




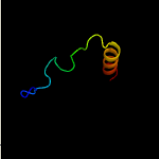



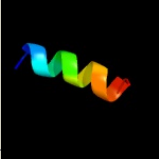



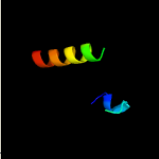

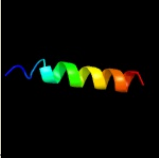

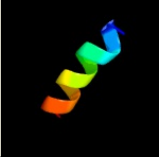



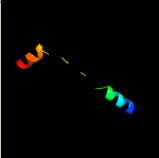


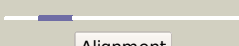








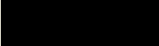
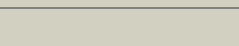
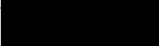

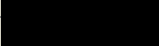

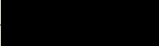


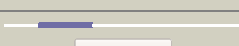

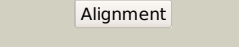

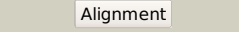



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3103c (-)_3471410_3471847
Date	Thu Aug 8 16:20:28 BST 2019
Unique Job ID	8d5fd477a6eddd34

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qlcd_	 Alignment		40.7	29	Fold: Single transmembrane helix Superfamily: Bacterial aa3 type cytochrome c oxidase subunit IV Family: Bacterial aa3 type cytochrome c oxidase subunit IV
2	c5t4oj_	 Alignment		20.4	17	PDB header: hydrolase Chain: J: PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
3	d1xl4a2	 Alignment		19.9	20	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
4	c6odm5_	 Alignment		19.8	29	PDB header: viral protein Chain: 5: PDB Molecule: triple capsid protein 1; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
5	c6dadD_	 Alignment		18.1	36	PDB header: calcium binding protein/membrane protein Chain: D: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: 1.65 angstrom crystal structure of the n97i ca/cam:cav1.2 iq domain2 complex
6	c6daeD_	 Alignment		17.4	36	PDB header: calcium binding protein/membrane protein Chain: D: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: 2.0 angstrom crystal structure of the d95v ca/cam:cav1.2 iq domain2 complex
7	c5ydnA_	 Alignment		17.2	31	PDB header: viral protein Chain: A: PDB Molecule: gene product j; PDBTitle: mu pahge neck subunit
8	d1m56d_	 Alignment		17.2	24	Fold: Single transmembrane helix Superfamily: Bacterial aa3 type cytochrome c oxidase subunit IV Family: Bacterial aa3 type cytochrome c oxidase subunit IV
9	c6daeC_	 Alignment		17.0	36	PDB header: calcium binding protein/membrane protein Chain: C: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: 2.0 angstrom crystal structure of the d95v ca/cam:cav1.2 iq domain2 complex
10	c2ls2A_	 Alignment		15.4	31	PDB header: metal transport Chain: A: PDB Molecule: high affinity copper uptake protein 1; PDBTitle: 1h chemical shift assignments for the first transmembrane domain from2 human copper transport 1
11	c3u3iA_	 Alignment		15.3	17	PDB header: rna binding protein Chain: A: PDB Molecule: nucleocapsid protein; PDBTitle: a rna binding protein from crimean-congo hemorrhagic fever virus

12	c6dadC_	 Alignment		15.2	36	PDB header: calcium binding protein/membrane protein Chain: C: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: 1.65 angstrom crystal structure of the n97i ca/cam:cav1.2 iq domain2 complex
13	c2mkaB_	 Alignment		15.0	25	PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
14	c2mk9A_	 Alignment		15.0	25	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3
15	c2mk9B_	 Alignment		15.0	25	PDB header: immune system Chain: B: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the dimeric transmembrane domain of toll-like2 receptor 3
16	c2mkaC_	 Alignment		15.0	25	PDB header: immune system Chain: C: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
17	c2mkaA_	 Alignment		15.0	25	PDB header: immune system Chain: A: PDB Molecule: toll-like receptor 3; PDBTitle: spatial structure of the toll-like receptor 3 transmembrane domain in2 the trimeric state
18	c2y69W_	 Alignment		14.7	22	PDB header: electron transport Chain: W: PDB Molecule: cytochrome c oxidase polypeptide 7a1; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
19	c2zkr3_	 Alignment		12.8	25	PDB header: ribosomal protein/rna Chain: 3: PDB Molecule: 60s ribosomal protein l39e; 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
20	c5h67C_	 Alignment		12.2	16	PDB header: dna binding protein/cell cycle Chain: C: PDB Molecule: segregation and condensation protein a; PDBTitle: crystal structure of the bacillus subtilis smc head domain complexed2 with the cognate scpa c-terminal domain and soaked atp
21	c6humQ_	 Alignment	not modelled	11.4	18	PDB header: proton transport Chain: Q: PDB Molecule: proton-translocating nadh-quinone dehydrogenase subunit q PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
22	c6fkip_	 Alignment	not modelled	10.9	17	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
23	c2be6D_	 Alignment	not modelled	10.8	36	PDB header: membrane protein Chain: D: PDB Molecule: voltage-dependent l-type calcium channel alpha-1c subunit; PDBTitle: 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex
24	c2dw3A_	 Alignment	not modelled	10.7	32	PDB header: photosynthesis Chain: A: PDB Molecule: intrinsic membrane protein pufx; PDBTitle: solution structure of the rhodobacter sphaeroides pufx2 membrane protein
25	c3zf7q_	 Alignment	not modelled	10.6	25	PDB header: ribosome Chain: Q: PDB Molecule: ribosomal protein l15; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
26	c4a1bB_	 Alignment	not modelled	10.3	13	PDB header: ribosome Chain: B: PDB Molecule: rpl39; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 3.
27	d1vqo2l	 Alignment	not modelled	10.0	27	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Ribosomal protein L39e Family: Ribosomal protein L39e
28	c5xnmT_	 Alignment	not modelled	9.8	23	PDB header: membrane protein Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: structure of unstacked c2s2m2-type psii-lhcii

						supercomplex from pism2 sativum PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
29	c5v2sA_	Alignment	not modelled	9.8	29	PDB header: ribosome Chain: F: PDB Molecule: 50s ribosomal protein l6p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by 2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
30	c3j21f_	Alignment	not modelled	9.6	25	PDB header: electron transport Chain: J: PDB Molecule: cytochrome c oxidase subunit 7a2, mitochondrial; PDBTitle: structure of human cytochrome c oxidase
31	c5z62j_	Alignment	not modelled	9.6	7	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
32	d1q90r_	Alignment	not modelled	9.3	26	PDB header: photosynthesis Chain: R: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
33	c1q90R_	Alignment	not modelled	9.3	26	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
34	c5mdxT_	Alignment	not modelled	9.2	23	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
35	c5mdxt_	Alignment	not modelled	9.2	23	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
36	c3jcut_	Alignment	not modelled	9.1	23	PDB header: membrane protein Chain: T: PDB Molecule: photosystem ii reaction center protein tc; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
37	c3jcuT_	Alignment	not modelled	9.1	23	PDB header: membrane protein Chain: T: PDB Molecule: photosystem ii reaction center protein tc; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
38	c3izso_	Alignment	not modelled	8.9	13	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein rpl28 (l15p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
39	c3i0mA_	Alignment	not modelled	8.9	38	PDB header: cell cycle Chain: A: PDB Molecule: dna repair and telomere maintenance protein nbs1; PDBTitle: structure of the s. pombe nbs1 fha/brct-repeat domain
40	c1jdmA_	Alignment	not modelled	8.0	39	PDB header: membrane protein Chain: A: PDB Molecule: sarcophilin; PDBTitle: nmr structure of sarcophilin
41	d1v54j_	Alignment	not modelled	8.0	7	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIa Family: Mitochondrial cytochrome c oxidase subunit VIIa
42	d2q07a3	Alignment	not modelled	7.8	44	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: AF0587 pre C-terminal domain-like
43	d2p7tc1	Alignment	not modelled	7.5	31	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
44	c2j7aC_	Alignment	not modelled	7.3	43	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome c quinol dehydrogenase nrhf; PDBTitle: crystal structure of cytochrome c nitrite reductase nrhf2 complex from desulfovibrio vulgaris
45	d1ehkb2	Alignment	not modelled	6.9	23	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
46	c5t42A_	Alignment	not modelled	6.3	25	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: structure of the ebola virus envelope protein mper/tm domain and its2 interaction with the fusion loop explains their fusion activity
47	c2kegA_	Alignment	not modelled	6.2	38	PDB header: antimicrobial protein Chain: A: PDB Molecule: plnk; PDBTitle: nmr structure of plantaricin k in dpc-micelles
48	c1jsuC_	Alignment	not modelled	5.9	31	PDB header: complex (transferase/cyclin/inhibitor) Chain: C: PDB Molecule: p27; PDBTitle: p27(kip1)/cyclin a/cdk2 complex
49	c5no8A_	Alignment	not modelled	5.8	35	PDB header: lyase Chain: A: PDB Molecule: bacell_00875; PDBTitle: polysaccharide lyase bacell_00875
50	c2ev2B_	Alignment	not modelled	5.7	15	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: structure of rv1264n, the regulatory domain of the mycobacterial2 adenylyl cylcase rv1264, at ph 8.5
51	c5mg3D_	Alignment	not modelled	5.5	7	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
52	c2ki9A_	Alignment	not modelled	5.5	37	PDB header: membrane protein Chain: A: PDB Molecule: cannabinoid receptor 2; PDBTitle: human cannabinoid receptor-2 helix 6
53	d1uptb_	Alignment	not modelled	5.4	21	Fold: GRIP domain Superfamily: GRIP domain Family: GRIP domain
						PDB header: photosynthesis

54	c6fosK_	Alignment	not modelled	5.4	24	Chain: K: PDB Molecule: photosystem i reaction center subunit x; PDBTitle: cyanidioschyzon merolae photosystem i
55	d1t98a2	Alignment	not modelled	5.4	14	Fold: STAT-like Superfamily: MukF C-terminal domain-like Family: MukF C-terminal domain-like
56	c3rgbA_	Alignment	not modelled	5.3	23	PDB header: oxidoreductase Chain: A: PDB Molecule: methane monoxygenase subunit b2; PDBTitle: crystal structure of particulate methane monoxygenase from2 methylococcus capsulatus (bath)
57	c1yewI_	Alignment	not modelled	5.3	23	PDB header: oxidoreductase, membrane protein Chain: I: PDB Molecule: particulate methane monoxygenase, b subunit; PDBTitle: crystal structure of particulate methane monoxygenase
58	c4zy8D_	Alignment	not modelled	5.2	75	PDB header: transport protein Chain: D: PDB Molecule: protein Ist4; PDBTitle: k. lactis Ist4 longin domain
59	c2hw0A_	Alignment	not modelled	5.2	15	PDB header: hydrolase, replication Chain: A: PDB Molecule: replicase; PDBTitle: nmr solution structure of the nuclease domain from the2 replicator initiator protein from porcine circovirus pcv2
60	c3rlbB_	Alignment	not modelled	5.2	14	PDB header: thiamine-binding protein Chain: B: PDB Molecule: thit; PDBTitle: crystal structure at 2.0 a of the s-component for thiamin from an ecf-2 type abc transporter
61	d3c07a2	Alignment	not modelled	5.1	25	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
62	c3on3B_	Alignment	not modelled	5.1	24	PDB header: oxidoreductase Chain: B: PDB Molecule: keto/oxoacid ferredoxin oxidoreductase, gamma subunit; PDBTitle: the crystal structure of keto/oxoacid ferredoxin oxidoreductase, gamma2 subunit from geobacter sulfurreducens pca
63	c5x5yF_	Alignment	not modelled	5.1	15	PDB header: membrane protein Chain: F: PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex