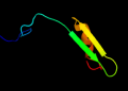
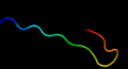
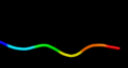
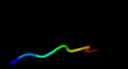


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P56257
Date	Thu Jan 5 12:06:19 GMT 2012
Unique Job ID	822a43d2819a0488

Detailed template information

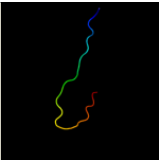
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2iuba1	 Alignment		35.7	27	Fold: CorA soluble domain-like Superfamily: CorA soluble domain-like Family: CorA soluble domain-like
2	c2bbjB_	 Alignment		22.0	27	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
3	d1dmla1	 Alignment		11.5	33	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
4	c3fo8D_	 Alignment		7.5	37	PDB header: viral protein Chain: D: PDB Molecule: tail sheath protein gp18; PDBTitle: crystal structure of the bacteriophage t4 tail sheath2 protein, protease resistant fragment gp18pr
5	c3nkgA_	 Alignment		7.1	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein geba250068378; PDBTitle: crystal structure of geba250068378 from sulfurospirillum deleyianum
6	c3ghpA_	 Alignment		6.9	75	PDB header: structural protein Chain: A: PDB Molecule: cellulosomal scaffoldin adaptor protein b; PDBTitle: structure of the second type ii cohesin module from the2 adaptor scaa scaffoldin of acetivibrio cellulolyticus3 (including long c-terminal linker)
7	d1t4za_	 Alignment		6.7	30	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: KaiB-like
8	d2bm3a1	 Alignment		6.5	75	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III
9	d1zv9a1	 Alignment		6.5	50	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III
10	d1tyja1	 Alignment		6.2	63	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III
11	c2b59A_	 Alignment		6.1	75	PDB header: hydrolase/structural protein Chain: A: PDB Molecule: cog1196: chromosome segregation atpases; PDBTitle: the type ii cohesin dockerin complex

12	c3fnkA_	Alignment		5.9	75	PDB header: structural protein Chain: A: PDB Molecule: cellulosomal scaffoldin adaptor protein b; PDBTitle: crystal structure of the second type ii cohesin module from2 the cellulosomal adaptor scaa scaffoldin of acetivibrio3 cellulolyticus
13	c3izbT_	Alignment		5.9	71	PDB header: ribosome Chain: T: PDB Molecule: 40s ribosomal protein rps21 (s21e); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
14	c1dmlG_	Alignment		5.4	33	PDB header: dna binding protein/transferase Chain: G: PDB Molecule: dna polymerase processivity factor; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-2 terminus of hsv pol

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[c3fcgB_](#)

Alignment



5.4

23

PDB header:membrane protein, protein transport
Chain: B: **PDB Molecule:**f1 capsule-anchoring protein;
PDBTitle: crystal structure analysis of the middle domain of the2
caf1a usher