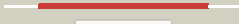

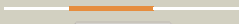
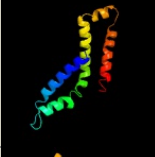

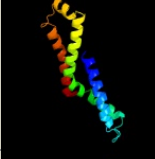



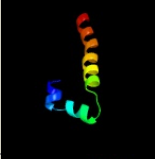



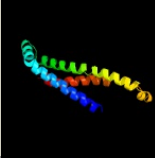



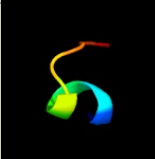

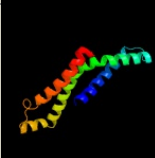




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0168 (yrbE1B)_197658_198527
 Date Tue Jul 23 14:50:22 BST 2019
 Unique Job ID 9a586973990a5c3c

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		82.7	13	PDB header: membrane protein Chain: G; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
3	c6mjpG_	 Alignment		65.1	16	PDB header: lipid transport Chain: G; PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
4	c5I75F_	 Alignment		63.5	12	PDB header: transport protein Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
5	c5I75G_	 Alignment		63.1	15	PDB header: transport protein Chain: G; PDB Molecule: fig000906: predicted permease; PDBTitle: a protein structure
6	c5x5yF_	 Alignment		46.8	14	PDB header: membrane protein Chain: F; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
7	c5xu1M_	 Alignment		16.2	11	PDB header: transport protein Chain: M; PDB Molecule: abc transporter permease; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
8	c6qvcB_	 Alignment		16.1	11	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
9	d2hafa1	 Alignment		15.7	30	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
10	c6mjpF_	 Alignment		14.4	13	PDB header: lipid transport Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
11	d2k0bx1	 Alignment		14.0	27	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain

12	c4migC_	Alignment		12.3	24	PDB header: oxidoreductase Chain: C: PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
13	c2m67A_	Alignment		12.0	18	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
14	c2hg5D_	Alignment		11.7	13	PDB header: membrane protein Chain: D: PDB Molecule: kcsc channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the e2 selectivity filter
15	c2hv8D_	Alignment		11.3	21	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
16	c1abzA_	Alignment		11.0	44	PDB header: de novo design Chain: A: PDB Molecule: alpha-t-alpha; PDBTitle: alpha-t-alpha, a de novo designed peptide, nmr, 232 structures
17	c1q7tA_	Alignment		10.8	36	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein rv1170; PDBTitle: rv1170 (mshb) from mycobacterium tuberculosis
18	d1z96a1	Alignment		10.5	24	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
19	c2aj2A_	Alignment		10.3	30	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.
20	c2kn8A_	Alignment		10.0	21	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
21	c5ghaF_	Alignment	not modelled	10.0	30	PDB header: transferase/transport protein Chain: F: PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
22	c1cf3A_	Alignment	not modelled	10.0	13	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from apergillus niger
23	c5sv0C_	Alignment	not modelled	9.5	18	PDB header: transport protein Chain: C: PDB Molecule: biopolymer transport protein exbb; PDBTitle: structure of the exbb/exbd complex from e. coli at ph 7.0
24	c2jy8A_	Alignment	not modelled	9.4	27	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
25	c2mfrA_	Alignment	not modelled	8.6	9	PDB header: transferase Chain: A: PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
26	d1q74a_	Alignment	not modelled	8.1	36	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
27	c5egiB_	Alignment	not modelled	7.4	6	PDB header: membrane protein Chain: B: PDB Molecule: uncharacterized protein y57a10a.10; PDBTitle: structure of a trimeric intracellular cation channel from c. elegans2 with bound ca2+
28	c5eikA_	Alignment	not modelled	6.9	11	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein y57a10a.28; PDBTitle: structure of a trimeric intracellular cation channel from c. elegans2 in the absence of ca2+
						PDB header: hydrolase

29	c3dfmA_	Alignment	not modelled	6.8	24	Chain: A; PDB Molecule: teicoplanin pseudoaglycone deacetylase orf2; PDBTitle: the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
30	c2onkC_	Alignment	not modelled	6.7	12	PDB header: membrane protein Chain: C; PDB Molecule: molybdate/tungstate abc transporter, permease PDBTitle: abc transporter modbc in complex with its binding protein2 moda
31	d2onkc1	Alignment	not modelled	6.7	12	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
32	c5nikK_	Alignment	not modelled	6.1	11	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
33	c6coyB_	Alignment	not modelled	6.1	14	PDB header: transport protein Chain: B; PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, transmembrane domain
34	c5l1xH_	Alignment	not modelled	5.7	32	PDB header: viral protein Chain: H; PDB Molecule: hmpv f1 subunit; PDBTitle: structure of the human metapneumovirus fusion protein in the2 postfusion conformation
35	c6iz0A_	Alignment	not modelled	5.7	15	PDB header: membrane protein Chain: A; PDB Molecule: trimeric intracellular cation channel type a; PDBTitle: crystal structure analysis of a eukaryotic membrane protein
36	d1i94m_	Alignment	not modelled	5.3	38	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
37	c2m7xA_	Alignment	not modelled	5.2	14	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
38	c4dagA_	Alignment	not modelled	5.2	32	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
39	d1g7oa1	Alignment	not modelled	5.1	16	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain