
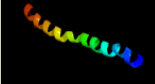
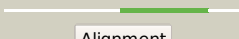
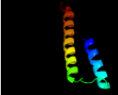
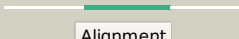

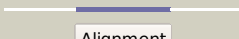

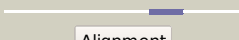

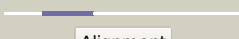








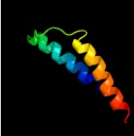

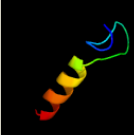

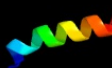


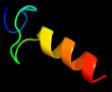






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1671_(-)_1896482_1896874
Date	Fri Aug 2 13:30:27 BST 2019
Unique Job ID	0658374469ee85c2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2m67A_</a>	 Alignment		67.0	19	<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
2	<a href="#">c6btmF_</a>	 Alignment		50.1	18	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> alternative complex iii subunit f; <b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
3	<a href="#">c5n9yB_</a>	 Alignment		41.1	10	<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
4	<a href="#">c4ev6E_</a>	 Alignment		19.3	13	<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
5	<a href="#">d2e9xb2</a>	 Alignment		15.3	27	<b>Fold:</b> GINS/PriA/YqbF domain <b>Superfamily:</b> PriA/YqbF domain <b>Family:</b> PSF2 N-terminal domain-like
6	<a href="#">d2axtj1</a>	 Alignment		15.2	30	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, Psbj <b>Family:</b> Psbj-like
7	<a href="#">c3a0hj_</a>	 Alignment		15.2	30	<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
8	<a href="#">c2hn8A_</a>	 Alignment		11.5	30	<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
9	<a href="#">c6humQ_</a>	 Alignment		11.3	58	<b>PDB header:</b> proton transport <b>Chain:</b> Q: <b>PDB Molecule:</b> proton-translocating nadh-quinone dehydrogenase subunit q <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
10	<a href="#">c2bbjB_</a>	 Alignment		10.4	12	<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
11	<a href="#">c1k6nH_</a>	 Alignment		9.9	37	<b>PDB header:</b> photosynthesis <b>Chain:</b> H: <b>PDB Molecule:</b> photosynthetic reaction center h subunit; <b>PDBTitle:</b> e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides

12	<a href="#">c2lcoA_</a>	Alignment		9.8	29	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> walp19-p8 peptide; <b>PDBTitle:</b> 1h and 15n assignments of walp19-p8 peptide in sds micelles
13	<a href="#">c2y0mB_</a>	Alignment		9.1	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> male-specific lethal 1 homolog; <b>PDBTitle:</b> crystal structure of the complex between dosage2 compensation factors msl1 and mof
14	<a href="#">d1y5ic1</a>	Alignment		8.6	19	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Respiratory nitrate reductase 1 gamma chain <b>Family:</b> Respiratory nitrate reductase 1 gamma chain
15	<a href="#">c2a2bA_</a>	Alignment		8.5	40	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin curvacin a; <b>PDBTitle:</b> curvacin a
16	<a href="#">c1eysH_</a>	Alignment		8.4	26	<b>PDB header:</b> electron transport <b>Chain:</b> H: <b>PDB Molecule:</b> photosynthetic reaction center; <b>PDBTitle:</b> crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
17	<a href="#">c2lcnA_</a>	Alignment		8.1	29	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> walp19-p10 peptide; <b>PDBTitle:</b> 1h and 15n assignments of walp19-p10 peptide in sds micelles
18	<a href="#">c6gcs6_</a>	Alignment		7.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 6: <b>PDB Molecule:</b> nd6 subunit (nu6m); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
19	<a href="#">d1ft8e_</a>	Alignment		7.4	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> RNA-binding domain, RBD <b>Family:</b> Non-canonical RBD domain
20	<a href="#">c4n9nA_</a>	Alignment		7.1	44	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> sterol uptake control protein 2, lysozyme; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae upc2 transcription2 factor fused with t4 lysozyme
21	<a href="#">c6nbxG_</a>	Alignment	not modelled	6.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
22	<a href="#">c5uzlA_</a>	Alignment	not modelled	6.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-acyltransferase; <b>PDBTitle:</b> brassica napus dgat1 exosite
23	<a href="#">c3fseB_</a>	Alignment	not modelled	6.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> two-domain protein containing dj-1/thij/pfpi-like and <b>PDBTitle:</b> crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
24	<a href="#">c5b2gG_</a>	Alignment	not modelled	6.6	30	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> endolysin,claudin-4; <b>PDBTitle:</b> crystal structure of human claudin-4 in complex with c-terminal2 fragment of clostridium perfringens enterotoxin
25	<a href="#">c2e9xF_</a>	Alignment	not modelled	6.4	27	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> dna replication complex gins protein psf2; <b>PDBTitle:</b> the crystal structure of human gins core complex
26	<a href="#">d2p7tc1</a>	Alignment	not modelled	6.4	43	<b>Fold:</b> Voltage-gated potassium channels <b>Superfamily:</b> Voltage-gated potassium channels <b>Family:</b> Voltage-gated potassium channels
27	<a href="#">c6c5wA_</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium uniporter; <b>PDBTitle:</b> crystal structure of the mitochondrial calcium uniporter
28	<a href="#">c3uk7B_</a>	Alignment	not modelled	6.2	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> class i glutamine amidotransferase-like domain-containing <b>PDBTitle:</b> crystal structure of arabidopsis thaliana dj-1d

29	<a href="#">c6ithA_</a>	Alignment	not modelled	6.1	33	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> syndecan-2; <b>PDBTitle:</b> structure of the transmembrane domain of syndecan 2 in micelles
30	<a href="#">c6bymA_</a>	Alignment	not modelled	6.0	40	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> sterol-binding protein; <b>PDBTitle:</b> crystal structure of the sterol-bound second start domain of yeast2 lam4
31	<a href="#">c3n23E_</a>	Alignment	not modelled	6.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> na+/k+ atpase gamma subunit transcript variant a; <b>PDBTitle:</b> crystal structure of the high affinity complex between ouabain and the2 e2p form of the sodium-potassium pump
32	<a href="#">c6ceiA_</a>	Alignment	not modelled	5.8	86	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> g117; <b>PDBTitle:</b> solution nmr structure of conotoxin g117 from conus geographus
33	<a href="#">c5kgmA_</a>	Alignment	not modelled	5.6	57	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> 2.95a resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form)
34	<a href="#">c4g4sP_</a>	Alignment	not modelled	5.5	23	<b>PDB header:</b> hydrolase/chaperone <b>Chain:</b> P: <b>PDB Molecule:</b> proteasome assembly chaperone 2; <b>PDBTitle:</b> structure of proteasome-pba1-pba2 complex
35	<a href="#">c3jc7B_</a>	Alignment	not modelled	5.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna replication complex gins protein psf2; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
36	<a href="#">c6d80A_</a>	Alignment	not modelled	5.2	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial calcium uniporter; <b>PDBTitle:</b> cryo-em structure of the mitochondrial calcium uniporter from n.2 fischeri bound to saposin
37	<a href="#">c3k9tA_</a>	Alignment	not modelled	5.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidase; <b>PDBTitle:</b> crystal structure of putative peptidase (np_348812.1) from clostridium2 acetobutylicum at 2.37 a resolution