
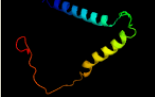


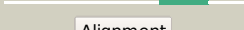
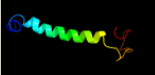

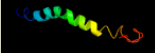




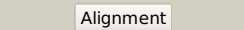
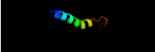
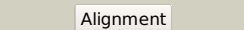
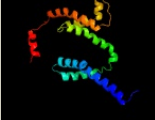
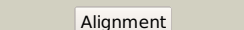
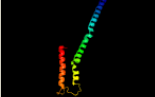
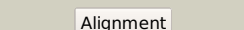

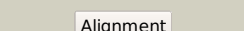
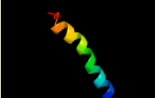


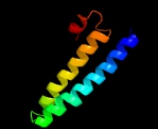
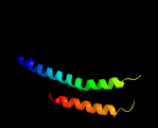
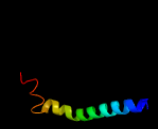
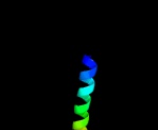

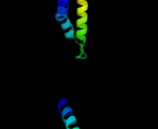
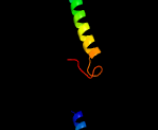


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0364 (-) _442396_443079
Date	Tue Jul 23 14:50:43 BST 2019
Unique Job ID	5338807ac2960b3e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4djiA_</a>	 Alignment		55.5	14	<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
2	<a href="#">c6adqP_</a>	 Alignment		50.4	21	<b>PDB header:</b> electron transport <b>Chain:</b> P: <b>PDB Molecule:</b> prokaryotic respiratory supercomplex associate factor 1 <b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
3	<a href="#">c6nbxG_</a>	 Alignment		43.4	15	<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)
4	<a href="#">d1fftb2</a>	 Alignment		29.5	20	<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
5	<a href="#">c4ev6E_</a>	 Alignment		28.6	10	<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
6	<a href="#">c3ukxC_</a>	 Alignment		27.7	25	<b>PDB header:</b> protein transport/inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> bimax2 peptide; <b>PDBTitle:</b> mouse importin alpha: bimax2 peptide complex
7	<a href="#">c2kncA_</a>	 Alignment		27.5	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiib; <b>PDBTitle:</b> platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
8	<a href="#">c2jlnA_</a>	 Alignment		24.4	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
9	<a href="#">c5n9yB_</a>	 Alignment		20.8	13	<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
10	<a href="#">c2na6A_</a>	 Alignment		19.3	32	<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
11	<a href="#">c2na6B_</a>	 Alignment		19.3	32	<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

12	<a href="#">c2na6C</a>	Alignment		19.3	32	<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
13	<a href="#">c4q2eA</a>	Alignment		18.5	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidate cytidyltransferase; <b>PDBTitle:</b> crystal structure of an intramembrane cdp-dag synthetase central for2 phospholipid biosynthesis (s200c/s258c, active mutant)
14	<a href="#">d2vv5a3</a>	Alignment		16.4	16	<b>Fold:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region <b>Family:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region
15	<a href="#">c2bbjB</a>	Alignment		16.1	15	<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
16	<a href="#">c2jp3A</a>	Alignment		14.6	17	<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
17	<a href="#">c5xsyB</a>	Alignment		14.2	6	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-gated sodium channel beta subunit 1; <b>PDBTitle:</b> structure of the nav1.4-beta1 complex from electric eel
18	<a href="#">d2oara1</a>	Alignment		12.9	8	<b>Fold:</b> Gated mechanosensitive channel <b>Superfamily:</b> Gated mechanosensitive channel <b>Family:</b> Gated mechanosensitive channel
19	<a href="#">d3dtub2</a>	Alignment		11.0	16	<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
20	<a href="#">c6hwhL</a>	Alignment		10.8	7	<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
21	<a href="#">c5xpdA</a>	Alignment	not modelled	10.5	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar transporter; <b>PDBTitle:</b> sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
22	<a href="#">d3ehbb2</a>	Alignment	not modelled	10.3	16	<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
23	<a href="#">c1fftG</a>	Alignment	not modelled	10.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> ubiquinol oxidase; <b>PDBTitle:</b> the structure of ubiquinol oxidase from escherichia coli
24	<a href="#">d1pw4a</a>	Alignment	not modelled	9.7	8	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
25	<a href="#">d1y5ic1</a>	Alignment	not modelled	9.0	14	<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
26	<a href="#">c6humE</a>	Alignment	not modelled	8.0	11	<b>PDB header:</b> proton transport <b>Chain:</b> E: <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit 4l; <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
27	<a href="#">c2micA</a>	Alignment	not modelled	8.0	11	<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
28	<a href="#">c2micB</a>	Alignment	not modelled	8.0	11	<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

29	<a href="#">c5ws4A_</a>	 Alignment	not modelled	7.8	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from <i>2 acinetobacter baumannii</i>
30	<a href="#">d2osoal</a>	 Alignment	not modelled	7.0	22	<b>Fold:</b> Ligand-binding domain in the NO signalling and Golgi transport <b>Superfamily:</b> Ligand-binding domain in the NO signalling and Golgi transport <b>Family:</b> MJ1460-like
31	<a href="#">c3hd6A_</a>	 Alignment	not modelled	6.2	9	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter rh type c; <b>PDBTitle:</b> crystal structure of the human rhesus glycoprotein rhcg
32	<a href="#">c3qngD_</a>	 Alignment	not modelled	6.1	8	<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 the <i>2 n,n'-diacetylchitobiose-specific phosphotransferase system</i>
33	<a href="#">c4z7fD_</a>	 Alignment	not modelled	6.1	10	<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
34	<a href="#">c3aygA_</a>	 Alignment	not modelled	6.0	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric oxide reductase; <b>PDBTitle:</b> crystal structure of nitric oxide reductase complex with hqno
35	<a href="#">c5oqtA_</a>	 Alignment	not modelled	6.0	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> amino acid transporter; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
36	<a href="#">d3ci0k2</a>	 Alignment	not modelled	5.8	7	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> GspK insert domain-like <b>Family:</b> GspK insert domain-like
37	<a href="#">c6c14A_</a>	 Alignment	not modelled	5.7	20	<b>PDB header:</b> membrane protein, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> protocadherin-15; <b>PDBTitle:</b> cryoem structure of mouse pcdh15-1ec-lhfpl5 complex
38	<a href="#">c6ei3A_</a>	 Alignment	not modelled	5.5	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> proton-dependent oligopeptide transporter family protein; <b>PDBTitle:</b> crystal structure of auto inhibited pot family peptide transporter
39	<a href="#">c1m57H_</a>	 Alignment	not modelled	5.5	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 <i>rhodobacter2 sphaeroides</i> (eq(i-286) mutant))
40	<a href="#">c3njcA_</a>	 Alignment	not modelled	5.5	13	<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 <i>bacillus subtilis.2 northeast structural genomics consortium target sr460.</i>
41	<a href="#">c2oarA_</a>	 Alignment	not modelled	5.4	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> large-conductance mechanosensitive channel; <b>PDBTitle:</b> mechanosensitive channel of large conductance (mscl)