

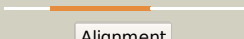

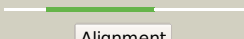

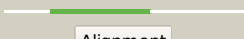





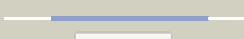

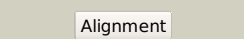

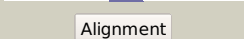

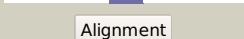

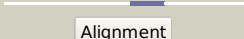


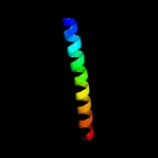
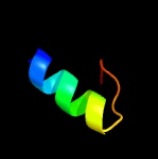
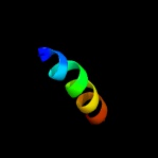
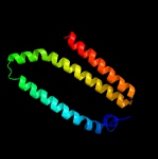

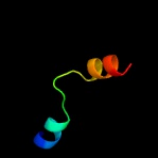




Phyre2

Email: mdejesus@rockefeller.edu
 Description: RVBD0167_(yrbE1A)_196859_197656
 Date: Tue Jul 23 14:50:21 BST 2019
 Unique Job ID: d8794692919d0cc1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4H_	 Alignment		100.0	21	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		80.6	15	PDB header: membrane protein Chain: G; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
3	c6mjpG_	 Alignment		51.6	13	PDB header: lipid transport Chain: G; PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
4	c5I75F_	 Alignment		50.5	15	PDB header: transport protein Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
5	c5I75G_	 Alignment		42.7	20	PDB header: transport protein Chain: G; PDB Molecule: fig000906: predicted permease; PDBTitle: a protein structure
6	c5x5yF_	 Alignment		26.7	16	PDB header: membrane protein Chain: F; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
7	c6qvcB_	 Alignment		20.0	12	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
8	c6mjpF_	 Alignment		17.6	15	PDB header: lipid transport Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
9	c5ghaF_	 Alignment		14.9	40	PDB header: transferase/transport protein Chain: F; PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
10	d2hafa1	 Alignment		14.2	50	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
11	c2mfrA_	 Alignment		11.3	24	PDB header: transferase Chain: A; PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles

12	d3dhwa1	Alignment		11.1	15	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
13	c2hg5D_	Alignment		10.9	10	PDB header: membrane protein Chain: D: PDB Molecule: kcsc channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
14	d1z96a1	Alignment		10.6	24	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
15	c2m67A_	Alignment		10.6	6	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
16	c3vvpA_	Alignment		10.5	16	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
17	c4migC_	Alignment		10.5	33	PDB header: oxidoreductase Chain: C: PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
18	c2hv8D_	Alignment		10.3	18	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
19	c6coyB_	Alignment		9.6	13	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, transmembrane domain
20	c5xu1M_	Alignment		9.2	14	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
21	d1g7oa1	Alignment	not modelled	9.0	16	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
22	c1abzA_	Alignment	not modelled	8.5	31	PDB header: de novo design Chain: A: PDB Molecule: alpha-t-alpha; PDBTitle: alpha-t-alpha, a de novo designed peptide, nmr, 232 structures
23	c2aj2A_	Alignment	not modelled	8.5	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.
24	c1cf3A_	Alignment	not modelled	8.3	25	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from apergillus niger
25	d2k0bx1	Alignment	not modelled	7.3	20	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
26	c3dfmA_	Alignment	not modelled	7.1	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
27	d1q74a_	Alignment	not modelled	6.8	32	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
28	c5mg3D_	Alignment	not modelled	6.8	7	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon

29	d2hjqal	Alignment	not modelled	6.8	20	Fold: LEM/SAP HeH motif Superfamily: Rho N-terminal domain-like Family: YqbF C-terminal domain-like
30	d2onkc1	Alignment	not modelled	6.3	11	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
31	c2onkC	Alignment	not modelled	6.3	11	PDB header: membrane protein Chain: C: PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
32	c5l1xH	Alignment	not modelled	6.2	42	PDB header: viral protein Chain: H: PDB Molecule: hmpv f1 subunit; PDBTitle: structure of the human metapneumovirus fusion protein in the2 postfusion conformation
33	d2ebfx2	Alignment	not modelled	6.2	24	Fold: EreA/ChaN-like Superfamily: EreA/ChaN-like Family: PMT domain-like
34	d1i94m	Alignment	not modelled	6.0	75	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
35	c5ws4A	Alignment	not modelled	6.0	15	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
36	c2jy8A	Alignment	not modelled	5.8	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
37	c4dagA	Alignment	not modelled	5.7	42	PDB header: viral protein/immune system Chain: A: PDB Molecule: fusion glycoprotein f0; PDBTitle: structure of the human metapneumovirus fusion protein with2 neutralizing antibody identifies a pneumovirus antigenic site
38	d1rhzb	Alignment	not modelled	5.6	12	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
39	c2m7xA	Alignment	not modelled	5.6	29	PDB header: membrane protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: structural and functional analysis of transmembrane segment iv of the2 salt tolerance protein sod2
40	c5wb0F	Alignment	not modelled	5.4	42	PDB header: viral protein Chain: F: PDB Molecule: fusion glycoprotein f0; PDBTitle: crystal structure of human metapneumovirus fusion glycoprotein2 stabilized in the prefusion state
41	c1zavV	Alignment	not modelled	5.1	41	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
42	d1zavu1	Alignment	not modelled	5.1	41	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain
43	c1zavW	Alignment	not modelled	5.1	41	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
44	c1zaxU	Alignment	not modelled	5.1	41	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
45	c1zaxV	Alignment	not modelled	5.1	41	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
46	c1zaxW	Alignment	not modelled	5.1	41	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
47	c1zavU	Alignment	not modelled	5.1	41	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
48	c1zaxY	Alignment	not modelled	5.1	41	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
49	c1zavX	Alignment	not modelled	5.1	41	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
50	c1zavY	Alignment	not modelled	5.1	41	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21