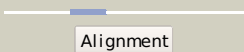

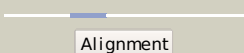

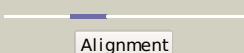

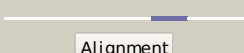

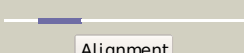

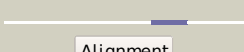



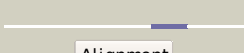




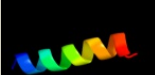

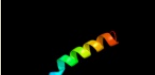



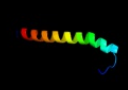



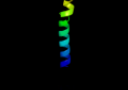



# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	C6Y4C1
Date	Sun Jul 8 11:45:08 BST 2012
Unique Job ID	5337bd441a2d6535

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1l4aE_</a>	 Alignment		24.6	33	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> E: <b>PDB Molecule:</b> synaphin a; <b>PDBTitle:</b> x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
2	<a href="#">c1kilE_</a>	 Alignment		21.3	33	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> complexin i snare-complex binding region; <b>PDBTitle:</b> three-dimensional structure of the complexin/snare complex
3	<a href="#">c3rl0j_</a>	 Alignment		18.4	27	<b>PDB header:</b> membrane protein/exocytosis <b>Chain:</b> J: <b>PDB Molecule:</b> syntaxin-1a; <b>PDBTitle:</b> truncated snare complex with complexin (p1)
4	<a href="#">c3bhpA_</a>	 Alignment		18.1	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0291 protein ynz; <b>PDBTitle:</b> crystal structure of upf0291 protein ynz from bacillus subtilis at resolution 2.0 a. northeast structural3 genomics consortium target sr384
5	<a href="#">c1dxzA_</a>	 Alignment		15.4	17	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholine receptor protein, alpha chain; <b>PDBTitle:</b> m2 transmembrane segment of alpha-subunit of nicotinic2 acetylcholine receptor from torpedo californica, nmr, 203 structures
6	<a href="#">c2jvdA_</a>	 Alignment		14.1	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0291 protein ynz; <b>PDBTitle:</b> solution nmr structure of the folded n-terminal fragment of2 upf0291 protein ynz from bacillus subtilis. northeast3 structural genomics target sr384-1-46
7	<a href="#">d1u58a2</a>	 Alignment		13.0	16	<b>Fold:</b> MHC antigen-recognition domain <b>Superfamily:</b> MHC antigen-recognition domain <b>Family:</b> MHC antigen-recognition domain
8	<a href="#">c2hepA_</a>	 Alignment		10.8	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0291 protein ynz; <b>PDBTitle:</b> solution nmr structure of the upf0291 protein ynz from2 bacillus subtilis. northeast structural genomics target3 sr384.
9	<a href="#">d2hepa1</a>	 Alignment		10.8	40	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> YnC-like <b>Family:</b> YnC-like
10	<a href="#">c1vryA_</a>	 Alignment		9.9	5	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine receptor alpha-1 chain; <b>PDBTitle:</b> second and third transmembrane domains of the alpha-12 subunit of human glycine receptor
11	<a href="#">d1gaka_</a>	 Alignment		9.3	22	<b>Fold:</b> Fertilization protein <b>Superfamily:</b> Fertilization protein <b>Family:</b> Fertilization protein

12	<a href="#">c3t98A_</a>	Alignment		9.0	32	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
13	<a href="#">c1b9xC_</a>	Alignment		8.6	17	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> protein (phosducin); <b>PDBTitle:</b> structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin
14	<a href="#">d1wgna_</a>	Alignment		7.2	19	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
15	<a href="#">c3cyoA_</a>	Alignment		7.2	10	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane protein; <b>PDBTitle:</b> structure of a longer thermalstable core domain of hiv-12 gp41 containing the enfuvirtide resistance mutation n43d3 and complementary mutation e137k
16	<a href="#">d1v54d_</a>	Alignment		7.1	16	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit IV <b>Family:</b> Mitochondrial cytochrome c oxidase subunit IV
17	<a href="#">c1gygA_</a>	Alignment		6.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase c; <b>PDBTitle:</b> r32 closed form of alpha-toxin from clostridium perfringens2 strain cer89l43
18	<a href="#">d1oede_</a>	Alignment		6.4	9	<b>Fold:</b> Neurotransmitter-gated ion-channel transmembrane pore <b>Superfamily:</b> Neurotransmitter-gated ion-channel transmembrane pore <b>Family:</b> Neurotransmitter-gated ion-channel transmembrane pore
19	<a href="#">d1v54i_</a>	Alignment		6.3	31	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIc <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIc
20	<a href="#">d2trcp_</a>	Alignment		5.8	33	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Phosducin
21	<a href="#">c1envA_</a>	Alignment	not modelled	5.8	0	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> hiv-1 envelope protein chimera consisting of a fragment of <b>PDBTitle:</b> atomic structure of the ectodomain from hiv-1 gp41
22	<a href="#">c2y69Q_</a>	Alignment	not modelled	5.7	16	<b>PDB header:</b> electron transport <b>Chain:</b> Q: <b>PDB Molecule:</b> cytochrome c oxidase subunit 4 isoform 1; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
23	<a href="#">c3a1qF_</a>	Alignment	not modelled	5.6	20	<b>PDB header:</b> gene regulation/signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> ubiquitin interaction motif-containing protein 1; <b>PDBTitle:</b> crystal structure of the mouse rap80 uims in complex with2 lys63-linked di-ubiquitin
24	<a href="#">d1rh5b_</a>	Alignment	not modelled	5.3	9	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Preprotein translocase SecE subunit <b>Family:</b> Preprotein translocase SecE subunit
25	<a href="#">d2buda1</a>	Alignment	not modelled	5.1	50	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Chromo domain-like <b>Family:</b> Chromo barrel domain