

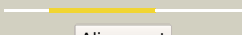


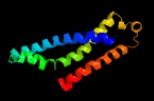
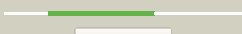
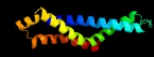


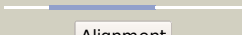
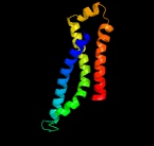
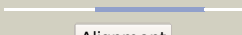
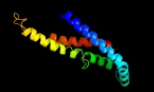
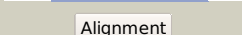



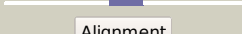

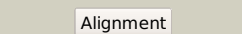
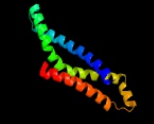


# Phyre2

Email: mdejesus@rockefeller.edu  
 Description: RVBD0587 (yrbE2A)\_685132\_685929  
 Date: Fri Jul 26 01:50:14 BST 2019  
 Unique Job ID: 4b78344e58f506c5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4H_</a>	 Alignment		100.0	22	<b>PDB header:</b> protein transport <b>Chain:</b> H; <b>PDB Molecule:</b> abc transporter permease; <b>PDBTitle:</b> cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
2	<a href="#">c5x5yG_</a>	 Alignment		74.4	14	<b>PDB header:</b> membrane protein <b>Chain:</b> G; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
3	<a href="#">c5I75F_</a>	 Alignment		64.1	16	<b>PDB header:</b> transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> a protein structure
4	<a href="#">c6mjpG_</a>	 Alignment		56.9	13	<b>PDB header:</b> lipid transport <b>Chain:</b> G; <b>PDB Molecule:</b> lps export abc transporter permease lptg; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae
5	<a href="#">c5I75G_</a>	 Alignment		37.2	17	<b>PDB header:</b> transport protein <b>Chain:</b> G; <b>PDB Molecule:</b> fig000906: predicted permease; <b>PDBTitle:</b> a protein structure
6	<a href="#">c5x5yF_</a>	 Alignment		22.6	15	<b>PDB header:</b> membrane protein <b>Chain:</b> F; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> a membrane protein complex
7	<a href="#">c5xu1M_</a>	 Alignment		22.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> M; <b>PDB Molecule:</b> abc transporter permease; <b>PDBTitle:</b> structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
8	<a href="#">c6qvcB_</a>	 Alignment		21.5	14	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> chloride channel protein 1; <b>PDBTitle:</b> cryoem structure of the human clc-1 chloride channel, cbs state 1
9	<a href="#">d2hafa1</a>	 Alignment		19.0	50	<b>Fold:</b> VC0467-like <b>Superfamily:</b> VC0467-like <b>Family:</b> VC0467-like
10	<a href="#">c5ghaF_</a>	 Alignment		17.7	40	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> sulfur carrier ttub; <b>PDBTitle:</b> sulfur transferase ttua in complex with sulfur carrier ttub
11	<a href="#">c6mjpF_</a>	 Alignment		16.4	18	<b>PDB header:</b> lipid transport <b>Chain:</b> F; <b>PDB Molecule:</b> fig000988: predicted permease; <b>PDBTitle:</b> lptb(e163q)fgc from vibrio cholerae

12	<a href="#">c2m67A_</a>	Alignment		15.6	6	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> full-length mercury transporter protein merf in lipid bilayer2 membranes
13	<a href="#">c2yvxD_</a>	Alignment		14.2	22	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte; <b>PDBTitle:</b> crystal structure of magnesium transporter mgte
14	<a href="#">c2aj2A_</a>	Alignment		14.0	50	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0301 protein vc0467; <b>PDBTitle:</b> x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.
15	<a href="#">c6coyB_</a>	Alignment		13.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> chloride channel protein 1; <b>PDBTitle:</b> human clc-1 chloride ion channel, transmembrane domain
16	<a href="#">c2hg5D_</a>	Alignment		13.3	13	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> kcsa channel; <b>PDBTitle:</b> cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
17	<a href="#">c2hv8D_</a>	Alignment		12.9	16	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> rab11 family-interacting protein 3; <b>PDBTitle:</b> crystal structure of gtp-bound rab11 in complex with fip3
18	<a href="#">c4migC_</a>	Alignment		12.4	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyranose 2-oxidase; <b>PDBTitle:</b> pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
19	<a href="#">c2mfrA_</a>	Alignment		11.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> insulin receptor; <b>PDBTitle:</b> solution structure of the transmembrane domain of the insulin receptor2 in micelles
20	<a href="#">c2kn8A_</a>	Alignment		11.7	29	<b>PDB header:</b> protein binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna cleavage and packaging protein large subunit, ul89; <b>PDBTitle:</b> nmr structure of the c-terminal domain of pul89
21	<a href="#">c2wwbB_</a>	Alignment	not modelled	10.7	11	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> protein transport protein sec61 subunit gamma; <b>PDBTitle:</b> cryo-em structure of the mammalian sec61 complex bound to the actively2 translating wheat germ 80s ribosome
22	<a href="#">d1z96a1</a>	Alignment	not modelled	10.5	24	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
23	<a href="#">c1cf3A_</a>	Alignment	not modelled	10.0	21	<b>PDB header:</b> oxidoreductase(flavoprotein) <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glucose oxidase); <b>PDBTitle:</b> glucose oxidase from apergillus niger
24	<a href="#">d1g7oa1</a>	Alignment	not modelled	8.8	15	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
25	<a href="#">c1abzA_</a>	Alignment	not modelled	8.2	33	<b>PDB header:</b> de novo design <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-t-alpha; <b>PDBTitle:</b> alpha-t-alpha, a de novo designed peptide, nmr, 232 structures
26	<a href="#">c6bs7A_</a>	Alignment	not modelled	7.8	41	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase from legionella2 pneumophila philadelphia 1
27	<a href="#">c1gw4A_</a>	Alignment	not modelled	7.5	27	<b>PDB header:</b> high density lipoproteins <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i; <b>PDBTitle:</b> the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
28	<a href="#">d1q74a_</a>	Alignment	not modelled	7.3	32	<b>Fold:</b> LmbE-like <b>Superfamily:</b> LmbE-like <b>Family:</b> LmbE-like

29	<a href="#">d2k0bx1</a>	Alignment	not modelled	7.2	20	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
30	<a href="#">c2m7xA</a>	Alignment	not modelled	7.1	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> na(+)/h(+) antiporter; <b>PDBTitle:</b> structural and functional analysis of transmembrane segment iv of the2 salt tolerance protein sod2
31	<a href="#">d2do8a1</a>	Alignment	not modelled	6.8	50	<b>Fold:</b> VC0467-like <b>Superfamily:</b> VC0467-like <b>Family:</b> VC0467-like
32	<a href="#">c5nikK</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> transport protein <b>Chain:</b> K; <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of the macab-tolc abc-type tripartite multidrug efflux pump
33	<a href="#">d3dhwa1</a>	Alignment	not modelled	6.3	16	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
34	<a href="#">d1i94m</a>	Alignment	not modelled	5.8	75	<b>Fold:</b> S13-like H2TH domain <b>Superfamily:</b> S13-like H2TH domain <b>Family:</b> Ribosomal protein S13
35	<a href="#">d1rhzb</a>	Alignment	not modelled	5.8	10	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Preprotein translocase SecE subunit <b>Family:</b> Preprotein translocase SecE subunit
36	<a href="#">c2jy8A</a>	Alignment	not modelled	5.8	20	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin-binding protein p62; <b>PDBTitle:</b> nmr structure of the ubiquitin associated (uba) domain of2 p62 (sqstm1) in complex with ubiquitin. rdc refined
37	<a href="#">d2hjqa1</a>	Alignment	not modelled	5.7	20	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> Rho N-terminal domain-like <b>Family:</b> YqbF C-terminal domain-like
38	<a href="#">c1vmaA</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
39	<a href="#">c2onkC</a>	Alignment	not modelled	5.5	12	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> molybdate/tungstate abc transporter, permease <b>PDBTitle:</b> abc transporter modbc in complex with its binding protein2 moda
40	<a href="#">d2onkc1</a>	Alignment	not modelled	5.5	12	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
41	<a href="#">c3dfmA</a>	Alignment	not modelled	5.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> teicoplanin pseudoaglycone deacetylase orf2; <b>PDBTitle:</b> the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
42	<a href="#">c1q7tA</a>	Alignment	not modelled	5.1	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein rv1170; <b>PDBTitle:</b> rv1170 (mshb) from mycobacterium tuberculosis
43	<a href="#">c2lxeA</a>	Alignment	not modelled	5.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> histone-lysine n-methyltransferase suvr4; <b>PDBTitle:</b> s4wyild