



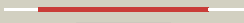







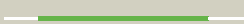




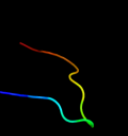












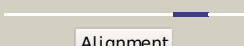
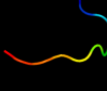
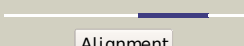

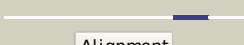





Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P61316
Date	Thu Jan 5 12:07:20 GMT 2012
Unique Job ID	649a31a7dbbcbdee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1iwlA_	 Alignment		100.0	99	Fold: LolA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: Outer-membrane lipoproteins carrier protein LolA
2	c2w7qB_	 Alignment		100.0	35	PDB header: protein transport Chain: B: PDB Molecule: outer-membrane lipoprotein carrier protein; PDBTitle: structure of pseudomonas aeruginosa lola
3	c3buuB_	 Alignment		99.7	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized lola superfamily protein ne2245; PDBTitle: crystal structure of lola superfamily protein ne2245 from2 nitrosomonas europaea
4	c3bk5A_	 Alignment		99.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative outer membrane lipoprotein-sorting protein; PDBTitle: crystal structure of putative outer membrane lipoprotein-sorting2 protein domain from vibrio parahaemolyticus
5	c2v43A_	 Alignment		99.0	10	PDB header: regulator Chain: A: PDB Molecule: sigma-e factor regulatory protein rseb; PDBTitle: crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
6	c2yzvA_	 Alignment		98.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha1012; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
7	c3mhaB_	 Alignment		58.3	13	PDB header: lipid binding protein Chain: B: PDB Molecule: lipoprotein lprg; PDBTitle: crystal structure of lprg from mycobacterium tuberculosis bound to pim
8	d2byoa1	 Alignment		25.7	9	Fold: LolA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: LppX-like
9	c3gf5A_	 Alignment		13.1	27	PDB header: structural protein Chain: A: PDB Molecule: major vault protein; PDBTitle: crystal structure of the p21 r1-r7 n-terminal domain of murine mvp
10	c3r2cJ_	 Alignment		11.5	33	PDB header: transcription/rna Chain: J: PDB Molecule: 30s ribosomal protein s10; PDBTitle: crystal structure of antitermination factors nusB and nusE in complex2 with boxA rna
11	c2f9jP_	 Alignment		9.3	21	PDB header: rna binding protein Chain: P: PDB Molecule: splicing factor 3b subunit 1; PDBTitle: 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155

12	d2jnaa1	 Alignment		9.1	41	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
13	dlo5ua_	 Alignment		8.8	18	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
14	dlquba5	 Alignment		7.2	13	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
15	dlc1za5	 Alignment		7.1	13	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
16	dlyrta1	 Alignment		7.1	9	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: N-acetylglucosamine-6-phosphate deacetylase, NagA
17	dlgwma_	 Alignment		6.1	11	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 29 carbohydrate binding module, CBM29
18	dlzaka2	 Alignment		5.8	15	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
19	c2ky8A_	 Alignment		5.7	33	PDB header: transcription/dna Chain: A: PDB Molecule: methyl-cpg-binding domain protein 2; PDBTitle: solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence

20 [dliwma_](#)

Alignment



5.6

10

Fold:LolA-like prokaryotic lipoproteins and lipoprotein localization factors

Superfamily:Prokaryotic lipoproteins and lipoprotein localization factors

Family:Outer membrane lipoprotein receptor LolB