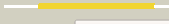
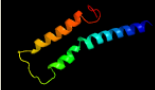
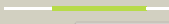




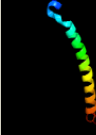



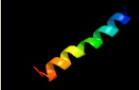
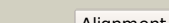
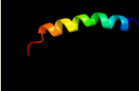

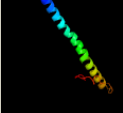





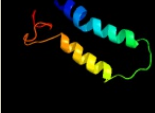


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2306B (-) _2577498_2577932
Date	Mon Aug 5 13:25:45 BST 2019
Unique Job ID	56f078546f2aff39

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5n9yB_</a>	 Alignment		75.6	16	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> zinc transport protein zntb; <b>PDBTitle:</b> the full-length structure of zntb
2	<a href="#">c4ev6E_</a>	 Alignment		62.8	11	<b>PDB header:</b> metal transport <b>Chain:</b> E; <b>PDB Molecule:</b> magnesium transport protein cora; <b>PDBTitle:</b> the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
3	<a href="#">c2w8aC_</a>	 Alignment		44.4	9	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
4	<a href="#">c1zrtD_</a>	 Alignment		41.1	4	<b>PDB header:</b> oxidoreductase/metal transport <b>Chain:</b> D; <b>PDB Molecule:</b> cytochrome c1; <b>PDBTitle:</b> rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
5	<a href="#">c4n7wA_</a>	 Alignment		30.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> transporter, sodium/bile acid symporter family; <b>PDBTitle:</b> crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
6	<a href="#">c2na6A_</a>	 Alignment		29.4	30	<b>PDB header:</b> apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
7	<a href="#">c2na6C_</a>	 Alignment		29.4	30	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
8	<a href="#">c4gn0D_</a>	 Alignment		28.9	11	<b>PDB header:</b> signaling protein <b>Chain:</b> D; <b>PDB Molecule:</b> hamp domain of af1503; <b>PDBTitle:</b> de novo phasing of a hamp-complex using an improved arcimboldo method
9	<a href="#">c1ciiA_</a>	 Alignment		28.2	29	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
10	<a href="#">c2na6B_</a>	 Alignment		25.7	30	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
11	<a href="#">c2bbjB_</a>	 Alignment		25.5	17	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter

12	<a href="#">c3j09A_</a>	Alignment		19.8	14	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A; <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
13	<a href="#">c4wv4A_</a>	Alignment		18.9	20	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 10; <b>PDBTitle:</b> heterodimer of taf8/taf10
14	<a href="#">c3cwbQ_</a>	Alignment		18.8	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q; <b>PDB Molecule:</b> mitochondrial cytochrome c1, heme protein; <b>PDBTitle:</b> chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
15	<a href="#">c5t4oJ_</a>	Alignment		18.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> J; <b>PDB Molecule:</b> atp synthase subunit b; <b>PDBTitle:</b> autoinhibited e. coli atp synthase state 1
16	<a href="#">c6an7D_</a>	Alignment		17.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> transport permease protein; <b>PDBTitle:</b> crystal structure of o-antigen polysaccharide abc-transporter
17	<a href="#">c2n28A_</a>	Alignment		16.4	24	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein vpu; <b>PDBTitle:</b> solid-state nmr structure of vpu
18	<a href="#">c3pcqX_</a>	Alignment		16.2	36	<b>PDB header:</b> photosynthesis <b>Chain:</b> X; <b>PDB Molecule:</b> photosystem i 4.8k protein; <b>PDBTitle:</b> femtosecond x-ray protein nanocrystallography
19	<a href="#">c3j08A_</a>	Alignment		15.0	14	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A; <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
20	<a href="#">c3sokB_</a>	Alignment		14.9	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> B; <b>PDB Molecule:</b> fimbrial protein; <b>PDBTitle:</b> dichelobacter nodosus pilin fima
21	<a href="#">c5wsuD_</a>	Alignment	not modelled	13.9	27	<b>PDB header:</b> motor protein/calcium binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> unconventional myosin-viia; <b>PDBTitle:</b> crystal structure of myosin viia iq5-sah in complex with apo-cam
22	<a href="#">d1pw4a_</a>	Alignment	not modelled	13.5	7	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
23	<a href="#">c1p84D_</a>	Alignment	not modelled	13.2	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> cytochrome c1, heme protein; <b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex
24	<a href="#">c5kk2E_</a>	Alignment	not modelled	12.8	7	<b>PDB header:</b> membrane protein, transport protein, sig <b>Chain:</b> E; <b>PDB Molecule:</b> voltage-dependent calcium channel gamma-2 subunit; <b>PDBTitle:</b> architecture of fully occupied glua2 ampa receptor - tarp complex2 elucidated by single particle cryo-electron microscopy
25	<a href="#">c4jo6Z_</a>	Alignment	not modelled	12.2	55	<b>PDB header:</b> unknown function <b>Chain:</b> Z; <b>PDB Molecule:</b> sbp-tag; <b>PDBTitle:</b> streptavidin complex with sbp-tag
26	<a href="#">c1qcrD_</a>	Alignment	not modelled	11.7	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> ubiquinol cytochrome c oxidoreductase; <b>PDBTitle:</b> crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
27	<a href="#">c1lifa_</a>	Alignment	not modelled	11.4	19	<b>PDB header:</b> virus <b>Chain:</b> A; <b>PDB Molecule:</b> inovirus; <b>PDBTitle:</b> molecular models and structural comparisons of native and2 mutant class i filamentous bacteriophages ff (fd, f1, m13),3 if1 and ike
28	<a href="#">c2mnsA_</a>	Alignment	not modelled	11.3	29	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> membrane fusion protein p15; <b>PDBTitle:</b> solution nmr structure of the reovirus p15 fusion-

28	<a href="#">c4mmsA</a>	Alignment	not modelled	11.5	29	associated small2 transmembrane (fast) protein fusion-inducing lipid packing sensor3 (flips) motif in dodecyl phosphocholine (dpc) micelles
29	<a href="#">c4jo6Y</a>	Alignment	not modelled	11.0	55	<b>PDB header:</b> unknown function <b>Chain:</b> Y; <b>PDB Molecule:</b> sbp-tag; <b>PDBTitle:</b> streptavidin complex with sbp-tag
30	<a href="#">c2na8A</a>	Alignment	not modelled	10.7	23	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> cytokine receptor common subunit beta; <b>PDBTitle:</b> transmembrane structure of the cytokine receptor common subunit beta
31	<a href="#">c6an7C</a>	Alignment	not modelled	10.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> transport permease protein; <b>PDBTitle:</b> crystal structure of o-antigen polysaccharide abc-transporter
32	<a href="#">c4inqA</a>	Alignment	not modelled	10.4	43	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> oxysterol-binding protein homolog 3; <b>PDBTitle:</b> crystal structure of osh3 ord in complex with pi(4)p from2 saccharomyces cerevisiae
33	<a href="#">c4b2zB</a>	Alignment	not modelled	9.9	57	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> oxysterol-binding protein homolog 6; <b>PDBTitle:</b> structure of osh6 in complex with phosphatidylserine
34	<a href="#">c5wvrA</a>	Alignment	not modelled	9.6	71	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> klla0c04147p; <b>PDBTitle:</b> crystal structure of osh1 ord domain in complex with cholesterol
35	<a href="#">c1ijjA</a>	Alignment	not modelled	9.5	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> erbB-2 receptor protein-tyrosine kinase; <b>PDBTitle:</b> solution structure of the neu/erbB-2 membrane spanning2 segment
36	<a href="#">c2micA</a>	Alignment	not modelled	9.5	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles
37	<a href="#">c2micB</a>	Alignment	not modelled	9.5	22	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles
38	<a href="#">d3cmco2</a>	Alignment	not modelled	9.5	14	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glycerolaldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
39	<a href="#">c5xamA</a>	Alignment	not modelled	9.4	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> protein translocase subunit secD; <b>PDBTitle:</b> crystal structure of secDf in i form at 4 a resolution
40	<a href="#">d1dssg2</a>	Alignment	not modelled	9.3	14	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glycerolaldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
41	<a href="#">c5zm8A</a>	Alignment	not modelled	9.1	71	<b>PDB header:</b> lipid transport <b>Chain:</b> A; <b>PDB Molecule:</b> oxysterol-binding protein-related protein 2; <b>PDBTitle:</b> crystal structure of orp2-ord in complex with pi(4,5)p2
42	<a href="#">c1m57H</a>	Alignment	not modelled	9.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H; <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
43	<a href="#">d2r31a1</a>	Alignment	not modelled	8.8	17	<b>Fold:</b> ATP12-like <b>Superfamily:</b> ATP12-like <b>Family:</b> ATP12-like
44	<a href="#">d2b4ro2</a>	Alignment	not modelled	8.7	18	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glycerolaldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
45	<a href="#">d2pkqo2</a>	Alignment	not modelled	8.7	14	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glycerolaldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
46	<a href="#">c2na9A</a>	Alignment	not modelled	8.5	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> cytokine receptor common subunit beta; <b>PDBTitle:</b> transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
47	<a href="#">d1obfo2</a>	Alignment	not modelled	8.5	14	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glycerolaldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
48	<a href="#">c1zi7C</a>	Alignment	not modelled	8.4	57	<b>PDB header:</b> lipid binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> kes1 protein; <b>PDBTitle:</b> structure of truncated yeast oxysterol binding protein osh4
49	<a href="#">d1i32a2</a>	Alignment	not modelled	8.1	21	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glycerolaldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
50	<a href="#">d1ggaa2</a>	Alignment	not modelled	8.0	18	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glycerolaldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
51	<a href="#">d1rm4a2</a>	Alignment	not modelled	7.9	14	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glycerolaldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
52	<a href="#">d1zhxa1</a>	Alignment	not modelled	7.8	57	<b>Fold:</b> Oxysterol-binding protein-like <b>Superfamily:</b> Oxysterol-binding protein-like <b>Family:</b> Oxysterol-binding protein
53	<a href="#">d1k3ta2</a>	Alignment	not modelled	7.7	21	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glycerolaldehyde-3-phosphate dehydrogenase-like, C-terminal domain

						<b>Family:</b> GAPDH-like <b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
54	<a href="#">d3gpdg2</a>	Alignment	not modelled	7.6	14	<b>Family:</b> GAPDH-like <b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem ii reaction center protein x; <b>PDBTitle:</b> cryo-em structure of the psii supercomplex from arabidopsis thaliana
55	<a href="#">c5mdxx_</a>	Alignment	not modelled	7.6	29	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem ii reaction center protein x; <b>PDBTitle:</b> cryo-em structure of the psii supercomplex from arabidopsis thaliana
56	<a href="#">c5mdxX_</a>	Alignment	not modelled	7.6	29	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
57	<a href="#">d2g82a2</a>	Alignment	not modelled	7.4	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> na(+)/h(+) antiporter; <b>PDBTitle:</b> crystal structure of sodium proton antiporter napa in outward-facing2 conformation.
58	<a href="#">c5bz3A_</a>	Alignment	not modelled	7.4	12	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
59	<a href="#">d1gado2</a>	Alignment	not modelled	7.1	14	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
60	<a href="#">c5x5yF_</a>	Alignment	not modelled	7.1	8	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 4 subunit a; <b>PDBTitle:</b> crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
61	<a href="#">c2inrA_</a>	Alignment	not modelled	6.3	16	<b>PDB header:</b> signaling protein/antagonist <b>Chain:</b> A: <b>PDB Molecule:</b> proteinase-activated receptor 1, lysozyme; <b>PDBTitle:</b> crystal structure of human protease-activated receptor 1 (par1) bound2 with antagonist vorapaxar at 2.2 angstrom
62	<a href="#">c3vw7A_</a>	Alignment	not modelled	6.1	10	<b>Fold:</b> Pili subunits <b>Superfamily:</b> Pili subunits <b>Family:</b> Pilin
63	<a href="#">d2pila_</a>	Alignment	not modelled	6.1	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter; <b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc
64	<a href="#">c4djiA_</a>	Alignment	not modelled	6.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome c1, heme protein; <b>PDBTitle:</b> x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
65	<a href="#">c2yiuE_</a>	Alignment	not modelled	6.0	4	<b>PDB header:</b> membrane protein,transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> large conductance mechanosensitive channel protein, <b>PDBTitle:</b> structure of an archaeal mechanosensitive channel in expanded state
66	<a href="#">c4y7jE_</a>	Alignment	not modelled	5.9	15	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
67	<a href="#">d1u8fo2</a>	Alignment	not modelled	5.8	14	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> protein translocase subunit secd; <b>PDBTitle:</b> em fitted model of bacterial holo-translocon
68	<a href="#">c5mg3D_</a>	Alignment	not modelled	5.7	7	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein detoxification 14; <b>PDBTitle:</b> crystal structure of eukaryotic mate transporter atdtx14
69	<a href="#">c5y50A_</a>	Alignment	not modelled	5.6	9	<b>PDB header:</b> hydrolase, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rna-dependent rna polymerase; <b>PDBTitle:</b> crystal structure of the viral otu domain protease from dera ghazi2 khan virus
70	<a href="#">c6dx2A_</a>	Alignment	not modelled	5.5	24	<b>PDB header:</b> lipoprotein(surface film) <b>Chain:</b> A: <b>PDB Molecule:</b> pulmonary surfactant-associated polypeptide c; <b>PDBTitle:</b> the nmr structure of the pulmonary surfactant-associated2 polypeptide sp-c in an apolar solvent contains a valyl-3 rich alpha-helix
71	<a href="#">c1spfA_</a>	Alignment	not modelled	5.4	36	<b>PDB header:</b> dna binding protein/replication <b>Chain:</b> C: <b>PDB Molecule:</b> ssdna-specific exonuclease; <b>PDBTitle:</b> dna replication protein
72	<a href="#">c5ghrC_</a>	Alignment	not modelled	5.3	67	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> sodium channel subunit beta-1; <b>PDBTitle:</b> structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
73	<a href="#">c6agfB_</a>	Alignment	not modelled	5.2	17	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein pb1-f2; <b>PDBTitle:</b> structural characterization and oligomerization of pb1-f2,2 a pro-apoptotic influenza a virus protein
74	<a href="#">c2hn8A_</a>	Alignment	not modelled	5.1	33	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> vit1; <b>PDBTitle:</b> crystal structure of iron transporter vit1 with zinc ions
75	<a href="#">c6iu3A_</a>	Alignment	not modelled	5.1	19	<b>Fold:</b> Pili subunits <b>Superfamily:</b> Pili subunits <b>Family:</b> Pilin
76	<a href="#">d1oqwa_</a>	Alignment	not modelled	5.1	12	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein w; <b>PDBTitle:</b> nipah virus w protein c-terminus in complex with importin alpha 3
77	<a href="#">c6bvVB_</a>	Alignment	not modelled	5.1	43	