
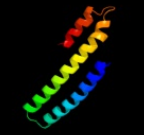

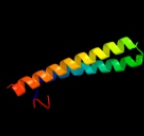











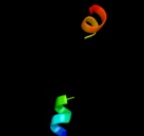

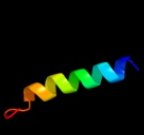



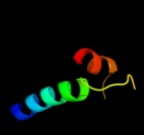

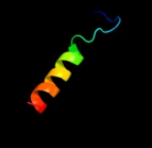

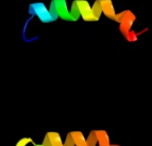
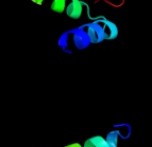
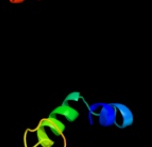

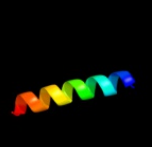
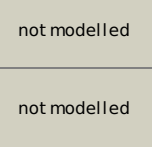


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P64530
Date	Thu Jan 5 12:09:14 GMT 2012
Unique Job ID	4b5cab8747d5a7a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hh7A_	 Alignment		99.9	16	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein csor; PDBTitle: crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
2	c3aaiB_	 Alignment		99.9	19	PDB header: transcription Chain: B: PDB Molecule: copper homeostasis operon regulatory protein; PDBTitle: x-ray crystal structure of csor from thermus thermophilus hb8
3	c1paqA_	 Alignment		39.1	15	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
4	d1paqa_	 Alignment		39.1	15	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
5	c3juia_	 Alignment		34.5	15	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
6	c2p5tA_	 Alignment		32.6	19	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator peza; PDBTitle: molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
7	c2nv2U_	 Alignment		25.1	21	PDB header: lyase/transferase Chain: U: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
8	c3zs9D_	 Alignment		16.5	50	PDB header: hydrolase/transport protein Chain: D: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
9	c2qycA_	 Alignment		12.2	5	PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
10	d1ivsa1	 Alignment		11.7	9	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Valyl-tRNA synthetase (ValRS) C-terminal domain
11	c3femB_	 Alignment		10.8	12	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae

12	c3cveC_	Alignment		8.9	18	PDB header: signaling protein Chain: C: PDB Molecule: homer protein homolog 1; PDBTitle: crystal structure of the carboxy terminus of homer1
13	d2igsal	Alignment		8.2	8	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PA2222-like
14	d1ev0a_	Alignment		8.1	25	Fold: Cell division protein MinE topological specificity domain Superfamily: Cell division protein MinE topological specificity domain Family: Cell division protein MinE topological specificity domain
15	d1kkg_	Alignment		8.0	4	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
16	d1obba2	Alignment		8.0	16	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
17	d1josa_	Alignment		7.2	9	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
18	d1tiza_	Alignment		6.9	7	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
19	c3oq3A_	Alignment		6.9	17	PDB header: cytokine/viral protein Chain: A: PDB Molecule: interferon alpha-5; PDBTitle: structural basis of type-i interferon sequestration by a poxvirus2 decoy receptor
20	c2ovcA_	Alignment		6.7	30	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily kqt member 4; PDBTitle: crystal structure of a coiled-coil tetramerization domain from kv7.42 channels
21	d2oa5a1	Alignment	not modelled	6.7	12	Fold: BLRF2-like Superfamily: BLRF2-like Family: BLRF2-like
22	c2gtlO_	Alignment	not modelled	6.2	21	PDB header: oxygen storage/transport Chain: O: PDB Molecule: extracellular hemoglobin linker I3 subunit; PDBTitle: lumbricus erythrocrutorin at 3.5a resolution
23	c1cffB_	Alignment	not modelled	6.0	30	PDB header: calmodulin Chain: B: PDB Molecule: protein (calcium pump); PDBTitle: nmr solution structure of a complex of calmodulin with a2 binding peptide of the ca2+-pump
24	c2kneB_	Alignment	not modelled	6.0	31	PDB header: metal transport Chain: B: PDB Molecule: atpase, ca++ transporting, plasma membrane 4; PDBTitle: calmodulin wraps around its binding domain in the plasma2 membrane ca2+ pump anchored by a novel 18-1 motif
25	d1up7a2	Alignment	not modelled	5.8	16	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
26	d1q4ra_	Alignment	not modelled	5.5	5	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
27	c3nepX_	Alignment	not modelled	5.1	21	PDB header: oxidoreductase Chain: X: PDB Molecule: malate dehydrogenase; PDBTitle: 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber