
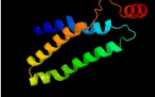





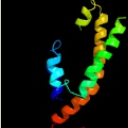





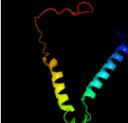







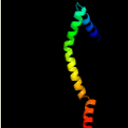
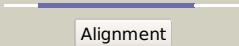


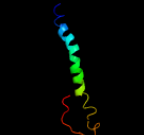

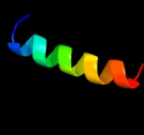
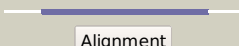

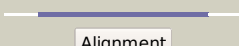

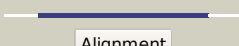

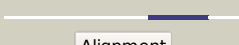
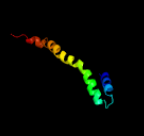
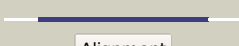


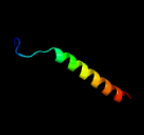
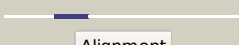
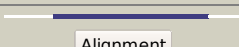

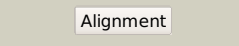


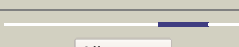


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD2637\_(dedA)\_2963596\_2964252  
 Date Wed Aug 7 12:50:28 BST 2019  
 Unique Job ID 833718106fc8cbfa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4j05A_</a>	 Alignment		70.2	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate transporter; <b>PDBTitle:</b> crystal structure of a eukaryotic phosphate transporter
2	<a href="#">c4huqS_</a>	 Alignment		64.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> S: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a transporter
3	<a href="#">c5a1sB_</a>	 Alignment		47.4	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> citrate-sodium symporter; <b>PDBTitle:</b> crystal structure of the sodium-dependent citrate symporter secits2 form salmonella enterica.
4	<a href="#">c3qngD_</a>	 Alignment		31.8	5	<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
5	<a href="#">c6hwhX_</a>	 Alignment		27.0	9	<b>PDB header:</b> electron transport <b>Chain:</b> X: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 4; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
6	<a href="#">c2kncA_</a>	 Alignment		26.9	5	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiib; <b>PDBTitle:</b> platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
7	<a href="#">c4djiA_</a>	 Alignment		26.7	10	<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
8	<a href="#">c4z7fD_</a>	 Alignment		26.1	11	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> folate ecf transporter; <b>PDBTitle:</b> crystal structure of folt bound with folic acid
9	<a href="#">c2bbjB_</a>	 Alignment		24.7	21	<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
10	<a href="#">c2n28A_</a>	 Alignment		21.3	26	<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
11	<a href="#">c2w8aC_</a>	 Alignment		14.2	18	<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

12	<a href="#">c5d7tC_</a>		Alignment		13.7	16	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> s-component for folate; <b>PDBTitle:</b> folate ecf transporter: apo state
13	<a href="#">d1fftb2</a>		Alignment		12.9	8	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
14	<a href="#">c6jnyA_</a>		Alignment		12.8	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> antiterminator q protein; <b>PDBTitle:</b> crystal structure of bacteriophage 21 q protein
15	<a href="#">c6iu3A_</a>		Alignment		12.6	15	<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
16	<a href="#">c5u1dB_</a>		Alignment		10.0	9	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> antigen peptide transporter 2; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
17	<a href="#">c4hzuS_</a>		Alignment		7.2	10	<b>PDB header:</b> hydrolase, transport protein <b>Chain:</b> S: <b>PDB Molecule:</b> predicted membrane protein; <b>PDBTitle:</b> structure of a bacterial energy-coupling factor transporter
18	<a href="#">c4ainB_</a>		Alignment		7.2	19	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of betp with asymmetric protomers.
19	<a href="#">c3qf4A_</a>		Alignment		7.0	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
20	<a href="#">c2momB_</a>		Alignment		6.2	24	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
21	<a href="#">c2momC_</a>		Alignment	not modelled	6.2	24	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> lysosome-associated membrane glycoprotein 2; <b>PDBTitle:</b> structural insights of tm domain of lamp-2a in dpc micelles
22	<a href="#">c2xq2A_</a>		Alignment	not modelled	5.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsplt
23	<a href="#">c3njcA_</a>		Alignment	not modelled	5.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yslb protein; <b>PDBTitle:</b> crystal structure of the yslb protein from bacillus subtilis.2 northeast structural genomics consortium target sr460.
24	<a href="#">c2yevB_</a>		Alignment	not modelled	5.8	8	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> structure of caa3-type cytochrome oxidase
25	<a href="#">c4px7A_</a>		Alignment	not modelled	5.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylglycerophosphatase; <b>PDBTitle:</b> crystal structure of lipid phosphatase e. coli pgpb
26	<a href="#">c1ijjA_</a>		Alignment	not modelled	5.4	13	<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
27	<a href="#">c6hwhL_</a>		Alignment	not modelled	5.3	4	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis