



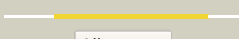
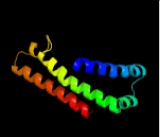



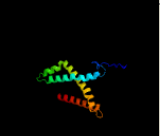

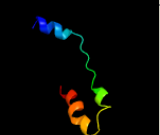
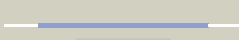


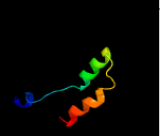





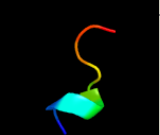








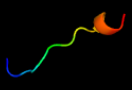


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1555_(frdD)_1760558_1760935
Date	Fri Aug 2 13:30:14 BST 2019
Unique Job ID	92fca238ff7fcb5b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1kf6d_</a>	 Alignment		100.0	31	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
2	<a href="#">d1nekc_</a>	 Alignment		93.2	12	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
3	<a href="#">d1nekd_</a>	 Alignment		72.0	14	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
4	<a href="#">c4ymkA_</a>	 Alignment		54.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase 1; <b>PDBTitle:</b> crystal structure of stearyl-coenzyme a desaturase 1
5	<a href="#">d1kf6c_</a>	 Alignment		50.4	14	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Fumarate reductase respiratory complex transmembrane subunits <b>Family:</b> Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
6	<a href="#">c2lj2A_</a>	 Alignment		28.1	37	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> integral membrane core domain of the mercury transporter merf in lipid2 bilayer membranes
7	<a href="#">c3vr6G_</a>	 Alignment		25.6	21	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome b-large subunit; <b>PDBTitle:</b> mitochondrial rhoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
8	<a href="#">c2m67A_</a>	 Alignment		22.9	37	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> full-length mercury transporter protein merf in lipid bilayer2 membranes
9	<a href="#">c1ciiA_</a>	 Alignment		17.3	38	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
10	<a href="#">c6bm8A_</a>	 Alignment		16.1	32	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of glycoprotein b from herpes simplex virus type i
11	<a href="#">c2m86A_</a>	 Alignment		15.6	67	<b>PDB header:</b> protein binding/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> mco-pmi; <b>PDBTitle:</b> solution structure of hdm2 with engineered cyclotide

12	<a href="#">c5h2sA_</a>	Alignment		14.5	46	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> piscidin-4; <b>PDBTitle:</b> solution structure of tilapia piscidin 4 (tp4) from oreochromis2 niloticus
13	<a href="#">c1yq3C_</a>	Alignment		13.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> succinate dehydrogenase cytochrome b, large subunit; <b>PDBTitle:</b> avian respiratory complex ii with oxaloacetate and ubiquinone
14	<a href="#">c2jo1A_</a>	Alignment		10.1	24	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
15	<a href="#">c5xmjG_</a>	Alignment		9.8	15	<b>PDB header:</b> electron transport <b>Chain:</b> G: <b>PDB Molecule:</b> fumarate reductase respiratory complex; <b>PDBTitle:</b> crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
16	<a href="#">c2y69Z_</a>	Alignment		9.7	12	<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
17	<a href="#">d1kwia_</a>	Alignment		9.5	25	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> Cystatin/monellin <b>Family:</b> Cathelicidin motif
18	<a href="#">d2c52b1</a>	Alignment		8.5	27	<b>Fold:</b> Nuclear receptor coactivator interlocking domain <b>Superfamily:</b> Nuclear receptor coactivator interlocking domain <b>Family:</b> Nuclear receptor coactivator interlocking domain
19	<a href="#">c2jp3A_</a>	Alignment		8.3	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fxyd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
20	<a href="#">c5wsnC_</a>	Alignment		8.2	31	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> e protein; <b>PDBTitle:</b> structure of japanese encephalitis virus
21	<a href="#">c4kslW_</a>	Alignment	not modelled	7.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> W: <b>PDB Molecule:</b> protein fam105b; <b>PDBTitle:</b> gumby/fam105b in complex with linear di-ubiquitin
22	<a href="#">c5vx3B_</a>	Alignment	not modelled	7.9	38	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> bcl-2-like protein 11; <b>PDBTitle:</b> bcl-xl in complex with bim-h3pc-rt
23	<a href="#">c2mkvA_</a>	Alignment	not modelled	7.6	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in micelles
24	<a href="#">c5z62M_</a>	Alignment	not modelled	7.2	19	<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
25	<a href="#">c6drmA_</a>	Alignment	not modelled	7.2	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> inactive ubiquitin thioesterase fam105a; <b>PDBTitle:</b> otu domain of fam105a
26	<a href="#">d1v54m_</a>	Alignment	not modelled	6.9	15	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
27	<a href="#">c2of6C_</a>	Alignment	not modelled	6.9	23	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> envelope glycoprotein e; <b>PDBTitle:</b> structure of immature west nile virus
28	<a href="#">c5ireA_</a>	Alignment	not modelled	6.6	23	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> e protein; <b>PDBTitle:</b> the cryo-em structure of zika virus

29	<a href="#">d1ok8a2</a>	Alignment	not modelled	6.6	7	<b>Fold:</b> Viral glycoprotein, central and dimerisation domains <b>Superfamily:</b> Viral glycoprotein, central and dimerisation domains <b>Family:</b> Viral glycoprotein, central and dimerisation domains
30	<a href="#">c4phtY_</a>	Alignment	not modelled	6.1	26	<b>PDB header:</b> protein transport <b>Chain:</b> Y: <b>PDB Molecule:</b> type ii secretion system protein I; <b>PDBTitle:</b> atpase gspe in complex with the cytoplasmic domain of gspl from the2 vibrio vulnificus type ii secretion system
31	<a href="#">c3jcul_</a>	Alignment	not modelled	6.1	19	<b>PDB header:</b> membrane protein <b>Chain:</b> L: <b>PDB Molecule:</b> protein photosystem ii reaction center protein I; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
32	<a href="#">c1p58C_</a>	Alignment	not modelled	6.0	8	<b>PDB header:</b> virus <b>Chain:</b> C: <b>PDB Molecule:</b> major envelope protein e; <b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
33	<a href="#">c4b03A_</a>	Alignment	not modelled	5.8	15	<b>PDB header:</b> virus <b>Chain:</b> A: <b>PDB Molecule:</b> dengue virus 1 e protein; <b>PDBTitle:</b> 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
34	<a href="#">c6ajjA_</a>	Alignment	not modelled	5.8	16	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> drug exporters of the rnd superfamily-like protein, <b>PDBTitle:</b> crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
35	<a href="#">c3c00A_</a>	Alignment	not modelled	5.8	45	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> escu; <b>PDBTitle:</b> crystal structural of the mutated g247t escu/spas c-terminal domain
36	<a href="#">c2l8sA_</a>	Alignment	not modelled	5.7	30	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
37	<a href="#">d2bh1a2</a>	Alignment	not modelled	5.7	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Cyto-EpsL domain
38	<a href="#">c5nmiK_</a>	Alignment	not modelled	5.6	46	<b>PDB header:</b> membrane protein <b>Chain:</b> K: <b>PDB Molecule:</b> arg-asn-trp-val-pro-thr-ala-gln-leu-trp-gly-ala-val-gly- <b>PDBTitle:</b> cytochrome bc1 bound to the inhibitor mjm170
39	<a href="#">c5nmiX_</a>	Alignment	not modelled	5.6	46	<b>PDB header:</b> membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> arg-asn-trp-val-pro-thr-ala-gln-leu-trp-gly-ala-val-gly- <b>PDBTitle:</b> cytochrome bc1 bound to the inhibitor mjm170
40	<a href="#">d1be3k_</a>	Alignment	not modelled	5.6	46	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) <b>Family:</b> Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
41	<a href="#">c2zxeG_</a>	Alignment	not modelled	5.4	24	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
42	<a href="#">c6h3aB_</a>	Alignment	not modelled	5.3	32	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin-dependent regulator <b>PDBTitle:</b> crystal structure of the kap1 rbcc domain in complex with the smarcad12 cue1 domain.
43	<a href="#">c4kt3B_</a>	Alignment	not modelled	5.1	57	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> structure of a type vi secretion system effector-immunity complex from2 pseudomonas protegens