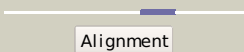
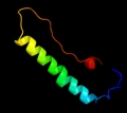
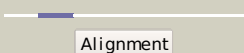

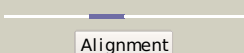
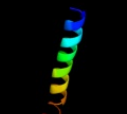
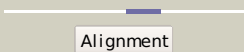

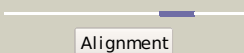


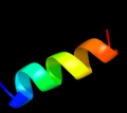


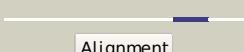

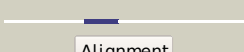

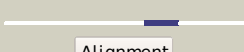
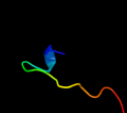




Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P27835
Date	Thu Jan 5 11:44:12 GMT 2012
Unique Job ID	ee10a5a7f838d33a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pidB_	 Alignment		15.3	17	PDB header: ligase Chain: B: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of human mitochondrial tyrosyl-trna synthetase in2 complex with an adenylate analog
2	c2wwaC_	 Alignment		13.4	38	PDB header: ribosome Chain: C: PDB Molecule: protein transport protein seb2; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
3	c3ipdB_	 Alignment		12.2	15	PDB header: exocytosis Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
4	c2vqzB_	 Alignment		11.8	22	PDB header: transcription Chain: B: PDB Molecule: polymerase basic protein 2; PDBTitle: structure of the cap-binding domain of influenza virus2 polymerase subunit pb2 with bound m7gtp
5	c2l9uA_	 Alignment		10.9	44	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
6	d2axtj1	 Alignment		10.6	47	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, PsbJ Family: PsbJ-like
7	c3d9wA_	 Alignment		10.2	30	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure analysis of nocardia farcinica arylamine2 n-acetyltransferase
8	d1qf8a_	 Alignment		8.8	73	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
9	c3dviB_	 Alignment		8.7	20	PDB header: membrane protein Chain: B: PDB Molecule: voltage-dependent n-type calcium channel subunit alpha-1b; PDBTitle: crystal structure of ca2+/cam-cav2.2 iq domain (without cloning2 artifact, hm to tv) complex
10	d1jb3a_	 Alignment		8.5	44	Fold: OB-fold Superfamily: TIMP-like Family: The laminin-binding domain of agrin
11	d1z9ha1	 Alignment		7.6	23	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain

12	c1m57H_	Alignment		7.4	6	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
13	c3io9B_	Alignment		7.1	33	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: biml12y in complex with mcl-1
14	d2b0la1	Alignment		6.6	60	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CodY HTH domain
15	c3dveB_	Alignment		6.6	20	PDB header: membrane protein Chain: B: PDB Molecule: voltage-dependent n-type calcium channel subunit alpha-1b; PDBTitle: crystal structure of ca2+/cam-cav2.2 iq domain complex
16	d1jwhc_	Alignment		5.8	73	Fold: Rubredoxin-like Superfamily: Casein kinase II beta subunit Family: Casein kinase II beta subunit
17	d1efya1	Alignment		5.8	31	Fold: Domain of poly(ADP-ribose) polymerase Superfamily: Domain of poly(ADP-ribose) polymerase Family: Domain of poly(ADP-ribose) polymerase
18	d2rd6a1	Alignment		5.7	31	Fold: Domain of poly(ADP-ribose) polymerase Superfamily: Domain of poly(ADP-ribose) polymerase Family: Domain of poly(ADP-ribose) polymerase
19	c1cw5A_	Alignment		5.6	67	PDB header: toxin Chain: A: PDB Molecule: type iia bacteriocin carnobacteriocin b2; PDBTitle: solution structure of carnobacteriocin b2
20	c2bbjB_	Alignment		5.5	16	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
21	c3rmrA_	Alignment	not modelled	5.5	37	PDB header: protein binding Chain: A: PDB Molecule: avirulence protein; PDBTitle: crystal structure of hyaloperonospora arabidopsidis atr1 effector2 domain
22	d1eysh2	Alignment	not modelled	5.5	26	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
23	c2hqlB_	Alignment	not modelled	5.4	22	PDB header: dna binding protein Chain: B: PDB Molecule: hypothetical protein mg376 homolog; PDBTitle: crystal structure of a small single-stranded dna binding2 protein from mycoplasma pneumoniae
24	d1y14b2	Alignment	not modelled	5.3	33	Fold: Dodecin subunit-like Superfamily: N-terminal, heterodimerisation domain of RBP7 (RpoE) Family: N-terminal, heterodimerisation domain of RBP7 (RpoE)
25	c2kegA_	Alignment	not modelled	5.3	35	PDB header: antimicrobial protein Chain: A: PDB Molecule: plnk; PDBTitle: nmr structure of plantaricin k in dpc-micelles
26	c2x11B_	Alignment	not modelled	5.2	36	PDB header: receptor/signaling protein Chain: B: PDB Molecule: ephrin-a5; PDBTitle: crystal structure of the complete epha2 ectodomain in2 complex with ephrin a5 receptor binding domain
27	d1shxa1	Alignment	not modelled	5.2	36	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Ephrin ectodomain