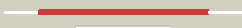









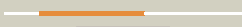


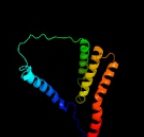
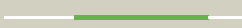
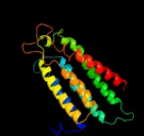



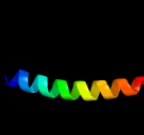

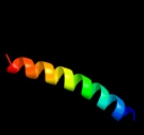


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1607_(chaA)_1806188_1807270
Date	Fri Aug 2 13:30:20 BST 2019
Unique Job ID	cf50b412117b7921

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4k1cB_	 Alignment		100.0	18	PDB header: membrane protein/metal transport Chain: B: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
2	c4k1cA_	 Alignment		100.0	18	PDB header: membrane protein/metal transport Chain: A: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
3	c4kjsB_	 Alignment		100.0	19	PDB header: transport protein Chain: B: PDB Molecule: cation exchanger yfke; PDBTitle: structure of native yfke
4	c4kppA_	 Alignment		100.0	17	PDB header: membrane protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
5	c3v5uA_	 Alignment		100.0	19	PDB header: metal transport Chain: A: PDB Molecule: uncharacterized membrane protein mj0091; PDBTitle: structure of sodium/calcium exchanger from methanocaldococcus2 jannaschii dsm 2661
6	c4djiA_	 Alignment		84.6	10	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
7	c4r0cB_	 Alignment		51.7	14	PDB header: membrane protein Chain: B: PDB Molecule: abgt putative transporter family; PDBTitle: crystal structure of the alcalivorax borkumensis ydah transporter2 reveals an unusual topology
8	c3j1zP_	 Alignment		50.1	13	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
9	c4iu8A_	 Alignment		46.8	13	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
10	d1xrda1	 Alignment		44.2	21	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
11	c1xrda_	 Alignment		44.2	21	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, alpha chain; PDBTitle: light-harvesting complex 1 alfa subunit from wild-type2 rhodospirillum rubrum

12	c4iu9A_	Alignment		43.5	13	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter
13	c6et5b_	Alignment		33.5	14	PDB header: photosynthesis Chain: B: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
14	c6hwhX_	Alignment		30.5	12	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
15	c4y7jE_	Alignment		27.0	11	PDB header: membrane protein,transport protein Chain: E: PDB Molecule: large conductance mechanosensitive channel protein, PDBTitle: structure of an archaeal mechanosensitive channel in expanded state
16	c3qngD_	Alignment		24.3	13	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
17	c2yvxD_	Alignment		22.0	15	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
18	c4r1iB_	Alignment		17.2	13	PDB header: membrane protein Chain: B: PDB Molecule: aminobenzoyl-glutamate transporter; PDBTitle: structure and function of neisseria gonorrhoeae mtrf illuminates a2 class of antimetabolite efflux pumps
19	d2yvxa3	Alignment		16.3	15	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like
20	c2oarA_	Alignment		15.1	13	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
21	d2oara1	Alignment	not modelled	14.4	19	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
22	c5mg3D_	Alignment	not modelled	13.5	15	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secD; PDBTitle: em fitted model of bacterial holo-translocon
23	c3jd8A_	Alignment	not modelled	13.2	14	PDB header: membrane protein Chain: A: PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom
24	c6j5i8_	Alignment	not modelled	11.6	11	PDB header: membrane protein Chain: 8: PDB Molecule: atp synthase protein 8; PDBTitle: cryo-em structure of the mammalian dp-state atp synthase
25	c5xpdA_	Alignment	not modelled	11.3	7	PDB header: transport protein Chain: A: PDB Molecule: sugar transporter; PDBTitle: sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
26	c4bduC_	Alignment	not modelled	8.7	21	PDB header: apoptosis Chain: C: PDB Molecule: green fluorescent protein, apoptosis regulator bax; PDBTitle: bax bh3-in-groove dimer (gfp)
27	c6ob7A_	Alignment	not modelled	8.5	9	PDB header: transport protein Chain: A: PDB Molecule: equilibrative nucleoside transporter 1; PDBTitle: human equilibrative nucleoside transporter-1, dilazep bound
28	d2iuba2	Alignment	not modelled	8.3	10	Fold: Transmembrane helix hairpin Superfamily: Magnesium transport protein CorA, transmembrane region Family: Magnesium transport protein CorA, transmembrane region PDB header: membrane protein

29	c6j5j8_	Alignment	not modelled	7.7	11	Chain: 8: PDB Molecule: atp synthase protein 8; PDBTitle: cryo-em structure of the mammalian e-state atp synthase
30	c6igz9_	Alignment	not modelled	7.1	25	PDB header: plant protein Chain: 9: PDB Molecule: lhca-i; PDBTitle: structure of psi-lhci
31	d1twfc2	Alignment	not modelled	6.0	50	Fold: Insert subdomain of RNA polymerase alpha subunit Superfamily: Insert subdomain of RNA polymerase alpha subunit Family: Insert subdomain of RNA polymerase alpha subunit
32	d1sqqa1	Alignment	not modelled	5.9	17	Fold: NusB-like Superfamily: NusB-like Family: RmsB N-terminal domain-like
33	d2nqwa1	Alignment	not modelled	5.6	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
34	c4he8M_	Alignment	not modelled	5.2	12	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-quinone oxidoreductase subunit 13; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus