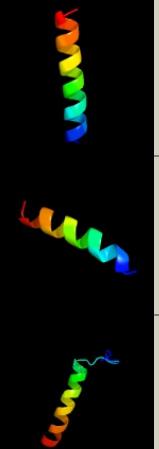
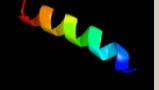
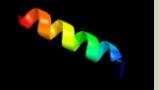
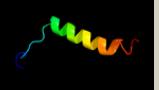
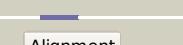
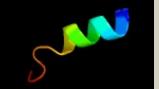
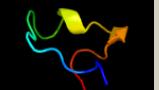
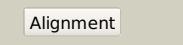


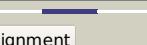
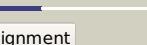
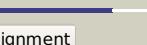
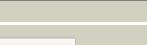
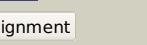
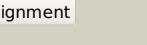
# Phyre<sup>2</sup>

Email	mdejesus@rockefeller.edu
Description	RVBD0011c_(-)_13714_13995
Date	Tue Jul 23 14:50:03 BST 2019
Unique Job ID	5a7909df80ac12c4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2mmuA</a>			99.9	100	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein crga; <b>PDBTitle:</b> structure of crga, a cell division structural and regulatory protein2 from mycobacterium tuberculosis, in lipid bilayers
2	<a href="#">c3j65n</a>			53.3	24	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein l28; <b>PDBTitle:</b> arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
3	<a href="#">c3mk7F</a>			50.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
4	<a href="#">c5z62J</a>			26.3	20	<b>PDB header:</b> electron transport <b>Chain:</b> J: <b>PDB Molecule:</b> cytochrome c oxidase subunit 7a2, mitochondrial; <b>PDBTitle:</b> structure of human cytochrome c oxidase
5	<a href="#">d1v54j</a>			25.3	17	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIa <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIa
6	<a href="#">c4zyoA</a>			24.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase; <b>PDBTitle:</b> crystal structure of human integral membrane stearoyl-coa desaturase2 with substrate
7	<a href="#">c4ymkA</a>			24.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase 1; <b>PDBTitle:</b> crystal structure of stearoyl-coenzyme a desaturase 1
8	<a href="#">c2y69Z</a>			21.5	23	<b>PDB header:</b> electron transport <b>Chain:</b> Z: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 8h; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
9	<a href="#">c2y69W</a>			21.3	17	<b>PDB header:</b> electron transport <b>Chain:</b> W: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 7a1; <b>PDBTitle:</b> bovine heart cytochrome c oxidase re-refined with molecular oxygen
10	<a href="#">c2n7rA</a>			19.9	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> nicastrin; <b>PDBTitle:</b> structure of the transmembrane domain of human nicastrin in dpc2 micelles
11	<a href="#">c3jcui</a>			16.0	23	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution

12	<a href="#">c5xnmj_</a>			15.8	32	<b>PDB header:</b> membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> structure of unstacked c2s2m2-type psii-lhcii supercomplex from <i>pisum2 sativum</i>
13	<a href="#">c2momC_</a>			13.8	29	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
14	<a href="#">c5z62M_</a>			13.6	23	<b>PDB header:</b> electron transport <b>Chain:</b> M: <b>PDB Molecule:</b> cytochrome c oxidase subunit 8a, mitochondrial; <b>PDBTitle:</b> structure of human cytochrome c oxidase
15	<a href="#">d1jb0f_</a>			12.6	44	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit III of photosystem I reaction centre, PsaF <b>Family:</b> Subunit III of photosystem I reaction centre, PsaF
16	<a href="#">c2momB_</a>			12.5	29	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
17	<a href="#">d1v54m_</a>			12.4	23	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIb (aka IX) <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIb (aka IX)
18	<a href="#">c4kt0F_</a>			11.6	44	<b>PDB header:</b> electron transport <b>Chain:</b> F: <b>PDB Molecule:</b> photosystem i subunit iii; <b>PDBTitle:</b> crystal structure of a virus like photosystem i from the2 cyanobacterium <i>synechocystis pcc 6803</i>
19	<a href="#">c6igzF_</a>			11.5	19	<b>PDB header:</b> plant protein <b>Chain:</b> F: <b>PDB Molecule:</b> psaf; <b>PDBTitle:</b> structure of psi-lhci
20	<a href="#">c6fhvA_</a>			10.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glucoamylase; <b>PDBTitle:</b> crystal structure of <i>penicillium oxalicum</i> glucoamylase
21	<a href="#">c1cn3F_</a>		not modelled	9.5	29	<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> fragment of coat protein vp2; <b>PDBTitle:</b> interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry
22	<a href="#">c6ijjF_</a>		not modelled	8.9	31	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> psaf; <b>PDBTitle:</b> photosystem i of <i>chlamydomonas reinhardtii</i>
23	<a href="#">c3hd7A_</a>		not modelled	8.7	5	<b>PDB header:</b> exocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
24	<a href="#">d1rkla_</a>		not modelled	7.6	29	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Oligosaccharyltransferase subunit ost4p <b>Family:</b> Oligosaccharyltransferase subunit ost4p
25	<a href="#">c1rkIA_</a>		not modelled	7.6	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> nmr structure of yeast oligosaccharyltransferase subunit2 ost4p
26	<a href="#">d1vema1</a>		not modelled	6.5	50	<b>PDB header:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> Starch-binding domain
27	<a href="#">c2z0bB_</a>		not modelled	6.2	50	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glycerophosphodiester phosphodiesterase 5; <b>PDBTitle:</b> crystal structure of cbm20 domain of human putative2 glycerophosphodiester phosphodiesterase 5 ( <i>kiaa1434</i> )
28	<a href="#">c2koga_</a>		not modelled	6.1	5	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> lipid-bound synaptobrevin solution nmr structure

29	<a href="#">c6fhwB_</a>		Alignment	not modelled	5.9	38	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glucoamylase p; <b>PDBTitle:</b> structure of hormoconis resinae glucoamylase
30	<a href="#">d1ppjd2</a>		Alignment	not modelled	5.6	22	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor <b>Family:</b> Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
31	<a href="#">c6btmC_</a>		Alignment	not modelled	5.6	13	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> alternative complex iii subunit c; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
32	<a href="#">c2xzn9_</a>		Alignment	not modelled	5.5	24	<b>PDB header:</b> ribosome <b>Chain:</b> 9; <b>PDB Molecule:</b> rps31e; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
33	<a href="#">c2xzm9_</a>		Alignment	not modelled	5.5	24	<b>PDB header:</b> ribosome <b>Chain:</b> 9; <b>PDB Molecule:</b> rps31e; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
34	<a href="#">d1kula_</a>		Alignment	not modelled	5.5	50	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> Starch-binding domain
35	<a href="#">c2ww9B_</a>		Alignment	not modelled	5.4	23	<b>PDB header:</b> ribosome <b>Chain:</b> B; <b>PDB Molecule:</b> protein transport protein ssh1; <b>PDBTitle:</b> cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
36	<a href="#">d2axtj1</a>		Alignment	not modelled	5.4	23	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, Psbj <b>Family:</b> Psbj-like
37	<a href="#">c3a0hJ_</a>		Alignment	not modelled	5.4	23	<b>PDB header:</b> electron transport <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
38	<a href="#">c4y3uB_</a>		Alignment	not modelled	5.4	40	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> cardiac phospholamban; <b>PDBTitle:</b> the structure of phospholamban bound to the calcium pump serca1a
39	<a href="#">d1cxla2</a>		Alignment	not modelled	5.1	38	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> Starch-binding domain
40	<a href="#">d1cgta2</a>		Alignment	not modelled	5.0	50	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> Starch-binding domain