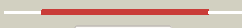
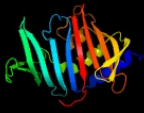

















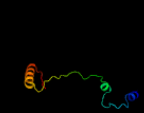





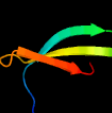

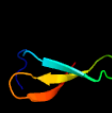

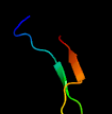



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1270c_(lprA)_1419020_1419754
 Date Wed Jul 31 22:05:36 BST 2019
 Unique Job ID 91324ac340e87512

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mhaB_	 Alignment		100.0	38	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	24	PDB header: lipid transport Chain: A: PDB Molecule: putative lipoprotein lprf; PDBTitle: crystal structure of lprf from mycobacterium bovis
4	c3buuB_	 Alignment		98.4	8	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		97.4	13	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		96.6	15	PDB header: membrane protein Chain: A: PDB Molecule: sigma factor algu regulatory protein mucb; PDBTitle: crystal structure of mucb
7	c3bk5A_	 Alignment		95.6	9	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
8	c2v43A_	 Alignment		94.6	12	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
9	c4z48B_	 Alignment		91.9	10	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	c3woaA_	 Alignment		67.1	12	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
11	c2w7qB_	 Alignment		65.0	8	PDB header: protein transport Chain: B: PDB Molecule: outer-membrane lipoprotein carrier protein; PDBTitle: structure of pseudomonas aeruginosa lola

12	d1mhna_	Alignment		24.4	14	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
13	d1iwa_	Alignment		24.1	13	Fold: LoIA-like prokaryotic lipoproteins and lipoprotein localization factors Superfamily: Prokaryotic lipoproteins and lipoprotein localization factors Family: Outer-membrane lipoproteins carrier protein LoIA
14	c4a4fA_	Alignment		22.6	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	c1g5vA_	Alignment		21.1	14	PDB header: translation Chain: A: PDB Molecule: survival motor neuron protein 1; PDBTitle: solution structure of the tudor domain of the human smn2 protein
16	c2d9tA_	Alignment		18.8	9	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
17	c3pnwX_	Alignment		18.7	9	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
18	d2d9ta1	Alignment		16.4	9	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
19	d1ueba2	Alignment		12.2	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
20	c3uc0B_	Alignment		11.1	28	PDB header: viral protein/immune system Chain: B: PDB Molecule: envelope protein; PDBTitle: crystal structure of domain i of the envelope glycoprotein ectodomain2 from dengue virus serotype 4 in complex with the fab fragment of the3 chimpanzee monoclonal antibody 5h2
21	c6gwjD_	Alignment	not modelled	9.0	10	PDB header: rna binding protein Chain: D: PDB Molecule: ekc/keops complex subunit gon7; PDBTitle: protein complex
22	c6h3iA_	Alignment	not modelled	8.9	21	PDB header: protein transport Chain: A: PDB Molecule: protein involved in gliding motility sprai; PDBTitle: structural snapshots of the type 9 protein translocon
23	c4onyB_	Alignment	not modelled	6.9	22	PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein family 5; PDBTitle: crystal structure of a abc transporter, periplasmic substrate-binding2 protein from brucella melitensis
24	c2m1hA_	Alignment	not modelled	6.7	6	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor s-ii; PDBTitle: solution structure of a pwwp domain from trypanosoma brucei
25	c5e7tl_	Alignment	not modelled	6.5	23	PDB header: viral protein Chain: I: PDB Molecule: major structural protein 1; PDBTitle: structure of the tripod (bpuct-a-i) from the baseplate of2 bacteriophage tuc2009
26	d1x9la_	Alignment	not modelled	6.0	15	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: DR1885-like metal-binding protein Family: DR1885-like metal-binding protein
27	d1j0ha2	Alignment	not modelled	6.0	15	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
28	c6epzA_	Alignment	not modelled	6.0	26	PDB header: transport protein Chain: A: PDB Molecule: periplasmic alpha-galactoside-binding protein; PDBTitle: structure of the periplasmic binding protein melb

					(atu4661) in complex2 with melibiose from agrobacterium fabrum c58
29	d1igqa_	Alignment	not modelled	5.8	19 Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Transcriptional repressor protein KorB
30	c4mjsQ_	Alignment	not modelled	5.8	11 PDB header: transferase/protein binding Chain: Q: PDB Molecule: protein kinase c zeta type; PDBTitle: crystal structure of a pb1 complex
31	d1erna2	Alignment	not modelled	5.5	15 Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
32	d2hqxa1	Alignment	not modelled	5.4	12 Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
33	c2hqxB_	Alignment	not modelled	5.4	12 PDB header: transcription Chain: B: PDB Molecule: p100 co-activator tudor domain; PDBTitle: crystal structure of human p100 tudor domain conserved2 region
34	d1zlqa1	Alignment	not modelled	5.4	22 Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
35	c4hzuS_	Alignment	not modelled	5.4	17 PDB header: hydrolase, transport protein Chain: S: PDB Molecule: predicted membrane protein; PDBTitle: structure of a bacterial energy-coupling factor transporter
36	d2z15a1	Alignment	not modelled	5.2	35 Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
37	c3m8uA_	Alignment	not modelled	5.2	17 PDB header: transport protein Chain: A: PDB Molecule: heme-binding protein a; PDBTitle: crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)
38	c3zk0A_	Alignment	not modelled	5.1	18 PDB header: chaperone Chain: A: PDB Molecule: sco3965; PDBTitle: the crystal structure of a cu(i) metallochaperone from2 streptomyces lividans in its apo form
39	c5o60Y_	Alignment	not modelled	5.0	11 PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l28; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis