 | d1nxza1 | Alignment | not modelled | 33.0 | 18 | **Fold:**PUA domain-like<br>**Superfamily:**PUA domain-like<br>**Family:**YggJ N-terminal domain-like |
| 45 | d3d37a2 | Alignment | not modelled | 32.2 | 18 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**Baseplate protein-like |
| 46 | d1pl8a1 | Alignment | not modelled | 30.9 | 18 | **Fold:**GroES-like<br>**Superfamily:**GroES-like<br>**Family:**Alcohol dehydrogenase-like, N-terminal domain |
| 47 | c2hcyD_ | Alignment | not modelled | 30.7 | 15 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**alcohol dehydrogenase 1;<br>**PDBTitle:** yeast alcohol dehydrogenase i, saccharomyces cerevisiae fermentative2 enzyme |
| 48 | c1cdoB_ | Alignment | not modelled | 30.4 | 17 | **PDB header:**oxidoreductase (ch-oh(d)-nad(a))<br>**Chain:** B: **PDB Molecule:**alcohol dehydrogenase;<br>**PDBTitle:** alcohol dehydrogenase (e.c.1.1.1.1) (ee isozyme) complexed with2 nicotinamide adenine dinucleotide (nad), and zinc |
| 49 | d2csja1 | Alignment | not modelled | 30.1 | 28 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 50 | c1uufA_ | Alignment | not modelled | 29.9 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**zinc-type alcohol dehydrogenase-like protein<br>**PDBTitle:** crystal structure of a zinc-type alcohol dehydrogenase-like2 protein yahk |
| 51 | d1ejia_ | Alignment | not modelled | 29.1 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 52 | c3g7kD_ | Alignment | not modelled | 27.9 | 25 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**3-methylitaconate isomerase;<br>**PDBTitle:** crystal structure of methylitaconate-delta-isomerase |
| 53 | d1uija1 | Alignment | not modelled | 27.8 | 10 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**Germin/Seed storage 7S protein |
| 54 | c3m6iA_ | Alignment | not modelled | 27.3 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**l-arabinitol 4-dehydrogenase;<br>**PDBTitle:** l-arabinitol 4-dehydrogenase |
| 55 | c1knwA_ | Alignment | not modelled | 27.2 | 8 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase;<br>**PDBTitle:** crystal structure of diaminopimelate decarboxylase |

| | | | | | | |
|---|---|---|---|---|---|---|
| 56 | d1knwa1 | Alignment | not modelled | 26.8 | 8 | **Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like<br>**Superfamily:**Alanine racemase C-terminal domain-like<br>**Family:**Eukaryotic ODC-like |
| 57 | c2vwpA_ | Alignment | not modelled | 26.5 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**glucose dehydrogenase;<br>**PDBTitle:** haloferax mediterranei glucose dehydrogenase in complex2 with nadph and zn. |
| 58 | c3ggeA_ | Alignment | not modelled | 26.5 | 28 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**pdz domain-containing protein gipc2;<br>**PDBTitle:** crystal structure of the pdz domain of pdz domain-containing protein2 gipc2 |
| 59 | c3uogB_ | Alignment | not modelled | 26.3 | 24 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**alcohol dehydrogenase;<br>**PDBTitle:** crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021 |
| 60 | d1rv3a_ | Alignment | not modelled | 26.1 | 14 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 61 | d1uepa_ | Alignment | not modelled | 25.8 | 17 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 62 | c2dphA_ | Alignment | not modelled | 25.6 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**formaldehyde dismutase;<br>**PDBTitle:** crystal structure of formaldehyde dismutase |
| 63 | c1rjwA_ | Alignment | not modelled | 25.2 | 27 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**alcohol dehydrogenase;<br>**PDBTitle:** crystal structure of nad(+)-dependent alcohol dehydrogenase2 from bacillus stearothermophilus strain lld-r |
| 64 | d2a7va1 | Alignment | not modelled | 25.1 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 65 | c2a7vA_ | Alignment | not modelled | 25.1 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase;<br>**PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2 |
| 66 | c3n0lA_ | Alignment | not modelled | 25.1 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase;<br>**PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni |
| 67 | c3n2bD_ | Alignment | not modelled | 24.5 | 13 | **PDB header:**lyase<br>**Chain:** D: **PDB Molecule:**diaminopimelate decarboxylase;<br>**PDBTitle:** 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae. |
| 68 | c2cf5A_ | Alignment | not modelled | 24.2 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**cinnamyl alcohol dehydrogenase;<br>**PDBTitle:** crystal structures of the arabidopsis cinnamyl alcohol2 dehydrogenases, atcad5 |
| 69 | d1kwaa_ | Alignment | not modelled | 23.7 | 28 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 70 | d1kola1 | Alignment | not modelled | 23.7 | 14 | **Fold:**GroES-like<br>**Superfamily:**GroES-like<br>**Family:**Alcohol dehydrogenase-like, N-terminal domain |
| 71 | c1f8fA_ | Alignment | not modelled | 23.3 | 33 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**benzyl alcohol dehydrogenase;<br>**PDBTitle:** crystal structure of benzyl alcohol dehydrogenase from acinetobacter2 calcoaceticus |
| 72 | d1ee6a_ | Alignment | not modelled | 23.2 | 29 | **Fold:**Single-stranded right-handed beta-helix<br>**Superfamily:**Pectin lyase-like<br>**Family:**Pectate lyase-like |
| 73 | c1ma0B_ | Alignment | not modelled | 23.2 | 23 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**glutathione-dependent formaldehyde dehydrogenase;<br>**PDBTitle:** ternary complex of human glutathione-dependent formaldehyde2 dehydrogenase with nad+ and dodecanoic acid |
| 74 | c3cosD_ | Alignment | not modelled | 23.1 | 24 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**alcohol dehydrogenase 4;<br>**PDBTitle:** crystal structure of human class ii alcohol dehydrogenase (adh4) in2 complex with nad and zn |
| 75 | c3bk7A_ | Alignment | not modelled | 23.1 | 28 | **PDB header:**hydrolyase/translation<br>**Chain:** A: **PDB Molecule:**abc transporter atp-binding protein;<br>**PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii |
| 76 | c3hu2C_ | Alignment | not modelled | 22.5 | 12 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase;<br>**PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs |
| 77 | c2xkxB_ | Alignment | not modelled | 22.3 | 35 | **PDB header:**structural protein<br>**Chain:** B: **PDB Molecule:**disks large homolog 4;<br>**PDBTitle:** single particle analysis of psd-95 in negative stain |
| 78 | d1uika1 | Alignment | not modelled | 22.3 | 7 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**Germin/Seed storage 7S protein |
| 79 | c2qg1A_ | Alignment | not modelled | 22.3 | 18 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**multiple pdz domain protein;<br>**PDBTitle:** crystal structure of the 11th pdz domain of mpdz (mupp1) |
| 80 | d1bj4a_ | Alignment | not modelled | 22.1 | 17 | **Fold:**PLP-dependent transferase-like<br>**Superfamily:**PLP-dependent transferases<br>**Family:**GABA-aminotransferase-like |
| 81 | c1hf3A_ | Alignment | not modelled | 22.0 | 28 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**alcohol dehydrogenase e chain;<br>**PDBTitle:** atomic x-ray structure of liver alcohol dehydrogenase2 containing cadmium and a hydroxide adduct to nadh |
| | | | | | | **Fold:**PDZ domain-like |

| | | | | | | |
|---|---|---|---|---|---|---|
| 82 | d1mfga_ | Alignment | not modelled | 21.9 | 26 | **Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 83 | c1d7kB_ | Alignment | not modelled | 21.7 | 12 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**human ornithine decarboxylase;<br>**PDBTitle:** crystal structure of human ornithine decarboxylase at 2.12 angstroms resolution |
| 84 | c3cyyA_ | Alignment | not modelled | 21.3 | 33 | **PDB header:**peptide binding protein<br>**Chain:** A: **PDB Molecule:**tight junction protein zo-1;<br>**PDBTitle:** the crystal structure of zo-1 pdz2 in complex with the cx43 peptide |
| 85 | d2f4pa1 | Alignment | not modelled | 21.2 | 26 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**TM1287-like |
| 86 | c3ecdC_ | Alignment | not modelled | 21.0 | 20 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**serine hydroxymethyltransferase 2;<br>**PDBTitle:** crystal structure of serine hydroxymethyltransferase from burkholderia2 pseudomallei |
| 87 | d1a8pa1 | Alignment | not modelled | 20.8 | 15 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Riboflavin synthase domain-like<br>**Family:**Ferredoxin reductase FAD-binding domain-like |
| 88 | d2h3la1 | Alignment | not modelled | 20.0 | 26 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 89 | d1wifa_ | Alignment | not modelled | 19.7 | 35 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 90 | d2byga1 | Alignment | not modelled | 19.3 | 39 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 91 | d1uija2 | Alignment | not modelled | 19.3 | 10 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**Germin/Seed storage 7S protein |
| 92 | d2f0aa1 | Alignment | not modelled | 19.1 | 33 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 93 | d1ujda_ | Alignment | not modelled | 19.0 | 28 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 94 | d1f3ta1 | Alignment | not modelled | 19.0 | 9 | **Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like<br>**Superfamily:**Alanine racemase C-terminal domain-like<br>**Family:**Eukaryotic ODC-like |
| 95 | c1u37A_ | Alignment | not modelled | 18.8 | 20 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding,<br>**PDBTitle:** auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains |
| 96 | c1u38A_ | Alignment | not modelled | 18.8 | 20 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**amyloid beta a4 precursor protein-binding,<br>**PDBTitle:** auto-inhibition mechanism of x11s/mints family scaffold2 proteins revealed by the closed conformation of the tandem3 pdz domains |
| 97 | c3b70A_ | Alignment | not modelled | 18.7 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**enoyl reductase;<br>**PDBTitle:** crystal structure of aspergillus terreus trans-acting lovastatin2 polyketide enoyl reductase (lovc) with bound nadp |
| 98 | d1qaua_ | Alignment | not modelled | 18.6 | 30 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**PDZ domain |
| 99 | d1dgwa_ | Alignment | not modelled | 18.5 | 12 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**Germin/Seed storage 7S protein |