# Phyre2

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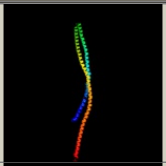
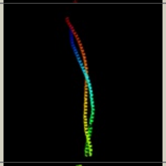
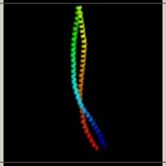
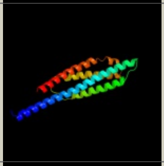
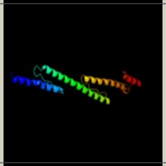
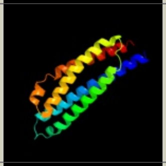
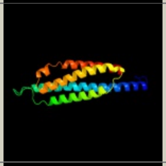
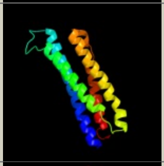
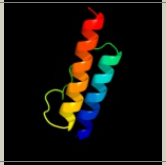
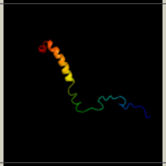
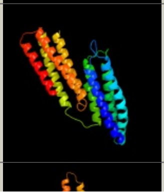
| Email | l.a.kelley@imperial.ac.uk |
| Description | P07017 |
| Date | Thu Jan 5 11:00:02 GMT 2012 |
| Unique Job ID | e43c6b1d80074314 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1qu7A_ | Alignment |  | 99.9 | 84 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i;<br>**PDBTitle:** four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor |
| 2 | c2ch7A_ | Alignment |  | 99.7 | 21 | **PDB header:**chemotaxis<br>**Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein;<br>**PDBTitle:** crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima |
| 3 | c3g67A_ | Alignment |  | 99.5 | 21 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein;<br>**PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima |
| 4 | c2d4uA_ | Alignment |  | 98.3 | 34 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i;<br>**PDBTitle:** crystal structure of the ligand binding domain of the bacterial serine2 chemoreceptor tsr |
| 5 | c3lnrA_ | Alignment |  | 98.1 | 12 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**aerotaxis transducer aer2;<br>**PDBTitle:** crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2 |
| 6 | d2asra_ | Alignment |  | 98.0 | 99 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Aspartate receptor, ligand-binding domain<br>**Family:**Aspartate receptor, ligand-binding domain |
| 7 | d2liga_ | Alignment |  | 98.0 | 69 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Aspartate receptor, ligand-binding domain<br>**Family:**Aspartate receptor, ligand-binding domain |
| 8 | d1vlta_ | Alignment |  | 97.5 | 70 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Aspartate receptor, ligand-binding domain<br>**Family:**Aspartate receptor, ligand-binding domain |
| 9 | d2asxa1 | Alignment |  | 97.0 | 27 | **Fold:**HAMP domain-like<br>**Superfamily:**HAMP domain-like<br>**Family:**HAMP domain |
| 10 | c2rm8A_ | Alignment |  | 96.7 | 19 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**sensory rhodopsin ii transducer;<br>**PDBTitle:** the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis |
| 11 | c1sj8A_ | Alignment |  | 94.9 | 9 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**talin 1;<br>**PDBTitle:** crystal structure of talin residues 482-789 |
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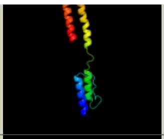
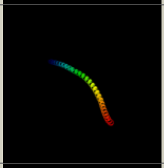
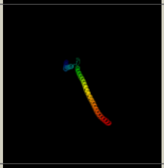
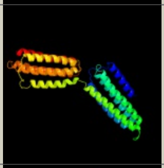
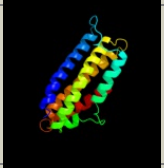
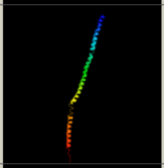
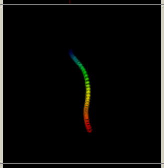
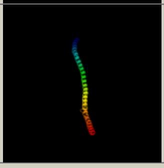
| 12 | c3zrwB_ | Alignment |  | 94.3 | 19 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**af1503 protein, osmolarity sensor protein envz;<br>**PDBTitle:** the structure of the dimeric hamp-dhp fusion a291v mutant |
| 13 | c2wpqA_ | Alignment |  | 93.0 | 12 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**trimeric autotransporter adhesin fragment;<br>**PDBTitle:** salmonella enterica sada 479-519 fused to gcn4 adaptors (2 sadak3, in-register fusion) |
| 14 | c3ojaB_ | Alignment |  | 80.6 | 12 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein<br>**PDBTitle:** crystal structure of lrim1/apl1c complex |
| 15 | c3dyjA_ | Alignment |  | 72.5 | 9 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**talin-1;<br>**PDBTitle:** crystal structure a talin rod fragment |
| 16 | c2kbbA_ | Alignment |  | 64.8 | 12 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**talin-1;<br>**PDBTitle:** nmr structure of the talin rod domain, 1655-1822 |
| 17 | c1deqO_ | Alignment |  | 61.7 | 16 | **PDB header:**<br>**PDB COMPND:** |
| 18 | c2qihA_ | Alignment |  | 56.6 | 12 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**protein uspa1;<br>**PDBTitle:** crystal structure of 527-665 fragment of uspa1 protein from2 moraxella catarrhalis |
| 19 | c3hd7A_ | Alignment |  | 53.6 | 26 | **PDB header:**exocytosis<br>**Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2;<br>**PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1 |
| 20 | c1ei3E_ | Alignment |  | 52.3 | 16 | **PDB header:**<br>**PDB COMPND:** |
| 21 | c1urqA_ | Alignment | not modelled | 52.1 | 21 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**m-tomosyn isoform;<br>**PDBTitle:** crystal structure of neuronal q-snares in complex with2 r-snare motif of tomosyn |
| 22 | c3b5nF_ | Alignment | not modelled | 48.2 | 12 | **PDB header:**membrane protein<br>**Chain:** F: **PDB Molecule:**protein sso1;<br>**PDBTitle:** structure of the yeast plasma membrane snare complex |
| 23 | c3ipdB_ | Alignment | not modelled | 46.6 | 13 | **PDB header:**exocytosis<br>**Chain:** B: **PDB Molecule:**syntaxin-1a;<br>**PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21 |
| 24 | c1sfcJ_ | Alignment | not modelled | 44.8 | 13 | **PDB header:**transport protein<br>**Chain:** J: **PDB Molecule:**protein (syntaxin 1a);<br>**PDBTitle:** neuronal synaptic fusion complex |
| 25 | c1n7sB_ | Alignment | not modelled | 42.6 | 15 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**syntaxin 1a;<br>**PDBTitle:** high resolution structure of a truncated neuronal snare2 complex |
| 26 | c1ei3C_ | Alignment | not modelled | 41.6 | 6 | **PDB header:**<br>**PDB COMPND:** |
| 27 | c1deqF_ | Alignment | not modelled | 40.2 | 5 | **PDB header:**<br>**PDB COMPND:** |
| 28 | c2ieqC_ | Alignment | not modelled | 37.7 | 14 | **PDB header:**viral protein<br>**Chain:** C: **PDB Molecule:**spike glycoprotein;<br>**PDBTitle:** core structure of s2 from the human coronavirus nl63 spike2 glycoprotein |
| 29 | c1n7sA_ | Alignment | not modelled | 37.1 | 25 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2;<br>**PDBTitle:** high resolution structure of a truncated neuronal snare2 |

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| | | | | | | complex |
| 30 | c3ghgK_ | Alignment | not modelled | 36.9 | 15 | **PDB header:**blood clotting<br>**Chain:** K: **PDB Molecule:**fibrinogen beta chain;<br>**PDBTitle:** crystal structure of human fibrinogen |
| 31 | c2npsA_ | Alignment | not modelled | 35.4 | 25 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 4;<br>**PDBTitle:** crystal structure of the early endosomal snare complex |
| 32 | c2vs0B_ | Alignment | not modelled | 33.5 | 13 | **PDB header:**cell invasion<br>**Chain:** B: **PDB Molecule:**virulence factor esxa;<br>**PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa |
| 33 | c2kseA_ | Alignment | not modelled | 33.5 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sensor protein qsec;<br>**PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor qsec, center for structures of3 membrane proteins (csmp) target 4311c |
| 34 | c2npsB_ | Alignment | not modelled | 33.5 | 16 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**syntaxin 13;<br>**PDBTitle:** crystal structure of the early endosomal snare complex |
| 35 | c3b5nE_ | Alignment | not modelled | 32.5 | 15 | **PDB header:**membrane protein<br>**Chain:** E: **PDB Molecule:**synaptobrevin homolog 1;<br>**PDBTitle:** structure of the yeast plasma membrane snare complex |
| 36 | c1sfcI_ | Alignment | not modelled | 30.4 | 26 | **PDB header:**transport protein<br>**Chain:** I: **PDB Molecule:**protein (synaptobrevin 2);<br>**PDBTitle:** neuronal synaptic fusion complex |
| 37 | c2efrB_ | Alignment | not modelled | 27.5 | 13 | **PDB header:**contractile protein<br>**Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 alpha chain;<br>**PDBTitle:** crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution |
| 38 | c1i49A_ | Alignment | not modelled | 25.0 | 13 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**arfaptin 2;<br>**PDBTitle:** crystal structure analysis of arfaptin |
| 39 | c1gl2A_ | Alignment | not modelled | 22.4 | 13 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**endobrevin;<br>**PDBTitle:** crystal structure of an endosomal snare core complex |
| 40 | c1m1jA_ | Alignment | not modelled | 21.4 | 6 | **PDB header:**blood clotting<br>**Chain:** A: **PDB Molecule:**fibrinogen alpha subunit;<br>**PDBTitle:** crystal structure of native chicken fibrinogen with two different2 bound ligands |
| 41 | c3gvmA_ | Alignment | not modelled | 18.4 | 11 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039;<br>**PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae |
| 42 | c2bezC_ | Alignment | not modelled | 17.3 | 16 | **PDB header:**viral protein<br>**Chain:** C: **PDB Molecule:**e2 glycoprotein;<br>**PDBTitle:** structure of a proteolitically resistant core from the2 severe acute respiratory syndrome coronavirus s2 fusion3 protein |
| 43 | c1l4aD_ | Alignment | not modelled | 17.1 | 7 | **PDB header:**endocytosis/exocytosis<br>**Chain:** D: **PDB Molecule:**s-snap25 fusion protein;<br>**PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei |
| 44 | c3arcl_ | Alignment | not modelled | 16.8 | 35 | **PDB header:**electron transport, photosynthesis<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution |
| 45 | c2npsD_ | Alignment | not modelled | 16.2 | 5 | **PDB header:**transport protein<br>**Chain:** D: **PDB Molecule:**syntaxin-6;<br>**PDBTitle:** crystal structure of the early endosomal snare complex |
| 46 | c1sfcD_ | Alignment | not modelled | 15.7 | 10 | **PDB header:**transport protein<br>**Chain:** D: **PDB Molecule:**protein (snap-25b);<br>**PDBTitle:** neuronal synaptic fusion complex |
| 47 | c3cwgA_ | Alignment | not modelled | 15.4 | 9 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**signal transducer and activator of transcription<br>**PDBTitle:** unphosphorylated mouse stat3 core fragment |
| 48 | c1nafA_ | Alignment | not modelled | 15.4 | 15 | **PDB header:**signaling protein, membrane protein<br>**Chain:** A: **PDB Molecule:**adp-ribosylation factor binding protein gga1;<br>**PDBTitle:** crystal structure of the human gga1 gat domain |
| 49 | c1kmiZ_ | Alignment | not modelled | 15.3 | 7 | **PDB header:**signaling protein<br>**Chain:** Z: **PDB Molecule:**chemotaxis protein chez;<br>**PDBTitle:** crystal structure of an e.coli chemotaxis protein, chez |
| 50 | d1ez3a_ | Alignment | not modelled | 14.8 | 12 | **Fold:**STAT-like<br>**Superfamily:**t-snare proteins<br>**Family:**t-snare proteins |
| 51 | c2d3eD_ | Alignment | not modelled | 14.5 | 8 | **PDB header:**contractile protein<br>**Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1<br>**PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin |
| 52 | c2d4yA_ | Alignment | not modelled | 14.1 | 9 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**flagellar hook-associated protein 1;<br>**PDBTitle:** crystal structure of a 49k fragment of hap1 (flgk) |
| 53 | c3prrL_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**photosynthesis<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer |
| 54 | c3kziL_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii |

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| 55 | c3prqL_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**photosynthesis<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer |
| 56 | c1s5lL_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**photosynthesis<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein;<br>**PDBTitle:** architecture of the photosynthetic oxygen evolving center |
| 57 | c3bz1L_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer |
| 58 | d2axtl1 | Alignment | not modelled | 13.7 | 35 | **Fold:**Single transmembrane helix<br>**Superfamily:**Photosystem II reaction center protein L, PsbL<br>**Family:**PsbL-like |
| 59 | c3bz2L_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer |
| 60 | c3a0hL_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of i-substituted photosystem ii complex |
| 61 | c3a0bl_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of br-substituted photosystem ii complex |
| 62 | c3a0bL_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of br-substituted photosystem ii complex |
| 63 | c1s5ll_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**photosynthesis<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein;<br>**PDBTitle:** architecture of the photosynthetic oxygen evolving center |
| 64 | c3arcL_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport, photosynthesis<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution |
| 65 | c3a0hl_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l;<br>**PDBTitle:** crystal structure of i-substituted photosystem ii complex |
| 66 | c2axtL_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein;<br>**PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus |
| 67 | c2axtl_ | Alignment | not modelled | 13.7 | 35 | **PDB header:**electron transport<br>**Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein;<br>**PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus |
| 68 | c1l7cA_ | Alignment | not modelled | 13.4 | 13 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**alpha e-catenin;<br>**PDBTitle:** alpha-catenin fragment, residues 385-651 |
| 69 | c1s94A_ | Alignment | not modelled | 13.0 | 11 | **PDB header:**endocytosis/exocytosis<br>**Chain:** A: **PDB Molecule:**s-syntaxin;<br>**PDBTitle:** crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei |
| 70 | d1s94a_ | Alignment | not modelled | 13.0 | 11 | **Fold:**STAT-like<br>**Superfamily:**t-snare proteins<br>**Family:**t-snare proteins |
| 71 | c1zvaA_ | Alignment | not modelled | 12.9 | 10 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**e2 glycoprotein;<br>**PDBTitle:** a structure-based mechanism of sars virus membrane fusion |
| 72 | c3ok8A_ | Alignment | not modelled | 12.4 | 8 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**brain-specific angiogenesis inhibitor 1-associated protein<br>**PDBTitle:** i-bar of pinkbar |
| 73 | d1i4da_ | Alignment | not modelled | 12.2 | 13 | **Fold:**BAR/IMD domain-like<br>**Superfamily:**BAR/IMD domain-like<br>**Family:**Arfaptin, Rac-binding fragment |
| 74 | d1eq1a_ | Alignment | not modelled | 11.9 | 9 | **Fold:**Apolipophorin-III<br>**Superfamily:**Apolipophorin-III<br>**Family:**Apolipophorin-III |
| 75 | d1r0da_ | Alignment | not modelled | 10.7 | 11 | **Fold:**I/LWEQ domain<br>**Superfamily:**I/LWEQ domain<br>**Family:**I/LWEQ domain |
| 76 | c3dtpA_ | Alignment | not modelled | 10.6 | 18 | **PDB header:**contractile protein<br>**Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and<br>**PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map |
| 77 | c1eboE_ | Alignment | not modelled | 10.2 | 18 | **PDB header:**viral protein<br>**Chain:** E: **PDB Molecule:**ebola virus envelope protein chimera consisting<br>**PDBTitle:** crystal structure of the ebola virus membrane-fusion2 subunit, gp2, from the envelope glycoprotein ectodomain |
| 78 | c3b5nL_ | Alignment | not modelled | 10.2 | 11 | **PDB header:**membrane protein<br>**Chain:** L: **PDB Molecule:**protein transport protein sec9;<br>**PDBTitle:** structure of the yeast plasma membrane snare complex |
| 79 | c1gl2D_ | Alignment | not modelled | 10.2 | 25 | **PDB header:**membrane protein<br>**Chain:** D: **PDB Molecule:**syntaxin 8;<br>**PDBTitle:** crystal structure of an endosomal snare core complex |
| 80 | c3c98B_ | Alignment | not modelled | 10.1 | 10 | **PDB header:**endocytosis/exocytosis<br>**Chain:** B: **PDB Molecule:**syntaxin-1a;<br>**PDBTitle:** revised structure of the munc18a-syntaxin1 complex |

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| 81 | c1l4aC_ | Alignment | not modelled | 10.1 | 7 | **PDB header:**endocytosis/exocytosis<br>**Chain:** C: **PDB Molecule:**s-snap25 fusion protein;<br>**PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei |
| 82 | c3gxvD_ | Alignment | not modelled | 10.0 | 15 | **PDB header:**hydrolase/replication<br>**Chain:** D: **PDB Molecule:**replicative dna helicase;<br>**PDBTitle:** three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase |
| 83 | c2dnxA_ | Alignment | not modelled | 9.8 | 9 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**syntaxin-12;<br>**PDBTitle:** solution structure of rsgi ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna |
| 84 | c3gxvC_ | Alignment | not modelled | 9.6 | 15 | **PDB header:**hydrolase/replication<br>**Chain:** C: **PDB Molecule:**replicative dna helicase;<br>**PDBTitle:** three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase |
| 85 | d1oxza_ | Alignment | not modelled | 9.5 | 15 | **Fold:**Spectrin repeat-like<br>**Superfamily:**GAT-like domain<br>**Family:**GAT domain |
| 86 | c1oxzA_ | Alignment | not modelled | 9.5 | 15 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**adp-ribosylation factor binding protein gga1;<br>**PDBTitle:** crystal structure of the human gga1 gat domain |
| 87 | c1wyyB_ | Alignment | not modelled | 9.2 | 16 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**e2 glycoprotein;<br>**PDBTitle:** post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein |
| 88 | d1wr6a1 | Alignment | not modelled | 9.1 | 9 | **Fold:**Spectrin repeat-like<br>**Superfamily:**GAT-like domain<br>**Family:**GAT domain |
| 89 | c2l9uA_ | Alignment | not modelled | 9.1 | 13 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-3;<br>**PDBTitle:** spatial structure of dimeric erbb3 transmembrane domain |
| 90 | c1junB_ | Alignment | not modelled | 9.0 | 25 | **PDB header:**transcription regulation<br>**Chain:** B: **PDB Molecule:**c-jun homodimer;<br>**PDBTitle:** nmr study of c-jun homodimer |
| 91 | d1t01a1 | Alignment | not modelled | 8.9 | 12 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**alpha-catenin/vinculin-like<br>**Family:**alpha-catenin/vinculin |
| 92 | c1n73C_ | Alignment | not modelled | 8.9 | 15 | **PDB header:**blood clotting<br>**Chain:** C: **PDB Molecule:**fibrin gamma chain;<br>**PDBTitle:** fibrin d-dimer, lamprey complexed with the peptide ligand: gly-his-2 arg-pro-amide |
| 93 | c1zv8I_ | Alignment | not modelled | 8.9 | 7 | **PDB header:**viral protein<br>**Chain:** I: **PDB Molecule:**e2 glycoprotein;<br>**PDBTitle:** a structure-based mechanism of sars virus membrane fusion |
| 94 | d1lvfa_ | Alignment | not modelled | 8.8 | 15 | **Fold:**STAT-like<br>**Superfamily:**t-snare proteins<br>**Family:**t-snare proteins |
| 95 | c1ciiA_ | Alignment | not modelled | 8.6 | 12 | **PDB header:**transmembrane protein<br>**Chain:** A: **PDB Molecule:**colicin ia;<br>**PDBTitle:** colicin ia |
| 96 | c3hnwB_ | Alignment | not modelled | 8.5 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750 |
| 97 | c2qrxA_ | Alignment | not modelled | 8.4 | 9 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**gm27569p;<br>**PDBTitle:** crystal structure of drosophila melanogaster translin2 protein |
| 98 | c2l16A_ | Alignment | not modelled | 8.2 | 14 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatad;<br>**PDBTitle:** solution structure of bacillus subtilits tatad protein in dpc micelles |
| 99 | c1y4cA_ | Alignment | not modelled | 8.1 | 10 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**maltose binding protein fused with designed<br>**PDBTitle:** designed helical protein fusion mbp |