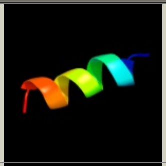
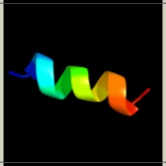
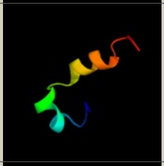
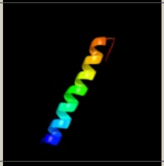
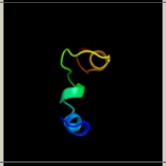
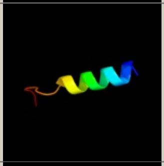
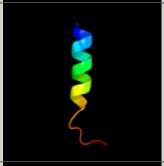
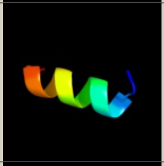
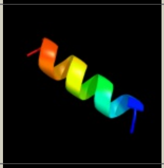
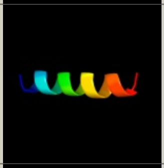
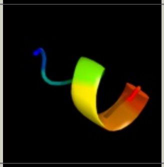
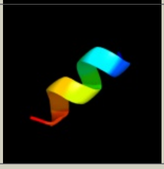
Phyre²

Email	l.a.kelley@imperial.ac.uk
Description	P77237
Date	Thu Jan 5 12:26:41 GMT 2012
Unique Job ID	e0ee91351ea76fe2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kdpH_	Alignment		23.8	36	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
2	c3kdpG_	Alignment		23.8	36	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**na+/k+ atpase gamma subunit transcript variant a; **PDBTitle:** crystal structure of the sodium-potassium pump
3	c2qjxA_	Alignment		22.7	32	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bim1; **PDBTitle:** structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
4	c2veqA_	Alignment		21.6	39	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** insights into kinetochore-dna interactions from the2 structure of cep3p
5	d2qjza1	Alignment		21.1	30	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
6	c2l2tA_	Alignment		18.6	27	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
7	c1wyoA_	Alignment		17.7	32	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microtubule-associated protein rp/eb family **PDBTitle:** solution structure of the ch domain of human microtubule-2 associated protein rp/eb family member 3
8	d1vk5a_	Alignment		12.9	30	**Fold:**Hypothetical protein At3g22680 **Superfamily:**Hypothetical protein At3g22680 **Family:**Hypothetical protein At3g22680
9	c1vk5A_	Alignment		12.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**expressed protein; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana at3g22680
10	d2gbsa1	Alignment		11.7	33	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
11	c3ixzB_	Alignment		11.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**potassium-transporting atpase subunit beta; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride

12	c3o0rC_	Alignment		11.1	35	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
13	d1m56d_	Alignment		10.7	40	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
14	c3b8eB_	Alignment		9.6	23	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
15	d1v5ka_	Alignment		9.5	32	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
16	c3dl8D_	Alignment		9.2	28	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**sece; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
17	c2kdnA_	Alignment		8.5	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein pfe0790c; **PDBTitle:** solution structure of pfe0790c, a putative bola-like2 protein from the protozoan parasite plasmodium falciparum.
18	c3o2eA_	Alignment		8.0	50	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**bola-like protein; **PDBTitle:** crystal structure of a bol-like protein from babesia bovis
19	d1ny8a_	Alignment		7.7	44	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
20	d1eysh2	Alignment		7.3	30	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
21	d1v9ja_	Alignment	not modelled	7.1	50	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**BolA-like **Family:**BolA-like
22	c3bq9A_	Alignment	not modelled	7.1	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
23	c3eopB_	Alignment	not modelled	7.0	20	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**thymocyte nuclear protein 1; **PDBTitle:** crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1
24	c3htuE_	Alignment	not modelled	6.1	25	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** crystal structure of the human vps25-vps20 subcomplex
25	c2ksdA_	Alignment	not modelled	5.2	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aerobic respiration control sensor protein arcb; **PDBTitle:** backbone structure of the membrane domain of e. coli2 histidine kinase receptor arcb, center for structures of3 membrane proteins (csmp) target 4310c
26	c2dhmA_	Alignment	not modelled	5.1	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bola; **PDBTitle:** solution structure of the bola protein from escherichia coli
27	d1xb4a2	Alignment	not modelled	5.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain