
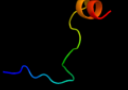



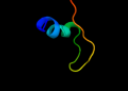
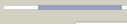
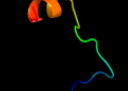












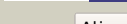

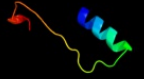

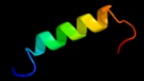
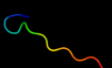
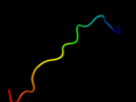
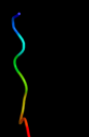


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A5A619
Date	Thu Jan 5 10:55:24 GMT 2012
Unique Job ID	a40be18e7f12bb4e

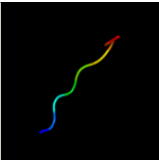
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v29b_	 Alignment		24.8	13	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
2	d1xg8a_	 Alignment		22.7	30	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: YuzD-like
3	d2pofa1	 Alignment		22.0	33	Fold: HIT-like Superfamily: HIT-like Family: CDH-like
4	d1ugpb_	 Alignment		20.0	35	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
5	c3dlrA_	 Alignment		18.5	42	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv2 integrase
6	c2x5cB_	 Alignment		13.5	75	PDB header: viral protein Chain: B: PDB Molecule: hypothetical protein orf131; PDBTitle: crystal structure of hypothetical protein orf131 from2 pyrobaculum spherical virus
7	d2qrda1	 Alignment		12.2	50	Fold: TBP-like Superfamily: KA1-like Family: Ssp2 C-terminal domain-like
8	c3qz9D_	 Alignment		12.1	20	PDB header: lyase Chain: D: PDB Molecule: co-type nitrile hydratase beta subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
9	c3l2tB_	 Alignment		9.5	42	PDB header: recombination/dna Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
10	d1c0ma2	 Alignment		8.8	8	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
11	d2ipqx1	 Alignment		7.7	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: STY4665 C-terminal domain-like

12	c2de0X_	Alignment		7.6	19	PDB header: transferase Chain: X: PDB Molecule: alpha-(1,6)-fucosyltransferase; PDBTitle: crystal structure of human alpha 1,6-fucosyltransferase, fut8
13	d1u5ta1	Alignment		6.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
14	c2x5fB_	Alignment		6.6	25	PDB header: transferase Chain: B: PDB Molecule: aspartate_tyrosine_phenylalanine pyridoxal-5' PDBTitle: crystal structure of the methicillin-resistant2 staphylococcus aureus sar2028, an3 aspartate_tyrosine_phenylalanine pyridoxal-5'-phosphate4 dependent aminotransferase
15	d1cxqa_	Alignment		6.4	8	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
16	c2b9sA_	Alignment		6.3	27	PDB header: isomerase/dna Chain: A: PDB Molecule: topoisomerase i-like protein; PDBTitle: crystal structure of heterodimeric I. donovani2 topoisomerase i-vanadate-dna complex
17	c3f1f4_	Alignment		5.8	67	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: crystal structure of a translation termination complex2 formed with release factor rf2. this file contains the 50s3 subunit of one 70s ribosome. the entire crystal structure4 contains two 70s ribosomes as described in remark 400.

18 [c2wh44_](#)

Alignment



5.3

67

PDB header:ribosome
Chain: 4: **PDB Molecule:**50s ribosomal protein l31;
PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome