
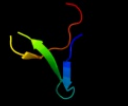





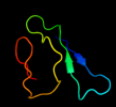
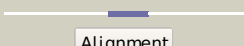
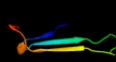
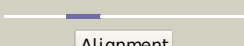
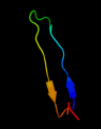
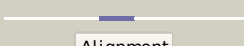
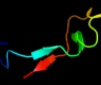

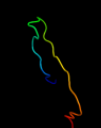






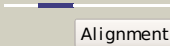

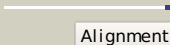













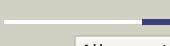

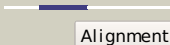

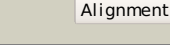
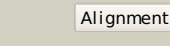

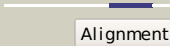

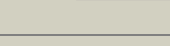


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	O13556
Date	Mon Jul 2 19:10:14 BST 2012
Unique Job ID	1ccd13067106070c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1j0sa_	 Alignment		26.3	30	Fold: beta-Trefoil Superfamily: Cytokine Family: Interleukin-1 (IL-1)
2	d1rwza1	 Alignment		20.3	13	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
3	c2h6oA_	 Alignment		19.3	22	PDB header: viral protein Chain: A: PDB Molecule: major outer envelope glycoprotein gp350; PDBTitle: epstein barr virus major envelope glycoprotein
4	c2vfbA_	 Alignment		14.2	17	PDB header: transferase Chain: A: PDB Molecule: arylamine n-acetyltransferase; PDBTitle: the structure of mycobacterium marinum arylamine n-2 acetyltransferase
5	d1ud9a1	 Alignment		12.0	5	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
6	c3bbnC_	 Alignment		11.8	13	PDB header: ribosome Chain: C: PDB Molecule: ribosomal protein s3; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
7	c3jrza_	 Alignment		10.2	23	PDB header: toxin Chain: A: PDB Molecule: ccdb; PDBTitle: ccdbvfi-formii-ph5.6
8	c2gy9C_	 Alignment		10.2	20	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal subunit protein s3; PDBTitle: structure of the 30s subunit of a pre-translocational e.2 coli ribosome obtained by fitting atomic models for rna and3 protein components into cryo-em map emd-1056
9	d1plqa1	 Alignment		10.1	15	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
10	d1t3ba2	 Alignment		8.6	19	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
11	c2uwiG_	 Alignment		8.3	57	PDB header: chaperone Chain: G: PDB Molecule: type iii export protein pscg; PDBTitle: structure of the heterotrimeric complex which regulates2 type iii secretion needle formation

12	d2nw8a1	 Alignment		8.2	25	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Bacterial tryptophan 2,3-dioxygenase
13	c3ph0C_	 Alignment		8.2	38	PDB header: chaperone Chain: C: PDB Molecule: ascg; PDBTitle: crystal structure of the heteromolecular chaperone, asce-ascg, from2 the type iii secretion system in aeromonas hydrophila
14	d1r0va3	 Alignment		8.1	23	Fold: MutS N-terminal domain-like Superfamily: tRNA-intron endonuclease N-terminal domain-like Family: tRNA-intron endonuclease N-terminal domain-like
15	c1hnwC_	 Alignment		8.0	20	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: structure of the thermus thermophilus 30s ribosomal subunit2 in complex with tetracycline
16	c1pnxC_	 Alignment		7.6	20	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: crystal structure of the wild type ribosome from e. coli, 2 30s subunit of 70s ribosome. this file, 1pnx, contains3 only molecules of the 30s ribosomal subunit. the 50s4 subunit is in the pdb file 1pny.
17	c2qbfC_	 Alignment		7.5	20	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: crystal structure of the bacterial ribosome from escherichia2 coli in complex with ribosome recycling factor (rrf). this3 file contains the 30s subunit of the second 70s ribosome.4 the entire crystal structure contains two 70s ribosomes and5 is described in remark 400.
18	d1gjwa1	 Alignment		6.5	36	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
19	c2nw7C_	 Alignment		6.4	25	PDB header: oxidoreductase Chain: C: PDB Molecule: tryptophan 2,3-dioxygenase; PDBTitle: crystal structure of tryptophan 2,3-dioxygenase (tdo) from2 xanthomonas campestris in complex with ferric heme.3 northeast structural genomics target xcr13
20	c1kuzB_	 Alignment		6.2	21	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: solution structure of the membrane proximal regions of2 alpha-iiB and beta-3 integrins
21	c3d12E_	 Alignment	not modelled	6.2	12	PDB header: hydrolase/membrane protein Chain: E: PDB Molecule: ephrin-b3; PDBTitle: crystal structures of nipah virus g attachment glycoprotein in complex2 with its receptor ephrin-b3
22	c1s1hN_	 Alignment	not modelled	6.2	50	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s29-b; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
23	d2qalc2	 Alignment	not modelled	6.0	20	Fold: Ribosomal protein S3 C-terminal domain Superfamily: Ribosomal protein S3 C-terminal domain Family: Ribosomal protein S3 C-terminal domain
24	c3utmC_	 Alignment	not modelled	6.0	24	PDB header: transferase/signaling protein Chain: C: PDB Molecule: axin-1; PDBTitle: crystal structure of a mouse tankyrase-axin complex
25	d1jjcb2	 Alignment	not modelled	6.0	33	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Domains B1 and B5 of PheRS-beta, PheT
26	c3k4xA_	 Alignment	not modelled	5.9	15	PDB header: dna binding protein/dna Chain: A: PDB Molecule: proliferating cell nuclear antigen; PDBTitle: eukaryotic sliding clamp pcna bound to dna
27	c2pnyA_	 Alignment	not modelled	5.8	16	PDB header: isomerase Chain: A: PDB Molecule: isopentenyl-diphosphate delta-isomerase 2; PDBTitle: structure of human isopentenyl-diphosphate delta-isomerase 2
28	c2p58C_	 Alignment	not modelled	5.6	21	PDB header: transport protein/chaperone Chain: C: PDB Molecule: putative type iii secretion protein yscg; PDBTitle: structure of the yersinia pestis type iii secretion system2

					needle protein yscf in complex with its chaperones3 ysce/yscg
29	c2iyjA_	Alignment	not modelled	5.6	19 PDB header: isomerase Chain: A: PDB Molecule: thiol disulfide interchange protein dsbc; PDBTitle: crystal structure of the n-terminal dimer domain of e.coli2 dsbc
30	d1w7ca1	Alignment	not modelled	5.5	10 Fold: Supersandwich Superfamily: Amine oxidase catalytic domain Family: Amine oxidase catalytic domain
31	d2axto1	Alignment	not modelled	5.3	15 Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: PsbO-like
32	c2zkqc_	Alignment	not modelled	5.1	16 PDB header: ribosomal protein/rna Chain: C: PDB Molecule: rna expansion segment es4; PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
33	c3h8dE_	Alignment	not modelled	5.1	63 PDB header: motor protein/signaling protein Chain: E: PDB Molecule: disabled homolog 2; PDBTitle: crystal structure of myosin vi in complex with dab2 peptide
34	d2uubc2	Alignment	not modelled	5.0	20 Fold: Ribosomal protein S3 C-terminal domain Superfamily: Ribosomal protein S3 C-terminal domain Family: Ribosomal protein S3 C-terminal domain