

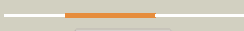




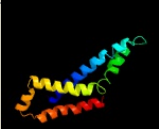







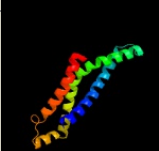








Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3500c_(yrbE4B)_3919399_3920241
 Date Fri Aug 9 18:20:17 BST 2019
 Unique Job ID 75b7a54d299edf34

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		83.0	17	PDB header: membrane protein Chain: G; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
3	c5I75F_	 Alignment		63.9	15	PDB header: transport protein Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
4	c5I75G_	 Alignment		52.9	10	PDB header: transport protein Chain: G; PDB Molecule: fig000906: predicted permease; PDBTitle: a protein structure
5	c6mjpG_	 Alignment		47.4	16	PDB header: lipid transport Chain: G; PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
6	c6qvcB_	 Alignment		30.6	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
7	c5x5yF_	 Alignment		23.4	13	PDB header: membrane protein Chain: F; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
8	c6mjpF_	 Alignment		16.3	12	PDB header: lipid transport Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
9	c4miqC_	 Alignment		14.6	24	PDB header: oxidoreductase Chain: C; PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
10	d2hafa1	 Alignment		14.6	10	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
11	c6coyB_	 Alignment		13.9	13	PDB header: transport protein Chain: B; PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, transmembrane domain

12	c5ghaF_	Alignment		13.6	10	PDB header: transferase/transport protein Chain: F: PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
13	c2hg5D_	Alignment		13.2	27	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	c2hv8D_	Alignment		12.4	16	PDB header: protein transport Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
15	c2mfrA_	Alignment		12.0	12	PDB header: transferase Chain: A: PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
16	c2kn8A_	Alignment		11.9	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
17	c1q7tA_	Alignment		10.3	36	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein rv1170; PDBTitle: rv1170 (mshb) from mycobacterium tuberculosis
18	c2aj2A_	Alignment		10.2	10	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.
19	c1cf3A_	Alignment		9.5	17	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from apergillus niger
20	c5sv0C_	Alignment		9.4	15	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
21	c2m67A_	Alignment	not modelled	9.2	0	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
22	c1abzA_	Alignment	not modelled	9.0	33	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	d1q74a_	Alignment	not modelled	7.8	36	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
24	c5l1xH_	Alignment	not modelled	7.4	47	PDB header: viral protein Chain: H: PDB Molecule: hmpv f1 subunit; PDBTitle: structure of the human metapneumovirus fusion protein in the2 postfusion conformation
25	d1z96a1	Alignment	not modelled	7.0	12	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
26	c4dagA_	Alignment	not modelled	6.8	47	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
27	c5xu1M_	Alignment	not modelled	6.7	8	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
28	c5wb0F_	Alignment	not modelled	6.5	47	PDB header: viral protein Chain: F: PDB Molecule: fusion glycoprotein f0; PDBTitle: crystal structure of human metapneumovirus fusion glycoprotein2 stabilized in the prefusion state PDB header: protein transport

29	c1vmaA_	Alignment	not modelled	6.5	25	Chain: A; PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from <i>Thermotoga maritima</i> at 1.60 Å resolution
30	d2hjqa1	Alignment	not modelled	6.5	12	Fold: LEM/SAP HeH motif Superfamily: Rho N-terminal domain-like Family: YqbF C-terminal domain-like
31	c6bs7A_	Alignment	not modelled	5.9	24	PDB header: ligase Chain: A; PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of adenylosuccinate synthetase from <i>Legionella pneumophila philadelphia 1</i>
32	c5bmoB_	Alignment	not modelled	5.8	38	PDB header: hydrolase Chain: B; PDB Molecule: putative uncharacterized protein Inmx; PDBTitle: Inmx protein, a putative glcnac-pi de-n-acetylase from <i>Streptomyces atroolivaceus</i>
33	c5l3sF_	Alignment	not modelled	5.6	42	PDB header: protein transport Chain: F; PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
34	c1gw4A_	Alignment	not modelled	5.6	27	PDB header: high density lipoproteins Chain: A; PDB Molecule: apoA-I; PDBTitle: the helix-hinge-helix structural motif in human apoA-I determined by NMR spectroscopy, 13 structure
35	c3vvpA_	Alignment	not modelled	5.6	12	PDB header: transport protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of Mate in complex with Br-Nrf
36	c2m7xA_	Alignment	not modelled	5.5	14	PDB header: membrane protein Chain: A; PDB Molecule: Na ⁺ /H ⁺ antiporter; PDBTitle: structural and functional analysis of transmembrane segment IV of the salt tolerance protein Sod2
37	c4ak9A_	Alignment	not modelled	5.5	25	PDB header: protein transport Chain: A; PDB Molecule: cpftsY; PDBTitle: structure of chloroplast ftsy from <i>Physcomitrella patens</i>
38	d1g7oa1	Alignment	not modelled	5.5	15	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
39	c2j7pA_	Alignment	not modelled	5.1	33	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
40	d2k0bx1	Alignment	not modelled	5.0	20	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
41	c2jy8A_	Alignment	not modelled	5.0	20	PDB header: protein binding Chain: A; PDB Molecule: ubiquitin-binding protein p62; PDBTitle: NMR structure of the ubiquitin-associated (UBA) domain of p62 (SQSTM1) in complex with ubiquitin. RDC refined
42	c1zaxU_	Alignment	not modelled	5.0	36	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
43	c1zaxW_	Alignment	not modelled	5.0	36	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
44	c1zaxV_	Alignment	not modelled	5.0	36	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
45	c1zavW_	Alignment	not modelled	5.0	36	PDB header: structural protein Chain: W; PDB Molecule: 50S ribosomal protein L7/L12; PDBTitle: ribosomal protein L10-L12 (ntd) complex, space group P21
46	c1zavV_	Alignment	not modelled	5.0	36	PDB header: structural protein Chain: V; PDB Molecule: 50S ribosomal protein L7/L12; PDBTitle: ribosomal protein L10-L12 (ntd) complex, space group P21
47	c1zavU_	Alignment	not modelled	5.0	36	PDB header: structural protein Chain: U; PDB Molecule: 50S ribosomal protein L7/L12; PDBTitle: ribosomal protein L10-L12 (ntd) complex, space group P21
48	d1zavu1	Alignment	not modelled	5.0	36	Fold: Ribosomal protein L7/L12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/L12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/L12, oligomerisation (N-terminal) domain
49	c1zaxY_	Alignment	not modelled	5.0	36	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
50	c1zavX_	Alignment	not modelled	5.0	36	PDB header: structural protein Chain: X; PDB Molecule: 50S ribosomal protein L7/L12; PDBTitle: ribosomal protein L10-L12 (ntd) complex, space group P21
51	c1zaxX_	Alignment	not modelled	5.0	36	PDB header: structural protein Chain: X; PDB Molecule: 50S ribosomal protein L7/L12; PDBTitle: ribosomal protein L10-L12 (ntd) complex, space group P212121, 2 form B