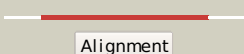
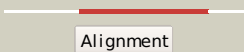
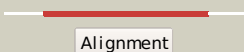
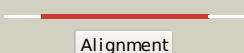
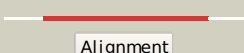
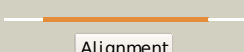
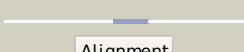
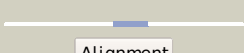
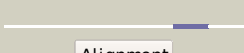
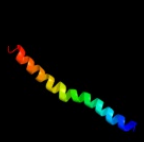


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ABD1
Date	Thu Jan 5 11:15:12 GMT 2012
Unique Job ID	70a11b18390b314b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hfxA_	 Alignment		100.0	29	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
2	c2w8aC_	 Alignment		100.0	27	PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
3	c2xq2A_	 Alignment		98.3	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vs9lt
4	d2a65a1	 Alignment		97.2	14	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
5	c2jlnA_	 Alignment		97.2	11	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
6	c3dh4A_	 Alignment		96.7	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
7	c3giaA_	 Alignment		90.6	9	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
8	c3lrcC_	 Alignment		88.3	14	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
9	c3gztF_	 Alignment		27.0	40	PDB header: virus Chain: F: PDB Molecule: outer capsid glycoprotein vp7; PDBTitle: vp7 reconstituted rotavirus dlp
10	c2kvIA_	 Alignment		24.5	40	PDB header: viral protein Chain: A: PDB Molecule: major outer capsid protein vp7; PDBTitle: nmr structure of the c-terminal domain of vp7
11	c2kncB_	 Alignment		19.8	10	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex

12	d2f2ha1	Alignment		10.2	40	Fold: Putative glucosidase YicI, C-terminal domain Superfamily: Putative glucosidase YicI, C-terminal domain Family: Putative glucosidase YicI, C-terminal domain
13	d1qmva_	Alignment		7.5	38	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
14	d1qq2a_	Alignment		7.2	31	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
15	c3pcqX_	Alignment		6.6	38	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem i 4.8k protein; PDBTitle: femtosecond x-ray protein nanocrystallography
16	c1vpzB_	Alignment		6.5	23	PDB header: rna binding protein Chain: B: PDB Molecule: carbon storage regulator homolog; PDBTitle: crystal structure of a putative carbon storage regulator protein2 (csra, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
17	c2jppB_	Alignment		6.4	15	PDB header: translation/rna Chain: B: PDB Molecule: translational repressor; PDBTitle: structural basis of rsmA/csra rna recognition: structure of2 rsmE bound to the shine-dalgarno sequence of hcna mrna
18	d1jb0x_	Alignment		6.3	38	Fold: Single transmembrane helix Superfamily: Subunit Psax of photosystem I reaction centre Family: Subunit Psax of photosystem I reaction centre
19	c1jb0X_	Alignment		6.3	38	PDB header: photosynthesis Chain: X: PDB Molecule: photosystem i subunit psax; PDBTitle: crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
20	c3kv1A_	Alignment		6.2	27	PDB header: transcription Chain: A: PDB Molecule: transcriptional repressor; PDBTitle: crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
21	d1jxha_	Alignment	not modelled	6.2	24	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
22	d1vpza_	Alignment	not modelled	5.9	23	Fold: CsrA-like Superfamily: CsrA-like Family: CsrA-like
23	c3l09B_	Alignment	not modelled	5.9	14	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
24	c3jycA_	Alignment	not modelled	5.5	11	PDB header: metal transport Chain: A: PDB Molecule: inward-rectifier k+ channel kir2.2; PDBTitle: crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
25	d2a7sa1	Alignment	not modelled	5.4	19	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
26	d1e2ya_	Alignment	not modelled	5.4	31	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
27	d1h6ia_	Alignment	not modelled	5.4	20	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
28	c3c02A_	Alignment	not modelled	5.3	16	PDB header: membrane protein Chain: A: PDB Molecule: aquaglyceroporin; PDBTitle: x-ray structure of the aquaglyceroporin from plasmodium falciparum

29	d2axtm1	Alignment	not modelled	5.3	27	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein M, PsbM Family: PsbM-like
30	c1t3oA	Alignment	not modelled	5.2	15	PDB header: rna binding protein Chain: A: PDB Molecule: carbon storage regulator; PDBTitle: solution structure of csra, a bacterial carbon storage2 regulatory protein
31	c2k10A	Alignment	not modelled	5.1	36	PDB header: antimicrobial protein Chain: A: PDB Molecule: ranatuerin-2csa; PDBTitle: conformational analysis of the broad-spectrum antibacterial2 peptide, rantuerin-2csa: identification of a full length3 helix-turn-helix motif