









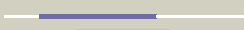


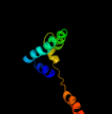

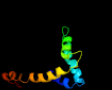

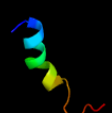

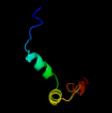

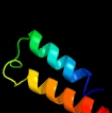

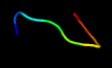

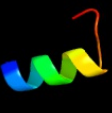
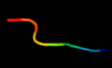
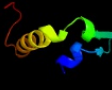


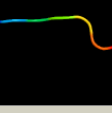


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1749c_(-)_1977335_1977892
Date	Fri Aug 2 13:30:35 BST 2019
Unique Job ID	52c107c054fbf014

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1bcc3	 Alignment		30.2	19	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
2	d1ppjc2	 Alignment		25.7	17	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
3	c4ojpC_	 Alignment		25.3	41	PDB header: viral protein Chain: C: PDB Molecule: tailspike protein; PDBTitle: crystal structure of putative tailspike protein (tsp1, orf210) from2 escherichia coli o157:h7 bacteriohage cba120 in complex with maltose
4	d3cx5c2	 Alignment		25.2	17	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
5	c3cwbC_	 Alignment		20.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome b; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
6	c4uisB_	 Alignment		18.8	11	PDB header: hydrolase Chain: B: PDB Molecule: gamma-secretase; PDBTitle: the cryoem structure of human gamma-secretase complex
7	c2qjkm_	 Alignment		14.6	26	PDB header: electron transport Chain: M: PDB Molecule: cytochrome b; PDBTitle: crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin
8	c3cx5N_	 Alignment		14.5	17	PDB header: oxidoreductase Chain: N: PDB Molecule: cytochrome b; PDBTitle: structure of complex iii with bound cytochrome c in reduced state and2 definition of a minimal core interface for electron transfer.
9	c5u1tB_	 Alignment		14.2	11	PDB header: hydrolase Chain: B: PDB Molecule: securin; PDBTitle: crystal structure of the saccharomyces cerevisiae separase-securin2 complex at 2.6 angstrom resolution
10	c5fsgA_	 Alignment		14.0	19	PDB header: viral protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, hantavirus PDBTitle: structure of the hantavirus nucleoprotein provides insights2 into the mechanism of rna encapsidation and a template for3 drug design
11	c6g7oA_	 Alignment		12.7	18	PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562; PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution

12	d1e57a_	Alignment		11.2	43	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP
13	d1mrza1	Alignment		11.2	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
14	c1jekB_	Alignment		11.0	58	PDB header: viral protein Chain: B: PDB Molecule: env polyprotein; PDBTitle: visna tm core structure
15	d1nekb2	Alignment		10.7	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
16	d1ddla_	Alignment		9.6	43	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP
17	c6onqA_	Alignment		9.4	17	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c xoxg; PDBTitle: crystal structure of c-type cytochrome xoxg from methylobacterium2 extorquens am1
18	d2hkja2	Alignment		8.8	27	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
19	d1lauya_	Alignment		8.7	50	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP
20	d1e57b_	Alignment		8.5	43	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP
21	c2lkgA_	Alignment	not modelled	8.4	12	PDB header: signaling protein Chain: A: PDB Molecule: acetylcholine receptor; PDBTitle: wsa major conformation
22	d1lauyb_	Alignment	not modelled	8.2	30	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tymoviridae-like VP
23	c6o7ua_	Alignment	not modelled	8.2	16	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
24	c3v8oB_	Alignment	not modelled	7.3	10	PDB header: structural protein Chain: B: PDB Molecule: filamin-c; PDBTitle: human filamin c ig - like domains 4 and 5
25	d2e74a1	Alignment	not modelled	6.7	15	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
26	d1nb9a_	Alignment	not modelled	6.3	11	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
27	d2axtc1	Alignment	not modelled	6.1	19	Fold: Photosystem II antenna protein-like Superfamily: Photosystem II antenna protein-like Family: Photosystem II antenna protein-like
28	c2axtc_	Alignment	not modelled	6.1	19	PDB header: electron transport Chain: C: PDB Molecule: photosystem ii cp43 protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
						Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H,

29	d1l9bh2	Alignment	not modelled	6.1	20	transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
30	d1q90b	Alignment	not modelled	6.0	13	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
31	c2lnyA	Alignment	not modelled	5.9	29	PDB header: de novo protein Chain: A: PDB Molecule: shb peptide; PDBTitle: shb peptide structure bound to negatively charged lipid-bilayer after2 molecular dynamics refinement
32	c2ww9B	Alignment	not modelled	5.8	15	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sss1; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
33	c5nvvA	Alignment	not modelled	5.7	40	PDB header: viral protein Chain: A: PDB Molecule: scrfp-tag,gp41; PDBTitle: nmr assignment and structure of a peptide derived from the fusion2 peptide of hiv-1 gp41 in the presence of dodecylphosphocholine3 micelles
34	c3u1lA	Alignment	not modelled	5.4	38	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine protease subunit ns2b; PDBTitle: dengue virus protease covalently bound to a peptide
35	c1p58F	Alignment	not modelled	5.3	33	PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
36	c2lvuA	Alignment	not modelled	5.1	71	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 10