
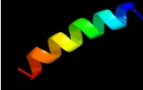
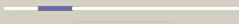

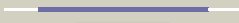
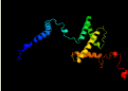



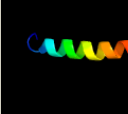







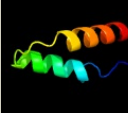


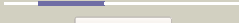

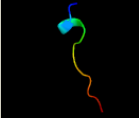
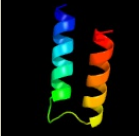


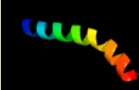

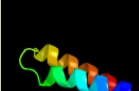



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1748 (-) _1976607_1977338
Date	Fri Aug 2 13:30:35 BST 2019
Unique Job ID	b359ba81d657e7e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6c6IN_	 Alignment		80.9	30	PDB header: membrane protein Chain: N: PDB Molecule: v0 assembly protein 1; PDBTitle: yeast vacuolar atpase vo in lipid nanodisc
2	c2qn5B_	 Alignment		19.4	64	PDB header: hydrolase inhibitor/hydrolase Chain: B: PDB Molecule: bowman-birk type bran trypsin inhibitor; PDBTitle: crystal structure and functional study of the bowman-birk2 inhibitor from rice bran in complex with bovine trypsin
3	c5ganA_	 Alignment		19.2	23	PDB header: transcription Chain: A: PDB Molecule: pre-mrna-splicing factor 8; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
4	c3ktcB_	 Alignment		16.7	10	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
5	c5doqC_	 Alignment		16.0	39	PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
6	c5ir6C_	 Alignment		16.0	39	PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
7	c2mf3A_	 Alignment		14.7	55	PDB header: toxin Chain: A: PDB Molecule: u2-segestritoxin-sf1a; PDBTitle: sgtx-sf1a
8	c5ow2A_	 Alignment		12.4	57	PDB header: viral protein Chain: A: PDB Molecule: capsid protein; PDBTitle: japanese encephalitis virus capsid protein
9	d1ks9a1	 Alignment		12.2	23	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Ketopantoate reductase PanE
10	c4xu6A_	 Alignment		12.1	58	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cross-linked mvins r77c trimer at 1.9a resolution
11	c3ez0D_	 Alignment		10.7	18	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein with ferritin-like fold; PDBTitle: crystal structure of protein of unknown function with ferritin-like fold (yp_832262.1) from arthrobacter sp. fb24 at 2.33 a resolution

12	c4uy87_	Alignment		10.3	80	PDB header: ribosome Chain: 7; PDB Molecule: tryptophanase; PDB Fragment: residues 7-85; PDBTitle: molecular basis for the ribosome functioning as a l-tryptophan sensor2 - cryo-em structure of a tnac stalled e.coli ribosome
13	c4b6aX_	Alignment		9.1	29	PDB header: ribosome Chain: X; PDB Molecule: 60s ribosomal protein l25; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
14	c3tufA_	Alignment		8.8	27	PDB header: signaling protein Chain: A; PDB Molecule: stage iii sporulation protein ah; PDBTitle: structure of the spoiii-spoiiiah pore forming complex.
15	c5wdaL_	Alignment		8.7	50	PDB header: protein transport Chain: L; PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus
16	d1sfka_	Alignment		8.2	46	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
17	d2pila_	Alignment		8.1	29	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
18	c5lj3F_	Alignment		8.1	50	PDB header: splicing Chain: F; PDB Molecule: pre-mrna-splicing factor cwc25; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
19	c3uz0A_	Alignment		7.9	27	PDB header: transport protein Chain: A; PDB Molecule: stage iii sporulation protein ah; PDBTitle: crystal structure of spoiiiah and spoiiq complex
20	c2mi2A_	Alignment		7.8	26	PDB header: transport protein Chain: A; PDB Molecule: sec-independent protein translocase protein tatb; PDBTitle: solution structure of the e. coli tatb protein in dpc micelles
21	c3mp7B_	Alignment	not modelled	7.3	50	PDB header: protein transport Chain: B; PDB Molecule: preprotein translocase subunit sece; PDBTitle: lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
22	d1rhzb_	Alignment	not modelled	7.1	33	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
23	c2r6fA_	Alignment	not modelled	7.1	33	PDB header: hydrolase Chain: A; PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra
24	c2ovcA_	Alignment	not modelled	7.0	23	PDB header: transport protein Chain: A; PDB Molecule: potassium voltage-gated channel subfamily kqt member 4; PDBTitle: crystal structure of a coiled-coil tetramerization domain from kv7.42 channels
25	c4atbC_	Alignment	not modelled	7.0	34	PDB header: immune system Chain: C; PDB Molecule: interleukin enhancer-binding factor 2; PDBTitle: crystal structure of the nf90-nf45 dimerisation domain2 complex with ctp
26	c4a17R_	Alignment	not modelled	6.8	29	PDB header: ribosome Chain: R; PDB Molecule: rpl23a; 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 2.
27	c1cn3F_	Alignment	not modelled	6.7	78	PDB header: viral protein Chain: F; PDB Molecule: fragment of coat protein vp2; PDBTitle: interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry
28	c3j39X_	Alignment	not modelled	6.7	29	PDB header: ribosome Chain: X; PDB Molecule: 60s ribosomal protein l23a; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins

29	c6itcB_	Alignment	not modelled	6.6	33	PDB header: protein transport Chain: B: PDB Molecule: translocating peptide; PDBTitle: structure of a substrate engaged seca-secy protein translocation2 machine
30	c6hu9e_	Alignment	not modelled	6.6	21	PDB header: oxidoreductase/electron transport Chain: E: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
31	c3lr6A_	Alignment	not modelled	6.5	9	PDB header: structural protein Chain: A: PDB Molecule: major ampullate spidroin 1; PDBTitle: self-assembly of spider silk proteins is controlled by a ph-sensitive2 relay
32	c4wfbQ_	Alignment	not modelled	6.5	38	PDB header: ribosome Chain: Q: PDB Molecule: 50s ribosomal protein l23; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with bc-3205
33	c6ansD_	Alignment	not modelled	6.3	17	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 burkholderia cenocepacia
34	d2joka1	Alignment	not modelled	6.3	18	Fold: SopE-like GEF domain Superfamily: SopE-like GEF domain Family: SopE-like GEF domain
35	d1muga_	Alignment	not modelled	6.2	22	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Mug-like
36	c3zf7X_	Alignment	not modelled	6.2	36	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l23a; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
37	c4g4mB_	Alignment	not modelled	6.2	30	PDB header: de novo protein Chain: B: PDB Molecule: alpha4f3(6-13); PDBTitle: crystal structure of the de novo designed fluorinated peptide2 alpha4f3(6-13)
38	c4g4mA_	Alignment	not modelled	6.1	30	PDB header: de novo protein Chain: A: PDB Molecule: alpha4f3(6-13); PDBTitle: crystal structure of the de novo designed fluorinated peptide2 alpha4f3(6-13)
39	c5yh1A_	Alignment	not modelled	6.1	14	PDB header: ribosomal protein Chain: A: PDB Molecule: member of s1p family of ribosomal proteins; PDBTitle: member of s1p family of ribosomal proteins pf0399 dhh domain
40	c5iz2A_	Alignment	not modelled	6.1	13	PDB header: structural protein Chain: A: PDB Molecule: major ampullate spidroin 1a; PDBTitle: crystal structure of the n. clavipes spidroin ntd at ph 6.5
41	c6akmA_	Alignment	not modelled	5.9	32	PDB header: protein binding Chain: A: PDB Molecule: suppressor of ikbke 1; PDBTitle: crystal structure of slmap-sike1 complex
42	c6re80_	Alignment	not modelled	5.8	83	PDB header: proton transport Chain: 0: PDB Molecule: asa-10: polytomella f-atp synthase associated subunit 10; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 2d,2 composite map
43	c5wx9A_	Alignment	not modelled	5.6	60	PDB header: dna binding protein/dna Chain: A: PDB Molecule: ethylene-responsive transcription factor erf096; PDBTitle: crystal structure of aterf96 with gcc-box
44	c5dkaA_	Alignment	not modelled	5.6	71	PDB header: replication Chain: A: PDB Molecule: cell division protein zapd; PDBTitle: the structure of escherichia coli zapd
45	c2ogdB_	Alignment	not modelled	5.6	13	PDB header: transferase Chain: B: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: t. brucei farnesyl diphosphate synthase complexed with bisphosphonate2 bph-527
46	c5f56A_	Alignment	not modelled	5.5	44	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded-dna-specific exonuclease; PDBTitle: structure of recj complexed with dna and ssb-ct
47	d1r6ra_	Alignment	not modelled	5.4	31	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
48	c1r6rA_	Alignment	not modelled	5.4	31	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of dengue virus capsid protein reveals a2 new fold
49	d1t92a_	Alignment	not modelled	5.4	43	Fold: Pili subunits Superfamily: Pili subunits Family: Pseudopilin
50	c2jowA_	Alignment	not modelled	5.3	16	PDB header: transport protein Chain: A: PDB Molecule: protein prgi; PDBTitle: differences in the electrostatic surfaces of the type iii2 secretion needle proteins
51	c6c4qA_	Alignment	not modelled	5.2	10	PDB header: transport protein Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: 1.16 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1-100) of polyketide synthase pks13 from3 mycobacterium tuberculosis
52	c3a7mA_	Alignment	not modelled	5.0	14	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: flagellar protein flit; PDBTitle: structure of flit, the flagellar type iii chaperone for flid
53	d1xa6a2	Alignment	not modelled	5.0	40	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain