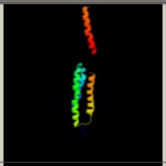
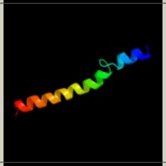
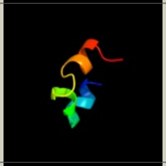
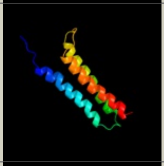
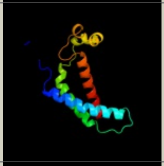
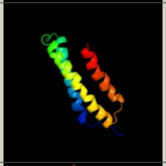
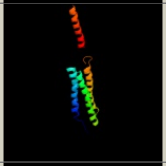
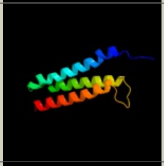
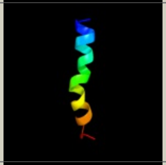
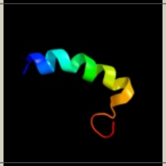
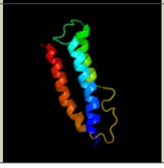
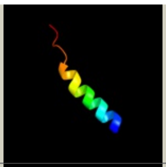
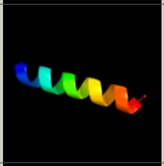
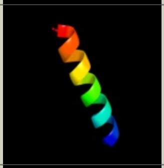
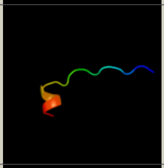
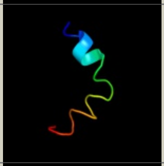
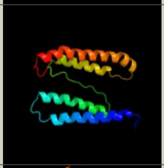
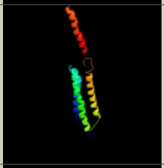
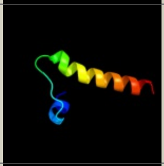
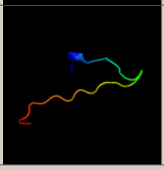
# Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ADJ8 |
| Date | Thu Jan 5 11:21:11 GMT 2012 |
| Unique Job ID | 1a93d2fa0f286f1e |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2bg9B_ | Alignment |  | 63.4 | 14 | **PDB header:**ion channel/receptor<br>**Chain:** B: **PDB Molecule:**acetylcholine receptor protein, beta chain;<br>**PDBTitle:** refined structure of the nicotinic acetylcholine receptor2 at 4a resolution. |
| 2 | c2kncB_ | Alignment |  | 60.6 | 10 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**integrin beta-3;<br>**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 3 | d1vpua_ | Alignment |  | 51.4 | 24 | **Fold:**HIV-1 VPU cytoplasmic domain<br>**Superfamily:**HIV-1 VPU cytoplasmic domain<br>**Family:**HIV-1 VPU cytoplasmic domain |
| 4 | c3riaC_ | Alignment |  | 44.1 | 7 | **PDB header:**transport protein/immune system<br>**Chain:** C: **PDB Molecule:**avermectin-sensitive glutamate-gated chloride channel glucl<br>**PDBTitle:** c. elegans glutamate-gated chloride channel (glucl) in complex with2 fab, ivermectin and iodide. |
| 5 | d1kqfc_ | Alignment |  | 43.1 | 14 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Formate dehydrogenase N, cytochrome (gamma) subunit |
| 6 | c2bg9A_ | Alignment |  | 32.4 | 14 | **PDB header:**ion channel/receptor<br>**Chain:** A: **PDB Molecule:**acetylcholine receptor protein, alpha chain;<br>**PDBTitle:** refined structure of the nicotinic acetylcholine receptor2 at 4a resolution. |
| 7 | c2bg9C_ | Alignment |  | 30.7 | 11 | **PDB header:**ion channel/receptor<br>**Chain:** C: **PDB Molecule:**acetylcholine receptor protein, delta chain;<br>**PDBTitle:** refined structure of the nicotinic acetylcholine receptor2 at 4a resolution. |
| 8 | c3eamB_ | Alignment |  | 26.6 | 9 | **PDB header:**membrane protein, transport protein<br>**Chain:** B: **PDB Molecule:**glr4197 protein;<br>**PDBTitle:** an open-pore structure of a bacterial pentameric ligand-2 gated ion channel |
| 9 | c1m8oB_ | Alignment |  | 23.4 | 12 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**platele integrin beta3 subunit: cytoplasmic<br>**PDBTitle:** platelet integrin alfaiib-beta3 cytoplasmic domain |
| 10 | c1s4xA_ | Alignment |  | 22.3 | 12 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin beta-3;<br>**PDBTitle:** nmr structure of the integrin b3 cytoplasmic domain in dpc2 micelles |
| 11 | c2ksrA_ | Alignment |  | 18.7 | 16 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**neuronal acetylcholine receptor subunit beta-2;<br>**PDBTitle:** nmr structures of tm domain of the n-acetylcholine receptor b2 subunit |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 12 | c3g9wC_ | Alignment |  | 14.6 | 14 | **PDB header:** cell adhesion<br>**Chain:** C: **PDB Molecule:** integrin beta-1d;<br>**PDBTitle:** crystal structure of talin2 f2-f3 in complex with the integrin beta1d2 cytoplasmic tail |
| 13 | c1q90L_ | Alignment |  | 11.1 | 30 | **PDB header:** photosynthesis<br>**Chain:** L: **PDB Molecule:** cytochrome b6f complex subunit petl;<br>**PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii |
| 14 | d1q90l_ | Alignment |  | 11.1 | 30 | **Fold:** Single transmembrane helix<br>**Superfamily:** PetL subunit of the cytochrome b6f complex<br>**Family:** PetL subunit of the cytochrome b6f complex |
| 15 | d1j46a_ | Alignment |  | 9.6 | 25 | **Fold:** HMG-box<br>**Superfamily:** HMG-box<br>**Family:** HMG-box |
| 16 | c1kuzB_ | Alignment |  | 9.2 | 14 | **PDB header:** cell adhesion<br>**Chain:** B: **PDB Molecule:** integrin beta-3;<br>**PDBTitle:** solution structure of the membrane proximal regions of2 alpha-iib and beta-3 integrins |
| 17 | d1uaza_ | Alignment |  | 8.1 | 13 | **Fold:** Family A G protein-coupled receptor-like<br>**Superfamily:** Family A G protein-coupled receptor-like<br>**Family:** Bacteriorhodopsin-like |
| 18 | c2bg9E_ | Alignment |  | 7.9 | 10 | **PDB header:** ion channel/receptor<br>**Chain:** E: **PDB Molecule:** acetylcholine receptor protein, gamma chain;<br>**PDBTitle:** refined structure of the nicotinic acetylcholine receptor2 at 4a resolution. |
| 19 | c3omyB_ | Alignment |  | 6.6 | 19 | **PDB header:** dna binding protein<br>**Chain:** B: **PDB Molecule:** protein tram;<br>**PDBTitle:** crystal structure of the ped208 tram n-terminal domain |
| 20 | d1i7na1 | Alignment |  | 6.1 | 33 | **Fold:** PreATP-grasp domain<br>**Superfamily:** PreATP-grasp domain<br>**Family:** Synapsin domain |
| 21 | c2etjA_ | Alignment | not modelled | 6.1 | 26 | **PDB header:** hydrolase<br>**Chain:** A: **PDB Molecule:** ribonuclease hii;<br>**PDBTitle:** crystal structure of ribonuclease hii (ec 3.1.26.4) (rnase hii)2 (tm0915) from thermotoga maritima at 1.74 a resolution |
| 22 | d2etja1 | Alignment | not modelled | 6.1 | 26 | **Fold:** Ribonuclease H-like motif<br>**Superfamily:** Ribonuclease H-like<br>**Family:** Ribonuclease H |
| 23 | d1qlec_ | Alignment | not modelled | 5.9 | 18 | **Fold:** Cytochrome c oxidase subunit III-like<br>**Superfamily:** Cytochrome c oxidase subunit III-like<br>**Family:** Cytochrome c oxidase subunit III-like |
| 24 | d1pk8a1 | Alignment | not modelled | 5.9 | 25 | **Fold:** PreATP-grasp domain<br>**Superfamily:** PreATP-grasp domain<br>**Family:** Synapsin domain |