

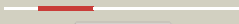
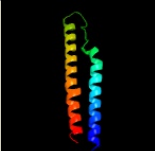

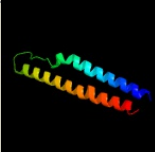



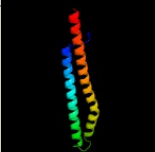





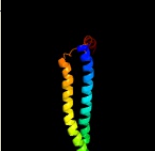





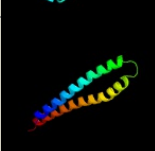


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1172c_(PE12)_1301760_1302686
 Date Wed Jul 31 22:05:26 BST 2019
 Unique Job ID cfc04f117e946ae5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	49	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	d2g38a1	 Alignment		100.0	32	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c2g38A_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c4wj2A_	 Alignment		83.1	16	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
5	c3gvmA_	 Alignment		58.2	14	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
6	c4iogD_	 Alignment		39.4	14	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
7	c2h3oA_	 Alignment		38.2	38	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: structure of merf, a membrane protein with two trans-2 membrane helices
8	d1wa8a1	 Alignment		33.2	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
9	c1wazA_	 Alignment		22.1	38	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: nmr structure determination of the bacterial mercury transporter,2 merf, in micelles
10	c2m67A_	 Alignment		21.7	36	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
11	c2vs0B_	 Alignment		21.2	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa

12	c3zbhC_	Alignment		20.9	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
13	c6cfzH_	Alignment		18.2	17	PDB header: nuclear protein Chain: H: PDB Molecule: dam1; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
14	c2lj2A_	Alignment		16.7	36	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: integral membrane core domain of the mercury transporter merf in lipid bilayer membranes
15	c4qncA_	Alignment		15.3	21	PDB header: membrane protein Chain: A: PDB Molecule: chemical transport protein; PDBTitle: crystal structure of a semisweet in an occluded state
16	d1vqw1	Alignment		14.0	24	Fold: Ribosomal protein L30p/L7e Superfamily: Ribosomal protein L30p/L7e Family: Ribosomal protein L30p/L7e
17	c5iqjB_	Alignment		13.4	50	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: 1.9 angstrom crystal structure of protein with unknown function from2 vibrio cholerae.
18	c3iz5e_	Alignment		13.0	47	PDB header: ribosome Chain: E: PDB Molecule: 60s ribosomal protein l11 (l5p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
19	c3j3bF_	Alignment		12.0	35	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the human 60s ribosomal proteins
20	c6d5fF_	Alignment		11.4	60	PDB header: virus Chain: F: PDB Molecule: fimbrial protein; PDBTitle: cryo-em reconstruction of membrane-enveloped filamentous virus sfv12 (sulfolobus filamentous virus 1)
21	c3j39F_	Alignment	not modelled	11.4	29	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
22	c3zf7w_	Alignment	not modelled	11.3	41	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l23, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
23	c3dyuB_	Alignment	not modelled	11.3	24	PDB header: transport protein Chain: B: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of snx9px-bar (230-595), h32
24	c2zkrw_	Alignment	not modelled	10.9	33	PDB header: ribosomal protein/rna Chain: W: PDB Molecule: rna expansion segment es10; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
25	d1lghb_	Alignment	not modelled	10.8	38	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
26	c3j21Y_	Alignment	not modelled	10.7	6	PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l30p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
27	c3j66s_	Alignment	not modelled	10.4	24	PDB header: ribosome Chain: S: PDB Molecule: PDBTitle: arx1 pre-60s particle. this entry contains the alternative position2 for rlp7.
28	c3onjA_	Alignment	not modelled	10.3	19	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain

29	c3izce_	Alignment	not modelled	9.3	41	PDB header: ribosome Chain: E: PDB Molecule: 60s ribosomal protein rpl11 (I5p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
30	c3fozB_	Alignment	not modelled	9.0	23	PDB header: transferase/rna Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate transferase; PDBTitle: structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
31	d1xmba2	Alignment	not modelled	8.8	29	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
32	c4a1cV_	Alignment	not modelled	8.6	29	PDB header: ribosome Chain: V: PDB Molecule: 60s ribosomal protein I7; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
33	d1p17b_	Alignment	not modelled	8.4	29	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
34	c4ud1B_	Alignment	not modelled	7.8	67	PDB header: viral protein Chain: B: PDB Molecule: n protein; PDBTitle: structure of the n terminal domain of the mers cov nucleocapsid
35	c4lwsA_	Alignment	not modelled	7.6	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
36	c5n4kA_	Alignment	not modelled	7.2	83	PDB header: rna binding protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: n-terminal domain of a human coronavirus nl63 nucleocapsid protein
37	c3jywF_	Alignment	not modelled	7.1	41	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein I7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
38	d2bxxa1	Alignment	not modelled	7.0	67	Fold: Coronavirus RNA-binding domain Superfamily: Coronavirus RNA-binding domain Family: Coronavirus RNA-binding domain
39	c4j72B_	Alignment	not modelled	6.9	22	PDB header: transferase Chain: B: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase
40	d2a5yb2	Alignment	not modelled	6.8	38	Fold: DEATH domain Superfamily: DEATH domain Family: Caspase recruitment domain, CARD
41	c3crqA_	Alignment	not modelled	6.6	22	PDB header: transferase Chain: A: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: structure of trna dimethylallyltransferase: rna2 modification through a channel
42	d2geca1	Alignment	not modelled	6.6	67	Fold: Coronavirus RNA-binding domain Superfamily: Coronavirus RNA-binding domain Family: Coronavirus RNA-binding domain
43	c2m7xA_	Alignment	not modelled	6.5	64	PDB header: membrane protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: structural and functional analysis of transmembrane segment iv of the2 salt tolerance protein sod2
44	d1sska_	Alignment	not modelled	6.5	83	Fold: Coronavirus RNA-binding domain Superfamily: Coronavirus RNA-binding domain Family: Coronavirus RNA-binding domain
45	c3exaD_	Alignment	not modelled	6.3	27	PDB header: transferase Chain: D: PDB Molecule: trna delta(2)-isopentenylpyrophosphate transferase; PDBTitle: crystal structure of the full-length trna isopentenylpyrophosphate2 transferase (bh2366) from bacillus halodurans, northeast structural3 genomics consortium target bhr41.
46	c5ireD_	Alignment	not modelled	6.2	38	PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus
47	c4g7xA_	Alignment	not modelled	6.2	67	PDB header: protein binding/protein binding Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a complex between the ctxphi piiii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
48	c1s1iF_	Alignment	not modelled	6.0	41	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein I7-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
49	c3hd4A_	Alignment	not modelled	6.0	83	PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: mhv nucleocapsid protein ntd
50	c5mlc8_	Alignment	not modelled	5.9	71	PDB header: ribosome Chain: 8: PDB Molecule: psrp6, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
51	c5mmi7_	Alignment	not modelled	5.8	71	PDB header: ribosome Chain: 7: PDB Molecule: 50s ribosomal protein 6, chloroplastic; PDBTitle: structure of the large subunit of the chloroplast ribosome
52	c1yfaA_	Alignment	not modelled	5.8	42	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase;

52	c1yza_	Alignment	not modelled	5.8	43	PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
53	d1yfza1	Alignment	not modelled	5.8	43	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
54	c3fhkF_	Alignment	not modelled	5.8	31	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
55	d2o8ra1	Alignment	not modelled	5.8	21	Fold: Spectrin repeat-like Superfamily: PPK N-terminal domain-like Family: PPK N-terminal domain-like
56	c4g7wB_	Alignment	not modelled	5.7	67	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of the minor coat protein2 piii from ctxphi
57	c2uwjG_	Alignment	not modelled	5.6	42	PDB header: chaperone Chain: G: PDB Molecule: type iii export protein pscg; PDBTitle: structure of the heterotrimeric complex which regulates type iii2 secretion needle formation
58	c4jzaB_	Alignment	not modelled	5.5	67	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a legionella phosphoinositide phosphatase:2 insights into lipid metabolism in pathogen host interaction
59	c4j72A_	Alignment	not modelled	5.5	22	PDB header: transferase Chain: A: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase