
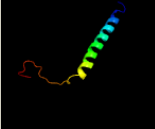



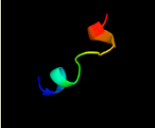

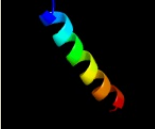







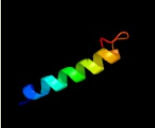





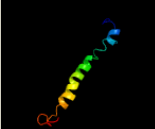


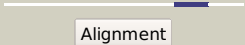



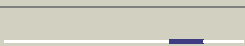

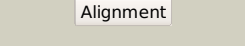

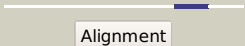
# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2395 (-) _2690082_2692085
Date	Mon Aug 5 13:25:55 BST 2019
Unique Job ID	20c32e077bb59529

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6cfwl_</a>	 Alignment		36.3	20	<b>PDB header:</b> membrane protein <b>Chain:</b> I: <b>PDB Molecule:</b> mbh subunit; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
2	<a href="#">d1y5ic1</a>	 Alignment		33.6	17	<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
3	<a href="#">c6c90B_</a>	 Alignment		32.0	33	<b>PDB header:</b> hydrolase/rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> zinc finger cchc domain-containing protein 8; <b>PDBTitle:</b> human mtr4 helicase in complex with zcchc8-ctd
4	<a href="#">c6igzM_</a>	 Alignment		30.0	33	<b>PDB header:</b> plant protein <b>Chain:</b> M: <b>PDB Molecule:</b> photosystem i reaction center subunit xii; <b>PDBTitle:</b> structure of psi-lhci
5	<a href="#">c6ithA_</a>	 Alignment		29.5	28	<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
6	<a href="#">c3orgB_</a>	 Alignment		26.8	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cmclc; <b>PDBTitle:</b> crystal structure of a eukaryotic clc transporter
7	<a href="#">c3qngD_</a>	 Alignment		24.7	12	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
8	<a href="#">c2latA_</a>	 Alignment		21.5	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> solution structure of a human minimembrane protein ost4
9	<a href="#">d1ymga1</a>	 Alignment		17.5	13	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
10	<a href="#">c1ymgA_</a>	 Alignment		17.5	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lens fiber major intrinsic protein; <b>PDBTitle:</b> the channel architecture of aquaporin o at 2.2 angstrom resolution
11	<a href="#">c3chxG_</a>	 Alignment		15.3	16	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> pmoc; <b>PDBTitle:</b> crystal structure of methylosinus trichosporium ob3b particulate2 methane monooxygenase (pmmo)

12	<a href="#">d1j4na_</a>	Alignment		13.8	12	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
13	<a href="#">c2na6B_</a>	Alignment		13.5	26	<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
14	<a href="#">c2na6A_</a>	Alignment		13.5	26	<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
15	<a href="#">c2na6C_</a>	Alignment		13.5	26	<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
16	<a href="#">c4nefB_</a>	Alignment		11.3	11	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> aquaporin-2; <b>PDBTitle:</b> x-ray structure of human aquaporin 2
17	<a href="#">d2fnoa1</a>	Alignment		11.3	20	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
18	<a href="#">c2n1pA_</a>	Alignment		11.2	30	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 5b, ns5b; <b>PDBTitle:</b> structure of the c-terminal membrane domain of hcv ns5b protein
19	<a href="#">c3rgbG_</a>	Alignment		10.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> methane monooxygenase subunit c2; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
20	<a href="#">c4a01B_</a>	Alignment		8.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> proton pyrophosphatase; <b>PDBTitle:</b> crystal structure of the h-translocating pyrophosphatase
21	<a href="#">c3rfrK_</a>	Alignment	not modelled	8.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> pmoc; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
22	<a href="#">d1dq3a3</a>	Alignment	not modelled	8.0	38	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Intein endonuclease
23	<a href="#">c3j1zP_</a>	Alignment	not modelled	7.6	11	<b>PDB header:</b> metal transport <b>Chain:</b> P: <b>PDB Molecule:</b> cation efflux family protein; <b>PDBTitle:</b> inward-facing conformation of the zinc transporter yiiP revealed by2 cryo-electron microscopy
24	<a href="#">c1yewC_</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> particulate methane monooxygenase subunit c2; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
25	<a href="#">c4rfsS_</a>	Alignment	not modelled	7.0	11	<b>PDB header:</b> hydrolase, transport protein <b>Chain:</b> S: <b>PDB Molecule:</b> substrate binding prtein s; <b>PDBTitle:</b> structure of a pantothenate energy coupling factor transporter
26	<a href="#">c5zghK_</a>	Alignment	not modelled	6.8	19	<b>PDB header:</b> photosynthesis <b>Chain:</b> K: <b>PDB Molecule:</b> psak; <b>PDBTitle:</b> cryo-em structure of the red algal psi-lhcr
27	<a href="#">c5azcA_</a>	Alignment	not modelled	6.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> prolipoprotein diacylglycerol transferase; <b>PDBTitle:</b> crystal structure of escherichia coli lgt in complex with2 phosphatidylglycerol
28	<a href="#">c1ckwA_</a>	Alignment	not modelled	6.4	33	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> protein (cystic fibrosis transmembrane <b>PDBTitle:</b> cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation

29	<a href="#">c6hwhb_</a>	 Alignment	not modelled	6.2	12	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquinol-cytochrome c reductase iron-sulfur subunit; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
30	<a href="#">c4djiA_</a>	 Alignment	not modelled	5.8	12	<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
31	<a href="#">c2ka1A_</a>	 Alignment	not modelled	5.2	45	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
32	<a href="#">c2ka1B_</a>	 Alignment	not modelled	5.2	45	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
33	<a href="#">c2ka2B_</a>	 Alignment	not modelled	5.2	45	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
34	<a href="#">c2ka2A_</a>	 Alignment	not modelled	5.2	45	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> bcl2/adenovirus e1b 19 kda protein-interacting <b>PDBTitle:</b> solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
35	<a href="#">c2nx9B_</a>	 Alignment	not modelled	5.1	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
36	<a href="#">c1jb0K_</a>	 Alignment	not modelled	5.1	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> K: <b>PDB Molecule:</b> photosystem 1 reaction centre subunit x; <b>PDBTitle:</b> crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
37	<a href="#">d1jb0k_</a>	 Alignment	not modelled	5.1	18	<b>Fold:</b> Photosystem I reaction center subunit X, PsaK <b>Superfamily:</b> Photosystem I reaction center subunit X, PsaK <b>Family:</b> Photosystem I reaction center subunit X, PsaK