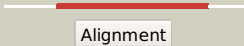

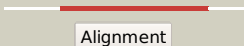

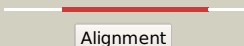




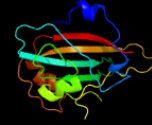


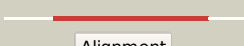
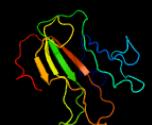








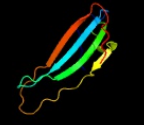




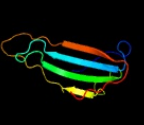





Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1911c_(lppC)_2157389_2157994
 Date Fri Aug 2 13:30:53 BST 2019
 Unique Job ID 1adf82024dfc0a8f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4begA	 Alignment		100.0	32	PDB header: lipid binding protein Chain: A; PDB Molecule: phosphatidylethanolamine binding protein; PDBTitle: structure of rv2140c, a phosphatidyl-ethanolamine binding protein from2 mycobacterium tuberculosis in complex with sulphate
2	c3n08A	 Alignment		100.0	37	PDB header: phosphatidylethanolamine-binding protein Chain: A; PDB Molecule: putative phosphatidylethanolamine-binding protein (pebp); PDBTitle: crystal structure of a putative phosphatidylethanolamine-binding2 protein (pebp) homolog ct736 from chlamydia trachomatis d/uw-3/cx
3	d1fuxa	 Alignment		100.0	29	Fold: PEBP-like Superfamily: PEBP-like Family: Prokaryotic PEBP-like proteins
4	d1fjja	 Alignment		100.0	30	Fold: PEBP-like Superfamily: PEBP-like Family: Prokaryotic PEBP-like proteins
5	c2evvD	 Alignment		100.0	27	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: hypothetical protein hp0218; PDBTitle: crystal structure of the pebp-like protein of unknown function hp02182 from helicobacter pylori
6	d1wpxb1	 Alignment		99.8	19	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
7	c2jyzA	 Alignment		99.8	27	PDB header: unknown function Chain: A; PDB Molecule: cg7054-pa; PDBTitle: cg7054 solution structure
8	c2r77A	 Alignment		99.8	23	PDB header: lipid binding protein Chain: A; PDB Molecule: phosphatidylethanolamine-binding protein, putative; PDBTitle: crystal structure of phosphatidylethanolamine-binding protein,2 pfl0955c, from plasmodium falciparum
9	c2gzaA	 Alignment		99.8	23	PDB header: lipid binding protein Chain: A; PDB Molecule: phosphatidylethanolamine-binding protein; PDBTitle: phosphatidylethanolamine-binding protein from plasmodium vivax
10	c5tvda	 Alignment		99.7	22	PDB header: unknown function Chain: A; PDB Molecule: tm16; PDBTitle: crystal structure of tm16
11	c1wkpA	 Alignment		99.7	19	PDB header: signaling protein Chain: A; PDB Molecule: flowering locus t protein; PDBTitle: flowering locus t (ft) from arabidopsis thaliana

12	c4ce4b_	Alignment		99.7	28	PDB header: ribosome Chain: B: PDB Molecule: unassigned rna; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
13	d1kn3a_	Alignment		99.7	22	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
14	d1a44a_	Alignment		99.7	23	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
15	d2qyqa1	Alignment		99.7	24	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
16	d1qoua_	Alignment		99.7	20	Fold: PEBP-like Superfamily: PEBP-like Family: Phosphatidylethanolamine binding protein
17	c4v1ab_	Alignment		99.6	27	PDB header: ribosome Chain: B: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
18	c1vw41_	Alignment		99.6	12	PDB header: ribosome Chain: 1: PDB Molecule: 54s ribosomal protein l35, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
19	c3j7y6_	Alignment		99.6	28	PDB header: ribosome Chain: 6: PDB Molecule: ml38; PDBTitle: structure of the large ribosomal subunit from human mitochondria
20	d1m4ka1	Alignment		25.3	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
21	d2dypd2	Alignment	not modelled	24.0	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
22	c3efyB_	Alignment	not modelled	22.9	22	PDB header: cell cycle Chain: B: PDB Molecule: cif (cell cycle inhibiting factor); PDBTitle: structure of the cyclomodulin cif from pathogenic2 escherichia coli
23	d1nkra2	Alignment	not modelled	21.3	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
24	d2dl2a1	Alignment	not modelled	18.5	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
25	d1ucta2	Alignment	not modelled	18.0	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
26	d1ugna2	Alignment	not modelled	16.1	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
27	d1m4ka2	Alignment	not modelled	13.9	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
28	c2vsdA_	Alignment	not modelled	13.4	19	PDB header: immune system receptor Chain: A: PDB Molecule: chir ab1; PDBTitle: crystal structure of chir-ab1
29	d1nkra1	Alignment	not modelled	11.3	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin

						Family: I set domains
30	c6fahE_	Alignment	not modelled	10.0	14	PDB header: flavoprotein Chain: E: PDB Molecule: caffeyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
31	c2e6pA_	Alignment	not modelled	9.4	23	PDB header: structural protein Chain: A: PDB Molecule: obscurin-like protein 1; PDBTitle: solution structure of the ig-like domain (714-804) from2 human obscurin-like protein 1
32	c1efvA_	Alignment	not modelled	9.3	24	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein; PDBTitle: three-dimensional structure of human electron transfer2 flavoprotein to 2.1 a resolution
33	d1efva2	Alignment	not modelled	9.1	24	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
34	d2dypd1	Alignment	not modelled	8.9	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: immunoglobulin Family: I set domains
35	d3clsd2	Alignment	not modelled	8.6	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
36	c4zgoA_	Alignment	not modelled	8.0	47	PDB header: cell cycle Chain: A: PDB Molecule: cell division cycle protein 123; PDBTitle: structure of c-terminally truncated cdc123 from schizosaccharomyces2 pombe
37	c3clrD_	Alignment	not modelled	7.8	22	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein subunit alpha; PDBTitle: crystal structure of the r236a etf mutant from m. methylotrophus
38	c4zgnA_	Alignment	not modelled	7.4	47	PDB header: cell cycle Chain: A: PDB Molecule: cell division cycle protein 123; PDBTitle: structure cdc123 complexed with the c-terminal domain of eif2gamma
39	c1ovzB_	Alignment	not modelled	6.7	24	PDB header: immune system Chain: B: PDB Molecule: immunoglobulin alpha fc receptor; PDBTitle: crystal structure of human fcari
40	d1jj2l_	Alignment	not modelled	6.6	19	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
41	d1ffki_	Alignment	not modelled	6.3	20	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: L15e
42	c3s6oD_	Alignment	not modelled	5.8	19	PDB header: hydrolase Chain: D: PDB Molecule: polysaccharide deacetylase family protein; PDBTitle: crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
43	c1efpC_	Alignment	not modelled	5.8	22	PDB header: electron transport Chain: C: PDB Molecule: protein (electron transfer flavoprotein); PDBTitle: electron transfer flavoprotein (etf) from paracoccus2 denitrificans
44	c1efxE_	Alignment	not modelled	5.5	15	PDB header: immune system Chain: E: PDB Molecule: natural killer cell receptor kir2dl2; PDBTitle: structure of a complex between the human natural killer2 cell receptor kir2dl2 and a class i mhc ligand hla-cw3
45	d1efpa2	Alignment	not modelled	5.5	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
46	c3kmlB_	Alignment	not modelled	5.4	40	PDB header: viral protein Chain: B: PDB Molecule: coat protein; PDBTitle: circular permutant of the tobacco mosaic virus