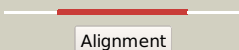



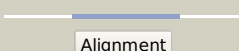
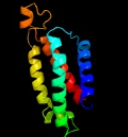
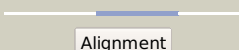


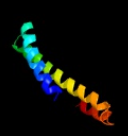
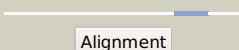

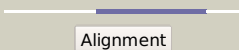

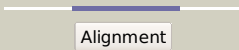

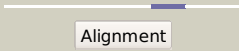

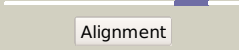





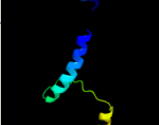





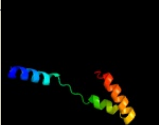


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3277 (-)_3659875_3660693
Date	Thu Aug 8 16:20:48 BST 2019
Unique Job ID	227a452766d31e6a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mm1A_	 Alignment		98.7	18	PDB header: membrane protein Chain: A: PDB Molecule: dolichol monophosphate mannose synthase; PDBTitle: dolichyl phosphate mannose synthase in complex with gdp and dolichyl2 phosphate mannose
2	c4px7A_	 Alignment		85.1	22	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pggp
3	c5khnB_	 Alignment		26.9	7	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
4	c6ebuA_	 Alignment		26.4	14	PDB header: hydrolase Chain: A: PDB Molecule: lpxe; PDBTitle: crystal structure of aquifex aeolicus lpXe
5	c4rfsS_	 Alignment		24.4	18	PDB header: hydrolase, transport protein Chain: S: PDB Molecule: substrate binding prtein s; PDBTitle: structure of a pantothenate energy coupling factor transporter
6	c4zigB_	 Alignment		22.5	62	PDB header: apoptosis Chain: B: PDB Molecule: bh3-interacting domain death agonist; PDBTitle: crystal structure of core/latch dimer of bax in complex with2 bidbh3mini
7	c6ajjA_	 Alignment		16.9	16	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
8	c4mt1A_	 Alignment		15.6	13	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
9	c5c0vA_	 Alignment		15.5	63	PDB header: rna binding protein Chain: A: PDB Molecule: la-related protein 1; PDBTitle: structure of the larp1-unique domain dm15
10	c4akrC_	 Alignment		14.3	88	PDB header: actin-binding protein Chain: C: PDB Molecule: f-actin-capping protein subunit alpha; PDBTitle: crystal structure of the cytoplasmic actin capping protein2 cap32_34 from dictyostelium discoideum
11	dlizna_	 Alignment		14.1	75	Fold: Subunits of heterodimeric actin filament capping protein Capz SuperFamily: Subunits of heterodimeric actin filament capping protein Capz Family: Capz alpha-1 subunit

12	c1zy3B_	Alignment		12.6	54	PDB header: apoptosis Chain: B: PDB Molecule: bh3-peptide from bh3 interacting domain death PDBTitle: structural model of complex of bcl-w protein with bid bh3-2 peptide
13	c6ithA_	Alignment		12.4	26	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
14	c4z38B_	Alignment		11.9	25	PDB header: transferase Chain: B: PDB Molecule: mlna; PDBTitle: crystal structure of enoyl reductase domain of mlna from the2 macrolactin biosynthesis cluster from bacillus amyloliquefaciens
15	c6k1hE_	Alignment		11.5	22	PDB header: protein transport Chain: E: PDB Molecule: pts mannose/fructose/sorbose transporter subunit iic; PDBTitle: structure of membrane protein
16	c2gv5C_	Alignment		11.2	75	PDB header: cell cycle Chain: C: PDB Molecule: sfi1p; PDBTitle: crystal structure of sfi1p/cdc31p complex
17	d1wpga4	Alignment		11.1	14	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
18	c6fosK_	Alignment		10.7	24	PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit x; PDBTitle: cyanidioschyzon merolae photosystem i
19	c5hk1A_	Alignment		10.0	20	PDB header: membrane protein Chain: A: PDB Molecule: sigma non-opioid intracellular receptor 1; PDBTitle: human sigma-1 receptor bound to pd144418
20	c2rdcA_	Alignment		9.9	30	PDB header: lipid binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
21	d1rhzb_	Alignment	not modelled	9.3	20	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
22	d1i17a_	Alignment	not modelled	9.1	46	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
23	c1pznG_	Alignment	not modelled	9.1	26	PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
24	d1ijwc_	Alignment	not modelled	9.0	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
25	d1gxua_	Alignment	not modelled	8.9	22	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
26	d1lg4a_	Alignment	not modelled	8.4	38	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
27	d1pzna2	Alignment	not modelled	8.4	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
28	c2fv2A_	Alignment	not modelled	8.3	19	PDB header: transcription Chain: A: PDB Molecule: rcd1 required for cell differentiation1 homolog; PDBTitle: crystal structure analysis of human rcd-1 conserved region
29	c2p64B_	Alignment	not modelled	8.3	27	PDB header: ligase Chain: B: PDB Molecule: f-box/wd repeat protein 1a;

						PDBTitle: d domain of b-trcp
30	d1w2ia_	Alignment	not modelled	8.2	22	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
31	d1z01a2	Alignment	not modelled	7.9	17	Fold: TBP-like Superfamily: Bet v1-like Family: Ring hydroxylating alpha subunit catalytic domain
32	c2dfIA_	Alignment	not modelled	7.9	26	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
33	c3ouxB_	Alignment	not modelled	7.8	23	PDB header: protein binding Chain: B: PDB Molecule: lymphoid enhancer-binding factor 1; PDBTitle: structure of beta-catenin with phosphorylated lef-1
34	d3d31c1	Alignment	not modelled	7.3	14	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
35	c3d31D_	Alignment	not modelled	7.3	14	PDB header: transport protein Chain: D: PDB Molecule: sulfate/molybdate abc transporter, permease protein; PDBTitle: modbc from methanosarcina acetivorans
36	d1v5wa_	Alignment	not modelled	7.2	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
37	c5id3C_	Alignment	not modelled	7.1	10	PDB header: transport protein Chain: C: PDB Molecule: mitochondrial calcium uniporter; PDBTitle: solution structure of the pore-forming region of c. elegans2 mitochondrial calcium uniporter (mcs)
38	c2r6gF_	Alignment	not modelled	7.1	11	PDB header: hydrolase/transport protein Chain: F: PDB Molecule: maltose transport system permease protein malf; PDBTitle: the crystal structure of the e. coli maltose transporter
39	c4b19A_	Alignment	not modelled	6.9	38	PDB header: toxin Chain: A: PDB Molecule: pepa1; PDBTitle: s. aureus pepa1 nmr structure
40	c4k0eC_	Alignment	not modelled	6.9	11	PDB header: transport protein Chain: C: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
41	d1hcra_	Alignment	not modelled	6.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
42	c3br8A_	Alignment	not modelled	6.7	17	PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: crystal structure of acylphosphatase from bacillus subtilis
43	c2r3bA_	Alignment	not modelled	6.5	23	PDB header: transferase Chain: A: PDB Molecule: yjef-related protein; PDBTitle: crystal structure of a ribokinase-like superfamily protein (ef1790)2 from enterococcus faecalis v583 at 1.80 a resolution
44	c5xpdA_	Alignment	not modelled	6.4	17	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
45	c5lnko_	Alignment	not modelled	6.4	9	PDB header: oxidoreductase Chain: O: PDB Molecule: PDBTitle: entire ovine respiratory complex i
46	c2gv1A_	Alignment	not modelled	6.3	29	PDB header: hydrolase Chain: A: PDB Molecule: probable acylphosphatase; PDBTitle: nmr solution structure of the acylphosphatase from2 eschaerichia coli
47	d2icha1	Alignment	not modelled	6.3	28	Fold: AtH-like Superfamily: AtH-like Family: AtH-like
48	c5ecfj_	Alignment	not modelled	6.3	10	PDB header: lipid binding protein Chain: J: PDB Molecule: cell wall antigen; PDBTitle: ligand binding domain 1 of penicillium marneffeii mp1 protein complexed2 with arachidonic acids
49	c5a96A_	Alignment	not modelled	6.3	50	PDB header: viral protein Chain: A: PDB Molecule: polyhedrin; PDBTitle: crystal structure of lymantria dispar cpv14 polyhedra
50	c1szpC_	Alignment	not modelled	6.2	37	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
51	c2oucB_	Alignment	not modelled	6.2	30	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the map kinase binding domain of mcp5
52	c6cc4A_	Alignment	not modelled	6.1	14	PDB header: transport protein Chain: A: PDB Molecule: soluble cytochrome b562, lipid ii flippase murj chimera; PDBTitle: structure of murj from escherichia coli
53	d1ulra_	Alignment	not modelled	6.0	21	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
54	d2acya_	Alignment	not modelled	6.0	17	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
55	d1szpa2	Alignment	not modelled	5.9	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
						Fold: AhpD-like

56	d2pfxa1	Alignment	not modelled	5.8	17	Superfamily: AhpD-like Family: Atu0492-like
57	d1apsa_	Alignment	not modelled	5.7	13	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
58	c2kl4A_	Alignment	not modelled	5.7	0	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2032 protein; PDBTitle: nmr structure of the protein nb7804a
59	c6j9nB_	Alignment	not modelled	5.5	25	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: acriic3; PDBTitle: nmehnh+acriic3
60	c3l8jA_	Alignment	not modelled	5.5	25	PDB header: protein binding Chain: A: PDB Molecule: programmed cell death protein 10; PDBTitle: crystal structure of ccm3, a cerebral cavernous malformation protein2 critical for vascular integrity
61	c2n5lA_	Alignment	not modelled	5.4	21	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: regnase-1 c-terminal domain
62	d1uj8a1	Alignment	not modelled	5.4	27	Fold: Another 3-helical bundle Superfamily: IscX-like Family: IscX-like
63	c2wwbB_	Alignment	not modelled	5.4	38	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sec61 subunit gamma; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
64	c6ijoL_	Alignment	not modelled	5.3	12	PDB header: photosynthesis Chain: L: PDB Molecule: psal; PDBTitle: photosystem i of chlamydomonas reinhardtii
65	c3jbrE_	Alignment	not modelled	5.3	17	PDB header: membrane protein Chain: E: PDB Molecule: voltage-dependent calcium channel gamma-1 subunit; PDBTitle: cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
66	c4cw5B_	Alignment	not modelled	5.1	23	PDB header: oxidoreductase Chain: B: PDB Molecule: dfna; PDBTitle: crystal structure of the enoyl reductase domain of dfna2 from bacillus amyloliquefaciens