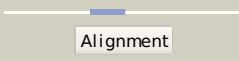
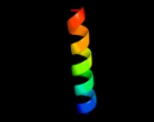


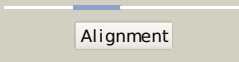

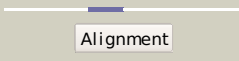

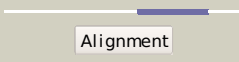

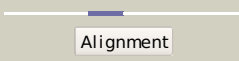

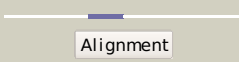
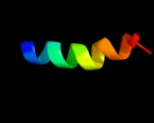
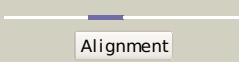
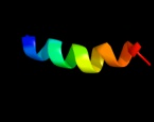
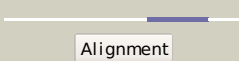

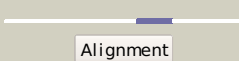
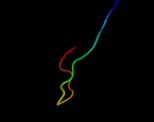
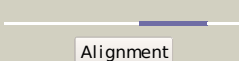







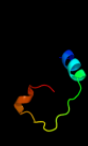




Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0ZSE6
Date	Wed Jun 6 09:28:32 BST 2012
Unique Job ID	97f40003d49e1245

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jp3A_			22.8	32	PDB header: transcription Chain: A; PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
2	c2zxeG_			21.1	21	PDB header: hydrolase/transport protein Chain: G; PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
3	d2axte1			20.5	13	Fold: Single transmembrane helix Superfamily: Cytochrome b559 subunits Family: Cytochrome b559 subunits
4	c2jo1A_			19.8	24	PDB header: hydrolase regulator Chain: A; PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in 2 micelles
5	c1x0gA_			17.0	21	PDB header: metal binding protein Chain: A; PDB Molecule: isca; PDBTitle: crystal structure of isca with the [2fe-2s] cluster
6	d2e74g1			15.5	12	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
7	c1vf5G_			15.0	12	PDB header: photosynthesis Chain: G; PDB Molecule: protein pet g; PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
8	d1vf5g_			15.0	12	Fold: Single transmembrane helix Superfamily: PetG subunit of the cytochrome b6f complex Family: PetG subunit of the cytochrome b6f complex
9	d1nt0a3			12.3	17	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
10	c2joxA_			10.7	26	PDB header: transcription Chain: A; PDB Molecule: churchill protein; PDBTitle: embryonic neural inducing factor churchill is not a dna-2 binding zinc finger protein: solution structure reveals a3 solvent-exposed beta-sheet and zinc binuclear cluster
11	c2d2aA_			10.0	22	PDB header: metal transport Chain: A; PDB Molecule: sufa protein; PDBTitle: crystal structure of escherichia coli sufa involved in2 biosynthesis of iron-sulfur clusters

12	d1ncfa3	Alignment		8.3	25	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
13	c1so9A_	Alignment		8.1	10	PDB header: metal transport Chain: A: PDB Molecule: cytochrome c oxidase assembly protein ctag; PDBTitle: solution structure of apocox11, 30 structures
14	d1so9a_	Alignment		8.1	10	Fold: Ctag/Cox11 Superfamily: Ctag/Cox11 Family: Ctag/Cox11
15	d1axha_	Alignment		8.1	25	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
16	c1p58C_	Alignment		7.9	11	PDB header: virus Chain: C: PDB Molecule: major envelope protein e; PDBTitle: complex organization of dengue virus membrane proteins as revealed by 2.9.5 angstrom cryo-em reconstruction
17	d1c99a_	Alignment		7.9	13	Fold: Transmembrane helix hairpin Superfamily: F1F0 ATP synthase subunit C Family: F1F0 ATP synthase subunit C
18	c2d1eA_	Alignment		7.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: phycocyanobilin:ferredoxin oxidoreductase; PDBTitle: crystal structure of pcy-a-biliverdin complex
19	d1ob1c1	Alignment		7.7	20	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Merozoite surface protein 1 (MSP-1)
20	d1n1ia1	Alignment		7.6	28	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Merozoite surface protein 1 (MSP-1)
21	c3n23E_	Alignment	not modelled	7.5	29	PDB header: hydrolase Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the high affinity complex between ouabain and the e2p form of the sodium-potassium pump
22	c2g18K_	Alignment	not modelled	7.5	22	PDB header: oxidoreductase Chain: K: PDB Molecule: phycocyanobilin:ferredoxin oxidoreductase; PDBTitle: crystal structure of nostoc sp. 7120 phycocyanobilin:ferredoxin2 oxidoreductase (pcya) apoprotein
23	c2kncA_	Alignment	not modelled	6.8	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alpha-iiB-beta3 transmembrane-cytoplasmic2 heterocomplex
24	d1b9wa1	Alignment	not modelled	6.7	28	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: Merozoite surface protein 1 (MSP-1)
25	c2gy9N_	Alignment	not modelled	6.2	26	PDB header: ribosome Chain: N: PDB Molecule: 30s ribosomal subunit protein s14; PDBTitle: structure of the 30s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and 3 protein components into cryo-em map emd-1056
26	c2y69Q_	Alignment	not modelled	5.9	11	PDB header: electron transport Chain: Q: PDB Molecule: cytochrome c oxidase subunit 4 isoform 1; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
27	c3iynR_	Alignment	not modelled	5.7	17	PDB header: virus Chain: R: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5

28	c2apnA_	Alignment	not modelled	5.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hi1723; PDBTitle: hi1723 solution structure
29	c2k1aA_	Alignment	not modelled	5.5	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: bicelle-embedded integrin alpha(iib) transmembrane segment
30	d1ncfb3	Alignment	not modelled	5.3	24	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
31	c1kdxB_	Alignment	not modelled	5.2	30	PDB header: transcription regulation complex Chain: B: PDB Molecule: creb; PDBTitle: kix domain of mouse cbp (creb binding protein) in complex2 with phosphorylated kinase inducible domain (pkid) of rat3 creb (cyclic amp response element binding protein), nmr 174 structures
32	d1v54d_	Alignment	not modelled	5.2	11	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit IV Family: Mitochondrial cytochrome c oxidase subunit IV
33	c3e07A_	Alignment	not modelled	5.1	25	PDB header: cytokine Chain: A: PDB Molecule: protein spaetzle; PDBTitle: crystal structure of spatze cystine knot
34	c1afoB_	Alignment	not modelled	5.1	24	PDB header: integral membrane protein Chain: B: PDB Molecule: glycophorin a; PDBTitle: dimeric transmembrane domain of human glycophorin a, nmr,2 20 structures