



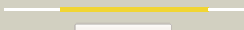

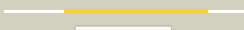
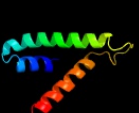
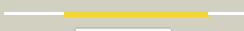







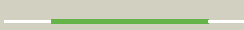
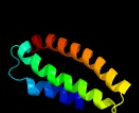
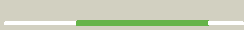
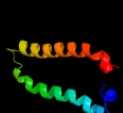

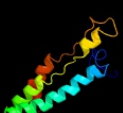
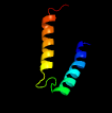










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1861 (-) _2109172_2109477
Date	Fri Aug 2 13:30:47 BST 2019
Unique Job ID	5325703871d7b91e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wufA_	 Alignment		88.0	19	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: structural basis for conductance through tric cation channels
2	d1l7va_	 Alignment		80.8	15	Fold: ABC transporter involved in vitamin B12 uptake, BtuC Superfamily: ABC transporter involved in vitamin B12 uptake, BtuC Family: ABC transporter involved in vitamin B12 uptake, BtuC
3	c5h36E_	 Alignment		78.5	20	PDB header: membrane protein Chain: E: PDB Molecule: uncharacterized protein tric; PDBTitle: crystal structures of the tric trimeric intracellular cation channel2 orthologue from rhodobacter sphaeroides
4	c5b57B_	 Alignment		78.4	17	PDB header: metal transport Chain: B: PDB Molecule: putative hemin abc transport system, membrane protein; PDBTitle: inward-facing conformation of abc heme importer bhuuv from2 burkholderia cenocepacia
5	c4dblB_	 Alignment		75.7	15	PDB header: transport protein Chain: B: PDB Molecule: vitamin b12 import system permease protein btuc; PDBTitle: crystal structure of e159q mutant of btucdf
6	c2nq2A_	 Alignment		69.6	21	PDB header: metal transport Chain: A: PDB Molecule: hypothetical abc transporter permease protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter.
7	c5h35C_	 Alignment		65.3	18	PDB header: immune system/membrane protein Chain: C: PDB Molecule: membrane protein tric; PDBTitle: crystal structures of the tric trimeric intracellular cation channel2 orthologue from sulfolobus solfataricus
8	c5wudA_	 Alignment		63.1	21	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structural basis for conductance through tric cation channels
9	c4hzuS_	 Alignment		51.0	21	PDB header: hydrolase, transport protein Chain: S: PDB Molecule: predicted membrane protein; PDBTitle: structure of a bacterial energy-coupling factor transporter
10	c4ikyA_	 Alignment		50.4	9	PDB header: transport protein Chain: A: PDB Molecule: di-tripeptide abc transporter (permease); PDBTitle: crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
11	c4rfsS_	 Alignment		46.6	19	PDB header: hydrolase, transport protein Chain: S: PDB Molecule: substrate binding pritein s; PDBTitle: structure of a pantothenate energy coupling factor transporter

12	c6e9oA	Alignment		45.6	22	PDB header: membrane protein Chain: A; PDB Molecule: d-galactonate transport; PDBTitle: e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
13	c4g1uB	Alignment		44.3	15	PDB header: transport protein/hydrolase Chain: B; PDB Molecule: hemin transport system permease protein hmuu; PDBTitle: x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
14	c6exsA	Alignment		38.6	12	PDB header: membrane protein Chain: A; PDB Molecule: peptide abc transporter permease; PDBTitle: crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
15	c1xooA	Alignment		19.8	36	PDB header: viral protein Chain: A; PDB Molecule: hemagglutinin; PDBTitle: nmr structure of g1s mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
16	c1iboA	Alignment		18.7	36	PDB header: viral protein Chain: A; PDB Molecule: hemagglutinin ha2 chain peptide; PDBTitle: nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 7.4
17	c1ibnA	Alignment		18.7	36	PDB header: viral protein Chain: A; PDB Molecule: hemagglutinin ha2 chain peptide; PDBTitle: nmr structure of hemagglutinin fusion peptide in dpc2 micelles at ph 5
18	c1xopA	Alignment		18.3	36	PDB header: viral protein Chain: A; PDB Molecule: hemagglutinin; PDBTitle: nmr structure of g1v mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5
19	c2kxaA	Alignment		17.9	36	PDB header: viral protein, immune system Chain: A; PDB Molecule: haemagglutinin ha2 chain peptide; PDBTitle: the hemagglutinin fusion peptide (h1 subtype) at ph 7.4
20	c2l4gA	Alignment		17.6	33	PDB header: viral protein Chain: A; PDB Molecule: haemagglutinin; PDBTitle: influenza haemagglutinin fusion peptide mutant g13a
21	c2ap8A	Alignment	not modelled	17.5	46	PDB header: antibiotic Chain: A; PDB Molecule: bombinin h4; PDBTitle: solution structure of bombinin h4 in dpc micelles
22	c5u9xA	Alignment	not modelled	17.4	64	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-k1; PDBTitle: ocellatin-lb2
23	c2ap7A	Alignment	not modelled	17.3	46	PDB header: antibiotic Chain: A; PDB Molecule: bombinin h2; PDBTitle: solution structure of bombinin h2 in dpc micelles
24	c5ua7A	Alignment	not modelled	17.1	64	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb2; PDBTitle: ocellatin-lb2, solution structure in sds micelle by nmr spectroscopy
25	c5u9rA	Alignment	not modelled	17.1	64	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb2; PDBTitle: ocellatin-lb2, solution structure in tfe by nmr spectroscopy
26	c3rlbB	Alignment	not modelled	16.5	20	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
27	d1rh1a2	Alignment	not modelled	15.1	25	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
28	c4w6vA	Alignment	not modelled	14.9	15	PDB header: transport protein Chain: A; PDB Molecule: di-/tripeptide transporter; PDBTitle: crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
29	c2dc1A	Alignment	not modelled	14.6	36	PDB header: viral protein Chain: A; PDB Molecule: hemagglutinin;

29	c2uc1A_	Alignment	not modelled	14.0	30	PDBTitle: nmr structure of influenza ha fusion peptide mutant w14a in2 dpc in ph5 PDB header: rna binding protein
30	c4ypiF_	Alignment	not modelled	14.1	23	Chain: F; PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of ebola virus nucleoprotein n-terminal fragment bound to a2 peptide derived from ebola vp35
31	c4ypiG_	Alignment	not modelled	14.1	23	PDB header: rna binding protein Chain: G; PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of ebola virus nucleoprotein n-terminal fragment bound to a2 peptide derived from ebola vp35
32	c2k21A_	Alignment	not modelled	14.0	26	PDB header: membrane protein Chain: A; PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c
33	c3phfX_	Alignment	not modelled	13.8	23	PDB header: viral protein Chain: X; PDB Molecule: envelope glycoprotein I; PDBTitle: crystal structure of the epstein-barr virus gh and gl complex
34	c5ua8A_	Alignment	not modelled	13.7	70	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-f1; PDBTitle: ocellatin-f1, solution structure in sds micelle by nmr spectroscopy
35	c5u9sA_	Alignment	not modelled	13.7	70	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-f1; PDBTitle: ocellatin-f1, solution structure in tfe by nmr spectroscopy
36	c5u9yA_	Alignment	not modelled	13.7	70	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-k1; PDBTitle: ocellatin-f1
37	c5u9qA_	Alignment	not modelled	13.5	70	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb1; PDBTitle: ocellatin-lb1
38	c5u9vA_	Alignment	not modelled	13.5	70	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb1; PDBTitle: ocellatin-lb1, solution structure in dpc micelle by nmr spectroscopy
39	c5ua6A_	Alignment	not modelled	13.5	70	PDB header: antimicrobial protein Chain: A; PDB Molecule: ocellatin-lb1; PDBTitle: ocellatin-lb1, solution structure in sds micelle by nmr spectroscopy
40	c2ndjA_	Alignment	not modelled	13.3	21	PDB header: membrane protein Chain: A; PDB Molecule: potassium voltage-gated channel subfamily e member 3; PDBTitle: structural basis for kcne3 and estrogen modulation of the kcnq12 channel
41	c5a40C_	Alignment	not modelled	13.1	13	PDB header: transport protein Chain: C; PDB Molecule: putative fluoride ion transporter crcb; PDBTitle: crystal structure of a dual topology fluoride ion channel.
42	c6e8wC_	Alignment	not modelled	12.2	15	PDB header: viral protein Chain: C; PDB Molecule: envelope glycoprotein gp160; PDBTitle: mper-tm domain of hiv-1 envelope glycoprotein (env)
43	c5egiB_	Alignment	not modelled	12.0	16	PDB header: membrane protein Chain: B; PDB Molecule: uncharacterized protein y57a10a.10; PDBTitle: structure of a trimeric intracellular cation channel from c. elegans2 with bound ca2+
44	c2m0qA_	Alignment	not modelled	11.1	26	PDB header: membrane protein Chain: A; PDB Molecule: potassium voltage-gated channel subfamily e member 2; PDBTitle: solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix
45	c2jrdA_	Alignment	not modelled	11.0	36	PDB header: viral protein Chain: A; PDB Molecule: hemagglutinin; PDBTitle: influenza hemagglutinin fusion domain mutant f9a
46	c4dveA_	Alignment	not modelled	10.0	13	PDB header: transport protein Chain: A; PDB Molecule: biotin transporter bioy; PDBTitle: crystal structure at 2.1 a of the s-component for biotin from an ecf-2 type abc transporter
47	c6g9xB_	Alignment	not modelled	10.0	12	PDB header: membrane protein Chain: B; PDB Molecule: major facilitator superfamily mfs_1; PDBTitle: crystal structure of a mfs transporter at 2.54 angstrom resolution
48	c5eh6A_	Alignment	not modelled	9.3	29	PDB header: membrane protein Chain: A; PDB Molecule: glycophorin-a; PDBTitle: crystal structure of the glycophorin a transmembrane monomer in2 lipidic cubic phase
49	c5eh4C_	Alignment	not modelled	9.3	29	PDB header: membrane protein Chain: C; PDB Molecule: glycophorin-a; PDBTitle: crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
50	c5eh4D_	Alignment	not modelled	9.3	29	PDB header: membrane protein Chain: D; PDB Molecule: glycophorin-a; PDBTitle: crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
51	c5eh4A_	Alignment	not modelled	9.3	29	PDB header: membrane protein Chain: A; PDB Molecule: glycophorin-a; PDBTitle: crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
52	c5eh4B_	Alignment	not modelled	9.3	29	PDB header: membrane protein Chain: B; PDB Molecule: glycophorin-a; PDBTitle: crystal structure of the glycophorin a transmembrane dimer in lipidic2 cubic phase
53	c5ed1A_	Alignment	not modelled	9.0	26	PDB header: transport protein Chain: A; PDB Molecule: putative hmp/thiamine permease protein ykoe; PDBTitle: crystal structure of an s-component of ecf transporter
54	c2ks1B_	Alignment	not modelled	8.8	23	PDB header: transferase Chain: B; PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation

55	c5v2sA_	Alignment	not modelled	8.7	20	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
56	c3b9yA_	Alignment	not modelled	8.5	25	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
57	c6humQ_	Alignment	not modelled	7.9	27	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
58	c2ifmA_	Alignment	not modelled	7.8	36	PDB header: virus Chain: A: PDB Molecule: pf1 filamentous bacteriophage; PDBTitle: pf1 filamentous bacteriophage: refinement of a molecular2 model by simulated annealing using 3.3 angstroms3 resolution x-ray fibre diffraction data
59	c1q11A_	Alignment	not modelled	7.8	36	PDB header: virus Chain: A: PDB Molecule: pf1 bacteriophage coat protein b; PDBTitle: inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
60	c5zjiI_	Alignment	not modelled	7.3	25	PDB header: membrane protein Chain: I: PDB Molecule: photosystem i reaction center subunit viii; PDBTitle: structure of photosystem i supercomplex with light-harvesting2 complexes i and ii
61	d2axtj1	Alignment	not modelled	7.1	28	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, PsbJ Family: PsbJ-like
62	c3a0hj_	Alignment	not modelled	7.1	28	PDB header: electron transport Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
63	c1ciiA_	Alignment	not modelled	6.8	18	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
64	d1n2fa_	Alignment	not modelled	6.1	12	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
65	c5nikK_	Alignment	not modelled	6.1	13	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
66	d1wj7a1	Alignment	not modelled	6.0	21	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
67	c4nozA_	Alignment	not modelled	5.8	18	PDB header: protein binding Chain: A: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of an organic hydroperoxide resistance protein from2 burkholderia cenocepacia
68	c5d7tC_	Alignment	not modelled	5.7	12	PDB header: transport protein Chain: C: PDB Molecule: s-component for folate; PDBTitle: folate ecf transporter: apo state
69	c2mp8A_	Alignment	not modelled	5.6	36	PDB header: antimicrobial protein Chain: A: PDB Molecule: nkr-5-3b; PDBTitle: nmr structure of nkr-5-3b
70	c2kncB_	Alignment	not modelled	5.4	17	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex