


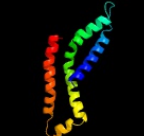



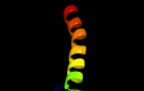

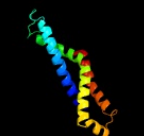


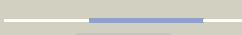
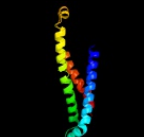



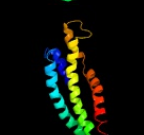






Phyre2

Email: mdejesus@rockefeller.edu
 Description: RVBD3501c_yrbE4A_3920276_3921040
 Date: Fri Aug 9 18:20:17 BST 2019
 Unique Job ID: 7fb979e27e8a3e3a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4H_	 Alignment		100.0	24	PDB header: protein transport Chain: H; PDB Molecule: abc transporter permease; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
2	c5x5yG_	 Alignment		84.3	15	PDB header: membrane protein Chain: G; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
3	c5I75F_	 Alignment		69.1	15	PDB header: transport protein Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
4	c5I75G_	 Alignment		68.1	27	PDB header: transport protein Chain: G; PDB Molecule: fig000906: predicted permease; PDBTitle: a protein structure
5	c6mjpG_	 Alignment		54.9	11	PDB header: lipid transport Chain: G; PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
6	c5x5yF_	 Alignment		30.8	15	PDB header: membrane protein Chain: F; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
7	c5xu1M_	 Alignment		27.2	15	PDB header: transport protein Chain: M; PDB Molecule: abc transporter permease; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
8	c6mjpF_	 Alignment		22.4	14	PDB header: lipid transport Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
9	c2yvxD_	 Alignment		19.6	22	PDB header: transport protein Chain: D; PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
10	d2hafa1	 Alignment		18.5	50	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
11	c1abzA_	 Alignment		17.9	25	PDB header: de novo design Chain: A; PDB Molecule: alpha-t-alpha; PDBTitle: alpha-t-alpha, a de novo designed peptide, nmr, 232 structures

12	c2kn8A_	Alignment		16.7	29	PDB header: protein binding, dna binding protein Chain: A; PDB Molecule: dna cleavage and packaging protein large subunit, ul89; PDBTitle: nmr structure of the c-terminal domain of pul89
13	c5ghaF_	Alignment		15.5	30	PDB header: transferase/transport protein Chain: F; PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
14	c2aj2A_	Alignment		13.4	50	PDB header: unknown function Chain: A; PDB Molecule: hypothetical upf0301 protein vc0467; PDBTitle: x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.
15	c5nikK_	Alignment		12.8	20	PDB header: transport protein Chain: K; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
16	d2ieaa3	Alignment		12.6	21	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
17	c2hv8D_	Alignment		12.3	14	PDB header: protein transport Chain: D; PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
18	c6qvcB_	Alignment		12.2	14	PDB header: membrane protein Chain: B; PDB Molecule: chloride channel protein 1; PDBTitle: cryoem structure of the human clc-1 chloride channel, cbs state 1
19	c2m67A_	Alignment		12.1	6	PDB header: transport protein Chain: A; PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
20	d1z96a1	Alignment		11.8	24	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
21	d1rhzb_	Alignment	not modelled	11.8	10	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
22	c4migC_	Alignment	not modelled	11.3	29	PDB header: oxidoreductase Chain: C; PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
23	d2k0bx1	Alignment	not modelled	9.7	20	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
24	c2mfrA_	Alignment	not modelled	9.6	21	PDB header: transferase Chain: A; PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
25	d1g7oa1	Alignment	not modelled	9.2	15	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
26	c1cf3A_	Alignment	not modelled	8.9	17	PDB header: oxidoreductase(flavoprotein) Chain: A; PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from aspergillus niger
27	c2hg5D_	Alignment	not modelled	8.6	7	PDB header: membrane protein Chain: D; PDB Molecule: kcsa channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
28	c3dfmA_	Alignment	not modelled	8.0	23	PDB header: hydrolase Chain: A; PDB Molecule: teicoplanin pseudoaglycone deacetylase orf2; PDBTitle: the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2

29	c2jy8A_	Alignment	not modelled	7.8	20	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin-binding protein p62; PDBTitle: nmr structure of the ubiquitin associated (uba) domain of2 p62 (sqstm1) in complex with ubiquitin. rdc refined
30	c2wwbB_	Alignment	not modelled	7.4	11	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sec61 subunit gamma; PDBTitle: cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
31	c3vvpA_	Alignment	not modelled	7.0	18	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
32	c1vmaA_	Alignment	not modelled	6.8	25	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
33	c5mg3D_	Alignment	not modelled	6.6	8	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
34	d1q74a_	Alignment	not modelled	6.5	36	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
35	d2do8a1	Alignment	not modelled	6.3	40	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
36	c4ak9A_	Alignment	not modelled	6.0	25	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
37	c5l3sF_	Alignment	not modelled	5.9	33	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
38	c2j7pA_	Alignment	not modelled	5.7	25	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
39	d2hjqa1	Alignment	not modelled	5.5	20	Fold: LEM/SAP HeH motif Superfamily: Rho N-terminal domain-like Family: YqbF C-terminal domain-like
40	c6cy1B_	Alignment	not modelled	5.5	33	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
41	c3mk7F_	Alignment	not modelled	5.3	11	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
42	c3b9qA_	Alignment	not modelled	5.2	25	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
43	d1i94m_	Alignment	not modelled	5.2	75	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13