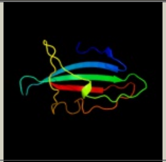
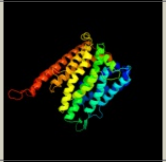
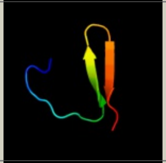
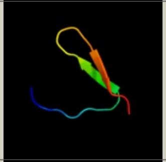
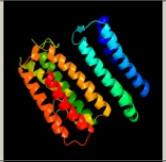
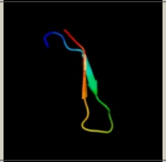
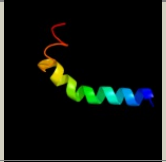
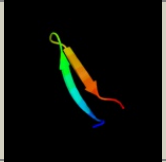
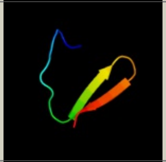
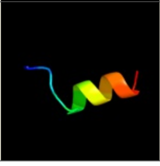
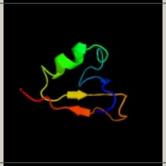
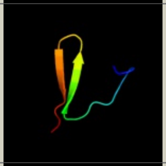
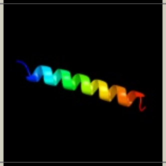
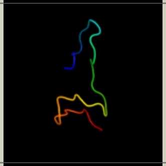
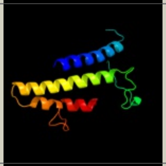
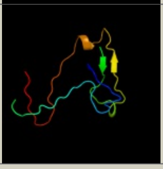
Phyre2

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P33927 |
| Date | Thu Jan 5 11:52:49 GMT 2012 |
| Unique Job ID | a27f3525d5524660 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3cfuA_ | Alignment |  | 63.9 | 14 | **PDB header:**lipoprotein<br>**Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yjha;<br>**PDBTitle:** crystal structure of the yjha protein from bacillus2 subtilis. northeast structural genomics consortium target3 sr562 |
| 2 | c3mk7K_ | Alignment |  | 51.6 | 12 | **PDB header:**oxidoreductase<br>**Chain:** K: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit n;<br>**PDBTitle:** the structure of cbb3 cytochrome oxidase |
| 3 | d2affa1 | Alignment |  | 47.6 | 28 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**FHA domain |
| 4 | c1r21A_ | Alignment |  | 46.8 | 30 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**antigen ki-67;<br>**PDBTitle:** solution structure of human ki67 fha domain |
| 5 | c3rkoN_ | Alignment |  | 46.7 | 13 | **PDB header:**oxidoreductase<br>**Chain:** N: **PDB Molecule:**nadh-quinone oxidoreductase subunit n;<br>**PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 6 | c3lkxB_ | Alignment |  | 29.6 | 25 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**nascent polypeptide-associated complex subunit alpha;<br>**PDBTitle:** human nac dimerization domain |
| 7 | c2jp3A_ | Alignment |  | 29.3 | 29 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4;<br>**PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles |
| 8 | c1agqB_ | Alignment |  | 27.3 | 42 | **PDB header:**growth factor<br>**Chain:** B: **PDB Molecule:**glial cell-derived neurotrophic factor;<br>**PDBTitle:** glial cell-derived neurotrophic factor from rat |
| 9 | d1udxa3 | Alignment |  | 26.2 | 29 | **Fold:**Obg GTP-binding protein C-terminal domain<br>**Superfamily:**Obg GTP-binding protein C-terminal domain<br>**Family:**Obg GTP-binding protein C-terminal domain |
| 10 | d2ff4a3 | Alignment |  | 20.9 | 29 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**FHA domain |
| 11 | d3b55a1 | Alignment |  | 18.1 | 13 | **Fold:**EreA/ChaN-like<br>**Superfamily:**EreA/ChaN-like<br>**Family:**EreA-like |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | c2radB_ | Alignment |  | 17.4 | 13 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**succinoglycan biosynthesis protein;<br>**PDBTitle:** crystal structure of the succinoglycan biosynthesis2 protein. northeast structural genomics consortium target3 bcr135 |
| 13 | c1lcyA_ | Alignment |  | 16.7 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**htra2 serine protease;<br>**PDBTitle:** crystal structure of the mitochondrial serine protease htra2 |
| 14 | c3gqsB_ | Alignment |  | 14.8 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**adenylate cyclase-like protein;<br>**PDBTitle:** crystal structure of the fha domain of ct664 protein from chlamydia2 trachomatis |
| 15 | c1bhbA_ | Alignment |  | 14.0 | 31 | **PDB header:**photoreceptor<br>**Chain:** A: **PDB Molecule:**bacteriorhodopsin;<br>**PDBTitle:** three-dimensional structure of (1-71) bacterioopsin2 solubilized in methanol-chloroform and sds micelles3 determined by 15n-1h heteronuclear nmr spectroscopy |
| 16 | d1dlpa1 | Alignment |  | 13.9 | 19 | **Fold:**beta-Prism II<br>**Superfamily:**alpha-D-mannose-specific plant lectins<br>**Family:**alpha-D-mannose-specific plant lectins |
| 17 | c3rkoM_ | Alignment |  | 12.5 | 15 | **PDB header:**oxidoreductase<br>**Chain:** M: **PDB Molecule:**nadh-quinone oxidoreductase subunit m;<br>**PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 18 | c2zpmA_ | Alignment |  | 11.9 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**regulator of sigma e protease;<br>**PDBTitle:** crystal structure analysis of pdz domain b |
| 19 | d1l9bm_ | Alignment |  | 11.5 | 23 | **Fold:**Bacterial photosystem II reaction centre, L and M subunits<br>**Superfamily:**Bacterial photosystem II reaction centre, L and M subunits<br>**Family:**Bacterial photosystem II reaction centre, L and M subunits |
| 20 | c3seeA_ | Alignment |  | 11.4 | 21 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**hypothetical sugar binding protein;<br>**PDBTitle:** crystal structure of a hypothetical sugar binding protein (bt_4411)2 from bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution |
| 21 | c2kklA_ | Alignment | not modelled | 10.2 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein mb1858;<br>**PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155). |
| 22 | c3poaA_ | Alignment | not modelled | 10.0 | 14 | **PDB header:**peptide binding protein<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8;<br>**PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions |
| 23 | c2l9uA_ | Alignment | not modelled | 9.9 | 31 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3;<br>**PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain |
| 24 | d2o3ga1 | Alignment | not modelled | 9.9 | 27 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CorC/HlyC domain-like |
| 25 | d2j8cm1 | Alignment | not modelled | 9.8 | 23 | **Fold:**Bacterial photosystem II reaction centre, L and M subunits<br>**Superfamily:**Bacterial photosystem II reaction centre, L and M subunits<br>**Family:**Bacterial photosystem II reaction centre, L and M subunits |
| 26 | d2f69a1 | Alignment | not modelled | 9.6 | 20 | **Fold:**open-sided beta-meander<br>**Superfamily:**Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain<br>**Family:**Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain |
| 27 | c2r76A_ | Alignment | not modelled | 9.6 | 15 | **PDB header:**lipoprotein<br>**Chain:** A: **PDB Molecule:**rare lipoprotein b;<br>**PDBTitle:** crystal structure of the rare lipoprotein b (so_1173) from shewanella2 oneidensis, northeast structural genomics consortium target sor91a |
| | | | | | | **Fold:**PDZ domain-like |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 28 | d2i4sa1 | Alignment | not modelled | 9.4 | 18 | **Superfamily:**PDZ domain-like<br>**Family:**EpsC C-terminal domain-like |
| 29 | c3pv4A_ | Alignment | not modelled | 9.3 | 33 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**degq;<br>**PDBTitle:** structure of legionella fallonii degq (delta-pdz2 variant) |
| 30 | d3dtua1 | Alignment | not modelled | 9.1 | 11 | **Fold:**Cytochrome c oxidase subunit I-like<br>**Superfamily:**Cytochrome c oxidase subunit I-like<br>**Family:**Cytochrome c oxidase subunit I-like |
| 31 | c2jo1A_ | Alignment | not modelled | 8.9 | 19 | **PDB header:**hydrolase regulator<br>**Chain:** A: **PDB Molecule:**phospholemman;<br>**PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles |
| 32 | d2bgca2 | Alignment | not modelled | 8.8 | 80 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**cAMP-binding domain-like<br>**Family:**Listeriolysin regulatory protein PrfA, N-terminal domain |
| 33 | d1hdmb2 | Alignment | not modelled | 8.7 | 83 | **Fold:**MHC antigen-recognition domain<br>**Superfamily:**MHC antigen-recognition domain<br>**Family:**MHC antigen-recognition domain |
| 34 | c4a0kB_ | Alignment | not modelled | 8.6 | 75 | **PDB header:**ligase/dna-binding protein/dna<br>**Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rbx1;<br>**PDBTitle:** structure of ddb1-ddb2-cul4a-rbx1 bound to a 12 bp abasic2 site containing dna-duplex |
| 35 | c3uotB_ | Alignment | not modelled | 8.5 | 7 | **PDB header:**cell cycle<br>**Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1;<br>**PDBTitle:** crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus |
| 36 | c2lezA_ | Alignment | not modelled | 8.5 | 20 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**secreted effector protein pipb2;<br>**PDBTitle:** solution nmr structure of n-terminal domain of salmonella effector2 protein pipb2. northeast structural genomics consortium (nesg) target3 stt318a |
| 37 | d2i6va1 | Alignment | not modelled | 8.4 | 18 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**EpsC C-terminal domain-like |
| 38 | d1x9la_ | Alignment | not modelled | 8.3 | 13 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**DR1885-like metal-binding protein<br>**Family:**DR1885-like metal-binding protein |
| 39 | d1rl2a2 | Alignment | not modelled | 8.1 | 20 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 40 | d2p13a1 | Alignment | not modelled | 8.0 | 16 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CorC/HlyC domain-like |
| 41 | c2q04C_ | Alignment | not modelled | 7.9 | 43 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**acetoin utilization protein;<br>**PDBTitle:** crystal structure of acetoin utilization protein (zp_00540088.1) from2 exiguobacterium sibiricum 255-15 at 2.33 a resolution |
| 42 | c2kjpA_ | Alignment | not modelled | 7.8 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein ylbl;<br>**PDBTitle:** solution structure of protein ylbl (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a |
| 43 | c1yj5C_ | Alignment | not modelled | 7.5 | 7 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain;<br>**PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme |
| 44 | c3ia8A_ | Alignment | not modelled | 7.5 | 29 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**thap domain-containing protein 4;<br>**PDBTitle:** the structure of the c-terminal heme nitrobindin domain of thap2 domain-containing protein 4 from homo sapiens |
| 45 | c2p3wB_ | Alignment | not modelled | 7.4 | 17 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**probable serine protease htra3;<br>**PDBTitle:** crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv) |
| 46 | c3htxA_ | Alignment | not modelled | 7.3 | 19 | **PDB header:**transferase/rna<br>**Chain:** A: **PDB Molecule:**hen1;<br>**PDBTitle:** crystal structure of small rna methyltransferase hen1 |
| 47 | c1hgvA_ | Alignment | not modelled | 7.3 | 21 | **PDB header:**virus<br>**Chain:** A: **PDB Molecule:**ph75 inovirus major coat protein;<br>**PDBTitle:** filamentous bacteriophage ph75 |
| 48 | d2qgma1 | Alignment | not modelled | 7.3 | 13 | **Fold:**EreA/ChaN-like<br>**Superfamily:**EreA/ChaN-like<br>**Family:**EreA-like |
| 49 | c2qgmA_ | Alignment | not modelled | 7.3 | 13 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**succinoglycan biosynthesis protein;<br>**PDBTitle:** crystal structure of succinoglycan biosynthesis protein at2 the resolution 1.7 a. northeast structural genomics3 consortium target bcr136. |
| 50 | d1eysm_ | Alignment | not modelled | 7.3 | 18 | **Fold:**Bacterial photosystem II reaction centre, L and M subunits<br>**Superfamily:**Bacterial photosystem II reaction centre, L and M subunits<br>**Family:**Bacterial photosystem II reaction centre, L and M subunits |
| 51 | c3rkoL_ | Alignment | not modelled | 7.3 | 13 | **PDB header:**oxidoreductase<br>**Chain:** L: **PDB Molecule:**nadh-quinone oxidoreductase subunit l;<br>**PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 52 | c3mpbA_ | Alignment | not modelled | 7.2 | 14 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**sugar isomerase;<br>**PDBTitle:** z5688 from e. coli o157:h7 bound to fructose |
|  |  |  |  |  |  | **Fold:**Cyclin-like |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 53 | d1gh6b2 | Alignment | not modelled | 7.2 | 27 | **Superfamily:**Cyclin-like<br>**Family:**Retinoblastoma tumor suppressor domains |
| 54 | c3i18A_ | Alignment | not modelled | 7.2 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**lmo2051 protein;<br>**PDBTitle:** crystal structure of the pdz domain of the sdrc-like protein2 (lmo2051) from listeria monocytogenes, northeast structural3 genomics consortium target lmr166b |
| 55 | c3stjC_ | Alignment | not modelled | 7.1 | 24 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**protease degq;<br>**PDBTitle:** crystal structure of the protease + pdz1 domain of degq from2 escherichia coli |
| 56 | c3eh4A_ | Alignment | not modelled | 7.0 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**cytochrome c oxidase subunit 1;<br>**PDBTitle:** structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus |
| 57 | c1sddB_ | Alignment | not modelled | 6.9 | 17 | **PDB header:**blood clotting<br>**Chain:** B: **PDB Molecule:**coagulation factor v;<br>**PDBTitle:** crystal structure of bovine factor vai |
| 58 | c3lw52_ | Alignment | not modelled | 6.9 | 21 | **PDB header:**photosynthesis<br>**Chain:** 2: **PDB Molecule:**type ii chlorophyll a/b binding protein from photosystem i;<br>**PDB Fragment:**residues 81-246; **PDBTitle:** improved model of plant photosystem i |
| 59 | d1q90r_ | Alignment | not modelled | 6.8 | 31 | **Fold:**Single transmembrane helix<br>**Superfamily:**ISP transmembrane anchor<br>**Family:**ISP transmembrane anchor |
| 60 | c1q90R_ | Alignment | not modelled | 6.8 | 31 | **PDB header:**photosynthesis<br>**Chain:** R: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit;<br>**PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii |
| 61 | c1dlpA_ | Alignment | not modelled | 6.8 | 19 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**lectin scafet precursor;<br>**PDBTitle:** structural characterization of the native fetuin-binding2 protein scilla campanulata agglutinin (scafet): a novel3 two-domain lectin |
| 62 | d1e57a_ | Alignment | not modelled | 6.7 | 29 | **Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins)<br>**Superfamily:**Positive stranded ssRNA viruses<br>**Family:**Tymoviridae-like VP |
| 63 | d1r45a_ | Alignment | not modelled | 6.6 | 11 | **Fold:**ADP-ribosylation<br>**Superfamily:**ADP-ribosylation<br>**Family:**ADP-ribosylating toxins |
| 64 | c1zrtD_ | Alignment | not modelled | 6.6 | 10 | **PDB header:**oxidoreductase/metal transport<br>**Chain:** D: **PDB Molecule:**cytochrome c1;<br>**PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound |
| 65 | d1uapa_ | Alignment | not modelled | 6.6 | 15 | **Fold:**OB-fold<br>**Superfamily:**TIMP-like<br>**Family:**Netrin-like domain (NTR/C345C module) |
| 66 | c2yvxD_ | Alignment | not modelled | 6.5 | 18 | **PDB header:**transport protein<br>**Chain:** D: **PDB Molecule:**mg2+ transporter mgte;<br>**PDBTitle:** crystal structure of magnesium transporter mgte |
| 67 | d1qbaa2 | Alignment | not modelled | 6.4 | 9 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Carbohydrate-binding domain<br>**Family:**Bacterial chitobiase, n-terminal domain |
| 68 | d1vqoa2 | Alignment | not modelled | 6.3 | 27 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 69 | c2rf9D_ | Alignment | not modelled | 6.3 | 43 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**erbb receptor feedback inhibitor 1;<br>**PDBTitle:** crystal structure of the complex between the egfr kinase2 domain and a mig6 peptide |
| 70 | d1i32a2 | Alignment | not modelled | 6.3 | 18 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |
| 71 | d1ggaa2 | Alignment | not modelled | 6.3 | 24 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |
| 72 | d2r7ga2 | Alignment | not modelled | 6.3 | 27 | **Fold:**Cyclin-like<br>**Superfamily:**Cyclin-like<br>**Family:**Retinoblastoma tumor suppressor domains |
| 73 | d2z9ia1 | Alignment | not modelled | 6.2 | 11 | **Fold:**PDZ domain-like<br>**Superfamily:**PDZ domain-like<br>**Family:**HtrA-like serine proteases |
| 74 | d2o1ra1 | Alignment | not modelled | 6.2 | 21 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CorC/HlyC domain-like |
| 75 | d2plia1 | Alignment | not modelled | 6.2 | 23 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CorC/HlyC domain-like |
| 76 | c2kl1A_ | Alignment | not modelled | 6.2 | 18 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**ylbl protein;<br>**PDBTitle:** solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c |
| 77 | c2bbjB_ | Alignment | not modelled | 6.1 | 12 | **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 |
| 78 | d2pkqo2 | Alignment | not modelled | 6.1 | 18 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | **Family:**GAPDH-like |
| 79 | d2brfa1 | Alignment | not modelled | 6.1 | 8 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**FHA domain |
| 80 | d1t3la2 | Alignment | not modelled | 6.1 | 36 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nucleotide and nucleoside kinases |
| 81 | c3llbA_ | Alignment | not modelled | 6.1 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1 |
| 82 | d1q90n_ | Alignment | not modelled | 6.1 | 35 | **Fold:**Single transmembrane helix<br>**Superfamily:**PetN subunit of the cytochrome b6f complex<br>**Family:**PetN subunit of the cytochrome b6f complex |
| 83 | d2c8aa1 | Alignment | not modelled | 6.1 | 11 | **Fold:**ADP-ribosylation<br>**Superfamily:**ADP-ribosylation<br>**Family:**ADP-ribosylating toxins |
| 84 | d1vjja2 | Alignment | not modelled | 6.0 | 8 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Transglutaminase, two C-terminal domains<br>**Family:**Transglutaminase, two C-terminal domains |
| 85 | d3deda1 | Alignment | not modelled | 6.0 | 16 | **Fold:**FAD-binding/transporter-associated domain-like<br>**Superfamily:**FAD-binding/transporter-associated domain-like<br>**Family:**CorC/HlyC domain-like |
| 86 | c3dedB_ | Alignment | not modelled | 6.0 | 16 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**probable hemolysin;<br>**PDBTitle:** c-terminal domain of probable hemolysin from chromobacterium violaceum |
| 87 | c1qcrD_ | Alignment | not modelled | 5.9 | 19 | **PDB header:**<br>**PDB COMPND:** |
| 88 | d1uhta_ | Alignment | not modelled | 5.9 | 18 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**FHA domain |
| 89 | d1e57b_ | Alignment | not modelled | 5.9 | 29 | **Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins)<br>**Superfamily:**Positive stranded ssRNA viruses<br>**Family:**Tymoviridae-like VP |
| 90 | c3cwbQ_ | Alignment | not modelled | 5.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein;<br>**PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d |
| 91 | c2l5bA_ | Alignment | not modelled | 5.8 | 33 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**activator of apoptosis harakiri;<br>**PDBTitle:** solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles |
| 92 | d1k3ta2 | Alignment | not modelled | 5.8 | 24 | **Fold:**FwdE/GAPDH domain-like<br>**Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain<br>**Family:**GAPDH-like |
| 93 | d2vera1 | Alignment | not modelled | 5.8 | 40 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Bacterial adhesins<br>**Family:**Dr-family adhesin |
| 94 | d1vf5c3 | Alignment | not modelled | 5.8 | 24 | **Fold:**Single transmembrane helix<br>**Superfamily:**Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor<br>**Family:**Cytochrome f subunit of the cytochrome b6f complex, transmembrane anchor |
| 95 | d1rhzb_ | Alignment | not modelled | 5.7 | 24 | **Fold:**Single transmembrane helix<br>**Superfamily:**Preprotein translocase SecE subunit<br>**Family:**Preprotein translocase SecE subunit |
| 96 | c2bovB_ | Alignment | not modelled | 5.7 | 11 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**mono-adp-ribosyltransferase c3;<br>**PDBTitle:** molecular recognition of an adp-ribosylating clostridium2 botulinum c3 exoenzyme by rala gtpase |
| 97 | c3p56F_ | Alignment | not modelled | 5.6 | 17 | **PDB header:**hydrolase/replication<br>**Chain:** F: **PDB Molecule:**ribonuclease h2 subunit c;<br>**PDBTitle:** the structure of the human rnase h2 complex defines key interaction2 interfaces relevant to enzyme function and human disease |
| 98 | d1ng0c_ | Alignment | not modelled | 5.6 | 38 | **Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins)<br>**Superfamily:**Positive stranded ssRNA viruses<br>**Family:**Tombusviridae-like VP |
| 99 | d1fftc_ | Alignment | not modelled | 5.5 | 7 | **Fold:**Cytochrome c oxidase subunit III-like<br>**Superfamily:**Cytochrome c oxidase subunit III-like<br>**Family:**Cytochrome c oxidase subunit III-like |