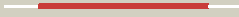




























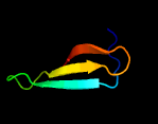



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1411c_(lprG)_1587778_1588488
Date	Wed Jul 31 22:05:52 BST 2019
Unique Job ID	b1c73d673a2e1d2b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mhaB_	 Alignment		100.0	100	PDB header: lipid binding protein Chain: B: PDB Molecule: lipoprotein lprg; PDBTitle: crystal structure of lprg from mycobacterium tuberculosis bound to pim
2	d2byoa1	 Alignment		100.0	30	Fold: LoLA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: LppX-like
3	c4qa8A_	 Alignment		100.0	30	PDB header: lipid transport Chain: A: PDB Molecule: putative lipoprotein lprf; PDBTitle: crystal structure of lprf from mycobacterium bovis
4	c3buuB_	 Alignment		98.6	12	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
5	c4mxtA_	 Alignment		98.0	11	PDB header: protein transport Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an outer-membrane lipoprotein carrier protein2 (bacuni_04723) from bacteroides uniformis atcc 8492 at 1.40 a3 resolution
6	c6in8A_	 Alignment		97.3	13	PDB header: membrane protein Chain: A: PDB Molecule: sigma factor algu regulatory protein mucb; PDBTitle: crystal structure of mucb
7	c2v43A_	 Alignment		94.9	15	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
8	c3bk5A_	 Alignment		92.6	10	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
9	c4z48B_	 Alignment		88.5	13	PDB header: structural biology, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf1329 family protein (despig_00262) from2 desulfovibrio piger atcc 29098 at 1.75 a resolution
10	c2w7qB_	 Alignment		86.1	9	PDB header: protein transport Chain: B: PDB Molecule: outer-membrane lipoprotein carrier protein; PDBTitle: structure of pseudomonas aeruginosa lola
11	d1iwla_	 Alignment		66.4	14	Fold: LoLA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: Outer-membrane lipoproteins carrier protein LoLA

12	c3woaA	Alignment		54.0	6	PDB header: dna binding protein, sugar binding prote Chain: A: PDB Molecule: repressor protein ci, maltose-binding periplasmic protein; PDBTitle: crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
13	c4mjsQ	Alignment		45.5	38	PDB header: transferase/protein binding Chain: Q: PDB Molecule: protein kinase c zeta type; PDBTitle: crystal structure of a pb1 complex
14	c4a4fA	Alignment		19.6	15	PDB header: rna binding protein Chain: A: PDB Molecule: survival of motor neuron-related-splicing factor 30; PDBTitle: solution structure of spf30 tudor domain in complex with symmetrically2 dimethylated arginine
15	d1mhna	Alignment		19.1	11	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
16	c3ls1A	Alignment		18.3	12	PDB header: photosynthesis Chain: A: PDB Molecule: sll1638 protein; PDBTitle: crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
17	d2d9ta1	Alignment		16.7	17	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
18	c3pnwX	Alignment		16.4	18	PDB header: protein binding/immune system Chain: X: PDB Molecule: tudor domain-containing protein 3; PDBTitle: crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab
19	c1g5vA	Alignment		16.2	11	PDB header: translation Chain: A: PDB Molecule: survival motor neuron protein 1; PDBTitle: solution structure of the tudor domain of the human smn2 protein
20	c2d9tA	Alignment		16.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tudor domain-containing protein 3; PDBTitle: solution structure of the tudor domain of tudor domain2 containing protein 3 from mouse
21	d1ueba2	Alignment	not modelled	14.5	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
22	c6gwjD	Alignment	not modelled	13.3	10	PDB header: rna binding protein Chain: D: PDB Molecule: ekc/keops complex subunit gon7; PDBTitle: protein complex
23	d1v0aa1	Alignment	not modelled	12.9	9	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: CBM11
24	d1jrma	Alignment	not modelled	12.1	24	Fold: YggU-like Superfamily: YggU-like Family: YggU-like
25	c6e5fA	Alignment	not modelled	9.1	23	PDB header: lipid binding protein Chain: A: PDB Molecule: lipid binding protein lpqn; PDBTitle: crystal structure of lpqn involved in cell envelope biogenesis of2 mycobacterium tuberculosis
26	d2gysa2	Alignment	not modelled	7.4	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
27	c2m1hA	Alignment	not modelled	7.1	11	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor s-ii; PDBTitle: solution structure of a pwwp domain from trypanosoma brucei
28	c4f98A	Alignment	not modelled	7.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf2790 family protein (pa3229) from2 pseudomonas aeruginosa pao1 at 1.26 a resolution
29	c2lojA	Alignment	not modelled	6.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: solution nmr structure of tstm1273 from salmonella

						typhimurium lt2,2 nesg target stt322, csgid target idp01027 and oosp target tstm1273
30	c2jraB_	Alignment	not modelled	6.2	10	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: protein rpa2121; PDBTitle: a novel domain-swapped solution nmr structure of protein rpa2121 from2 rhodopseudomonas palustris. northeast structural genomics target rpt6
31	c5o60Y_	Alignment	not modelled	6.0	21	PDB header: ribosome Chain: Y; PDB Molecule: 50s ribosomal protein l28; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
32	c6gvwJ_	Alignment	not modelled	5.9	33	PDB header: signaling protein Chain: J; PDB Molecule: brca1-a complex subunit rap80; PDBTitle: crystal structure of the brca1-a complex
33	c5e7tl_	Alignment	not modelled	5.5	21	PDB header: viral protein Chain: I; PDB Molecule: major structural protein 1; PDBTitle: structure of the tripod (bppuct-a-l) from the baseplate of2 bacteriophage tuc2009
34	c3p8dB_	Alignment	not modelled	5.5	16	PDB header: protein binding Chain: B; PDB Molecule: medulloblastoma antigen mu-mb-50.72; PDBTitle: crystal structure of the second tudor domain of human phf20 (homodimer2 form)
35	c2x34A_	Alignment	not modelled	5.4	18	PDB header: carbohydrate-binding protein Chain: A; PDB Molecule: cellulose-binding protein, x158; PDBTitle: structure of a polyisoprenoid binding domain from saccharophagus2 degradans implicated in plant cell wall breakdown
36	c5x7hA_	Alignment	not modelled	5.2	13	PDB header: transferase Chain: A; PDB Molecule: cycloisomaltooligosaccharide glucanotransferase; PDBTitle: crystal structure of paenibacillus sp. 598k2 cycloisomaltooligosaccharide glucanotransferase complexed with3 cycloisomaltoheptaose
37	c2hqxB_	Alignment	not modelled	5.2	9	PDB header: transcription Chain: B; PDB Molecule: p100 co-activator tudor domain; PDBTitle: crystal structure of human p100 tudor domain conserved2 region