








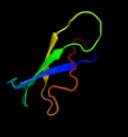





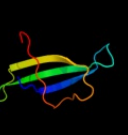



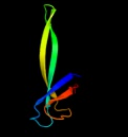

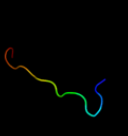
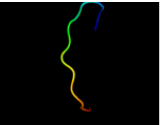

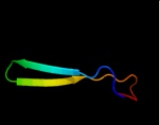

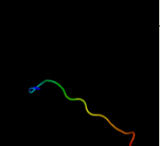

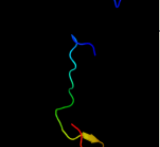
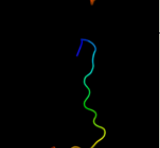



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AEJ8
Date	Thu Jan 5 11:23:31 GMT 2012
Unique Job ID	d60b99f087419ed0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qw7a1	 Alignment		100.0	39	Fold: OB-fold Superfamily: EutN/CcmL-like Family: EutN/CcmL-like
2	d2hd3a1	 Alignment		100.0	97	Fold: OB-fold Superfamily: EutN/CcmL-like Family: EutN/CcmL-like
3	d2rcfa1	 Alignment		100.0	41	Fold: OB-fold Superfamily: EutN/CcmL-like Family: EutN/CcmL-like
4	d1jjcb3	 Alignment		36.5	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Myf domain
5	c2akwB_	 Alignment		29.7	17	PDB header: ligase Chain: B; PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: crystal structure of t.thermophilus phenylalanyl-trna synthetase2 complexed with p-cl-phenylalanine
6	d2z1ca1	 Alignment		20.5	29	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
7	c3bbnQ_	 Alignment		19.4	16	PDB header: ribosome Chain: Q; PDB Molecule: ribosomal protein s17; PDBTitle: homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
8	c3bu2B_	 Alignment		17.0	18	PDB header: rna binding protein Chain: B; PDB Molecule: putative trna-binding protein; PDBTitle: crystal structure of a trna-binding protein from2 staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target syr77
9	d2ot2a1	 Alignment		16.7	36	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
10	d2gy9q1	 Alignment		15.8	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
11	d2z1ea2	 Alignment		15.5	38	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like

12	c3d3rA	Alignment		13.8	29	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hupc/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
13	c1rfoC	Alignment		13.8	55	PDB header: viral protein Chain: C: PDB Molecule: whisker antigen control protein; PDBTitle: trimeric foldon of the t4 phagehead fibrin
14	d2id1a1	Alignment		13.1	20	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: lojap/YbeB-like
15	d3d3ra1	Alignment		12.9	21	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
16	d2zoda2	Alignment		11.2	31	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
17	c3balB	Alignment		10.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: acetylacetone-cleaving enzyme; PDBTitle: crystal structure of an acetylacetone dioxygenase from2 acinetobacter johnsonii
18	d1e8ca2	Alignment		10.7	19	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
19	d2jfga2	Alignment		10.2	24	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
20	d1g2914	Alignment		9.4	22	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
21	c1avyA	Alignment	not modelled	7.7	55	PDB header: coiled coil Chain: A: PDB Molecule: fibrin; PDBTitle: fibrin deletion mutant m (bacteriophage t4)
22	c1ox3A	Alignment	not modelled	7.5	55	PDB header: chaperone Chain: A: PDB Molecule: fibrin; PDBTitle: crystal structure of mini-fibrin
23	d1wpga1	Alignment	not modelled	7.3	28	Fold: Double-stranded beta-helix Superfamily: Calcium ATPase, transduction domain A Family: Calcium ATPase, transduction domain A
24	d3c9ua2	Alignment	not modelled	7.2	38	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
25	c3mvnA	Alignment	not modelled	7.2	31	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- PDBTitle: crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
26	d1c0aa2	Alignment	not modelled	7.1	15	Fold: DCoH-like Superfamily: GAD domain-like Family: GAD domain
27	c1e8cB	Alignment	not modelled	7.0	19	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramoylalanyl-d-glutamate--2,6- PDBTitle: structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
28	c3b8eC	Alignment	not modelled	6.9	31	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump

29	d1vk3a3	Alignment	not modelled	6.8	17	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
30	c3upsA	Alignment	not modelled	6.6	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: iojap-like protein; PDBTitle: crystal structure of iojap-like protein from zymomonas mobilis
31	d1ylqa1	Alignment	not modelled	6.5	20	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
32	d2atzal	Alignment	not modelled	6.3	25	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: HP0184-like
33	c2opkC	Alignment	not modelled	6.1	70	PDB header: isomerase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
34	d2c42a3	Alignment	not modelled	6.0	35	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
35	c1s1hQ	Alignment	not modelled	5.9	13	PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein s11; 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.
36	c3b9bA	Alignment	not modelled	5.9	28	PDB header: hydrolase Chain: A: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
37	c3fq6A	Alignment	not modelled	5.6	40	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
38	c3ixzA	Alignment	not modelled	5.6	28	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
39	c3p9zA	Alignment	not modelled	5.2	12	PDB header: ligase Chain: A: PDB Molecule: uroporphyrinogen iii cosynthase (hemd); PDBTitle: crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
40	c3ajvA	Alignment	not modelled	5.2	29	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: splicing endonuclease from aeropyrum pernix
41	c1v1hB	Alignment	not modelled	5.1	50	PDB header: adenovirus Chain: B: PDB Molecule: fibrin, fiber protein; PDBTitle: adenovirus fibre shaft sequence n-terminally fused to the2 bacteriophage t4 fibrin foldon trimerisation motif with3 a short linker
42	c2gq1A	Alignment	not modelled	5.1	20	PDB header: hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphatase; PDBTitle: crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
43	d2o5aa1	Alignment	not modelled	5.1	24	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: iojap/YbeB-like