

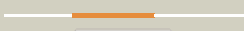

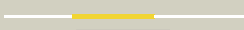


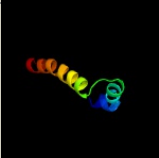

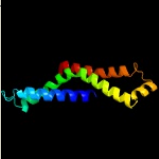

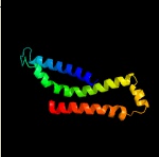

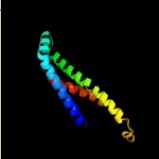

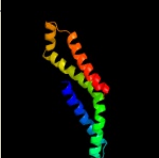

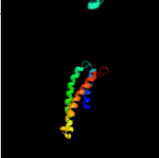

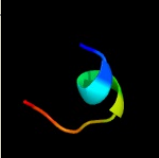

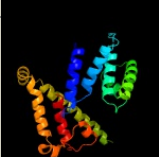











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0588 (yrbE2B)_685931_686818
Date	Fri Jul 26 01:50:14 BST 2019
Unique Job ID	0a57c924cdc0d390

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4H_</a>	 Alignment		100.0	21	<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		88.9	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		70.9	12	<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="#">c5I75G_</a>	 Alignment		70.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> G; <b>PDB Molecule:</b> fig000906: predicted permease; <b>PDBTitle:</b> a protein structure
5	<a href="#">c6mjpG_</a>	 Alignment		62.4	16	<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
6	<a href="#">c5x5yF_</a>	 Alignment		50.2	13	<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		38.7	12	<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="#">c6mjpF_</a>	 Alignment		31.6	12	<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
9	<a href="#">c2yvxD_</a>	 Alignment		22.1	16	<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
10	<a href="#">d2hafa1</a>	 Alignment		21.8	30	<b>Fold:</b> VC0467-like <b>Superfamily:</b> VC0467-like <b>Family:</b> VC0467-like
11	<a href="#">c6qvcB_</a>	 Alignment		20.1	11	<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

12	<a href="#">d1z96a1</a>	Alignment		16.8	24	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
13	<a href="#">c2aj2A</a>	Alignment		16.6	30	<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.
14	<a href="#">c2kn8A</a>	Alignment		16.1	21	<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
15	<a href="#">c5ghaF</a>	Alignment		16.0	30	<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
16	<a href="#">c5sv0C</a>	Alignment		15.3	16	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> biopolymer transport protein exbb; <b>PDBTitle:</b> structure of the exbb/exbd complex from e. coli at ph 7.0
17	<a href="#">d2k0bx1</a>	Alignment		15.2	27	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
18	<a href="#">c2hv8D</a>	Alignment		12.3	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
19	<a href="#">c2m67A</a>	Alignment		11.9	18	<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
20	<a href="#">c2hg5D</a>	Alignment		11.5	16	<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
21	<a href="#">c1q7tA</a>	Alignment	not modelled	11.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv1170; <b>PDBTitle:</b> rv1170 (mshb) from mycobacterium tuberculosis
22	<a href="#">c1abzA</a>	Alignment	not modelled	10.8	44	<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
23	<a href="#">c5ws4A</a>	Alignment	not modelled	10.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
24	<a href="#">c2jy8A</a>	Alignment	not modelled	9.7	27	<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
25	<a href="#">c3dfmA</a>	Alignment	not modelled	9.6	23	<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
26	<a href="#">c6bs7A</a>	Alignment	not modelled	9.5	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="#">c5nikK</a>	Alignment	not modelled	9.1	7	<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
						<b>Fold:</b> TK C-terminal domain-like

28	<a href="#">d2ieaa3</a>	Alignment	not modelled	9.0	17	<b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
29	<a href="#">d1q74a</a>	Alignment	not modelled	8.8	40	<b>Fold:</b> LmbE-like <b>Superfamily:</b> LmbE-like <b>Family:</b> LmbE-like
30	<a href="#">d2do8a1</a>	Alignment	not modelled	8.4	40	<b>Fold:</b> VC0467-like <b>Superfamily:</b> VC0467-like <b>Family:</b> VC0467-like
31	<a href="#">d2hjqa1</a>	Alignment	not modelled	8.4	20	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> Rho N-terminal domain-like <b>Family:</b> YqbF C-terminal domain-like
32	<a href="#">d1i94m</a>	Alignment	not modelled	7.7	38	<b>Fold:</b> S13-like H2TH domain <b>Superfamily:</b> S13-like H2TH domain <b>Family:</b> Ribosomal protein S13
33	<a href="#">d1g7oa1</a>	Alignment	not modelled	7.5	16	<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
34	<a href="#">d2ebfx2</a>	Alignment	not modelled	7.2	29	<b>Fold:</b> EreA/ChaN-like <b>Superfamily:</b> EreA/ChaN-like <b>Family:</b> PMT domain-like
35	<a href="#">c4migC</a>	Alignment	not modelled	7.2	19	<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
36	<a href="#">c3vvpA</a>	Alignment	not modelled	6.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of mate in complex with br-nrf
37	<a href="#">c5ch4E</a>	Alignment	not modelled	6.7	11	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> protein translocase subunit sece; <b>PDBTitle:</b> peptide-bound state of thermus thermophilus secyeg
38	<a href="#">c1cf3A</a>	Alignment	not modelled	6.6	13	<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
39	<a href="#">d3dhwa1</a>	Alignment	not modelled	6.6	15	<b>Fold:</b> MetI-like <b>Superfamily:</b> MetI-like <b>Family:</b> MetI-like
40	<a href="#">c1gw4A</a>	Alignment	not modelled	6.6	36	<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
41	<a href="#">c3mk7F</a>	Alignment	not modelled	6.5	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
42	<a href="#">c2lxeA</a>	Alignment	not modelled	6.5	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histone-lysine n-methyltransferase suvr4; <b>PDBTitle:</b> s4wyild
43	<a href="#">c3n4qA</a>	Alignment	not modelled	6.2	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> terminase subunit u189 protein; <b>PDBTitle:</b> human cytomegalovirus terminase nuclease domain, mn soaked
44	<a href="#">c6humQ</a>	Alignment	not modelled	6.1	14	<b>PDB header:</b> proton transport <b>Chain:</b> Q: <b>PDB Molecule:</b> proton-translocating nadh-quinone dehydrogenase subunit q <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
45	<a href="#">c1wr1B</a>	Alignment	not modelled	6.1	29	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein dsk2; <b>PDBTitle:</b> the complex structure of dsk2p uba with ubiquitin
46	<a href="#">c5azcA</a>	Alignment	not modelled	5.8	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> prolipoprotein diacylglycerol transferase; <b>PDBTitle:</b> crystal structure of escherichia coli lgt in complex with2 phosphatidylglycerol
47	<a href="#">c2jy5A</a>	Alignment	not modelled	5.8	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquilin-1; <b>PDBTitle:</b> nmr structure of ubiquilin 1 uba domain
48	<a href="#">c4w86B</a>	Alignment	not modelled	5.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xyloglucan-specific endo-beta-1,4-glucanase; <b>PDBTitle:</b> crystal structure of xeg5a, a gh5 xyloglucan-specific endo-beta-1,4-2 glucanase from ruminal metagenomic library, in complex with glucose3 and tris
49	<a href="#">d2bwba1</a>	Alignment	not modelled	5.7	27	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
50	<a href="#">c3n4pA</a>	Alignment	not modelled	5.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> terminase subunit u189 protein; <b>PDBTitle:</b> human cytomegalovirus terminase nuclease domain
51	<a href="#">c5egiB</a>	Alignment	not modelled	5.6	6	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein y57a10a.10; <b>PDBTitle:</b> structure of a trimeric intracellular cation channel from c. elegans2 with bound ca2+
52	<a href="#">c2n0pA</a>	Alignment	not modelled	5.6	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein aq_1974; <b>PDBTitle:</b> solution structure of aquifex aeolicus aq1974
53	<a href="#">d1veja1</a>	Alignment	not modelled	5.6	29	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
54	<a href="#">c5eikA</a>	Alignment	not modelled	5.6	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein y57a10a.28; <b>PDBTitle:</b> structure of a trimeric intracellular cation channel from c.

						elegans2 in the absence of ca2+
55	<a href="#">c5fiyE_</a>	Alignment	not modelled	5.6	50	<b>PDB header:</b> apoptosis <b>Chain:</b> E: <b>PDB Molecule:</b> prkc apoptosis wt1 regulator protein; <b>PDBTitle:</b> crystal structure of coiled coil domain of pawr
56	<a href="#">c1zaxV_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> V: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
57	<a href="#">c1zavW_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> W: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
58	<a href="#">c1zavV_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> V: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
59	<a href="#">d1zavu1</a>	Alignment	not modelled	5.5	36	<b>Fold:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Superfamily:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain <b>Family:</b> Ribosomal protein L7/12, oligomerisation (N-terminal) domain
60	<a href="#">c1zavU_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
61	<a href="#">c1zaxU_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> U: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
62	<a href="#">c1zaxW_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> W: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
63	<a href="#">c1zaxY_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> Y: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
64	<a href="#">c1zavY_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> Y: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
65	<a href="#">c1zaxX_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> X: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p212121,2 form b
66	<a href="#">c1zavX_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> structural protein <b>Chain:</b> X: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> ribosomal protein l10-l12(ntd) complex, space group p21
67	<a href="#">c2mfrA_</a>	Alignment	not modelled	5.5	6	<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
68	<a href="#">c5eulE_</a>	Alignment	not modelled	5.4	12	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> preprotein translocase sece subunit; <b>PDBTitle:</b> structure of the seca-secy complex with a translocating polypeptide2 substrate
69	<a href="#">c1dd3D_</a>	Alignment	not modelled	5.3	36	<b>PDB header:</b> ribosome <b>Chain:</b> D: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> crystal structure of ribosomal protein l12 from thermotoga maritima
70	<a href="#">c1dd3C_</a>	Alignment	not modelled	5.3	36	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> 50s ribosomal protein l7/l12; <b>PDBTitle:</b> crystal structure of ribosomal protein l12 from thermotoga maritima
71	<a href="#">c2cwbA_</a>	Alignment	not modelled	5.2	27	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of immunoglobulin g binding protein g <b>PDBTitle:</b> solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
72	<a href="#">c5i34B_</a>	Alignment	not modelled	5.2	41	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> adenylosuccinate synthetase from cryptococcus neoformans complexed2 with gdp and imp
73	<a href="#">c2bkiA_</a>	Alignment	not modelled	5.2	20	<b>PDB header:</b> motor protein/metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> unconventional myosin; <b>PDBTitle:</b> myosin vi nucleotide-free (mdinsert2-iq) crystal structure
74	<a href="#">c3dinD_</a>	Alignment	not modelled	5.1	17	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> preprotein translocase subunit sece; <b>PDBTitle:</b> crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
75	<a href="#">c5d3aA_</a>	Alignment	not modelled	5.1	33	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> kinesin-like protein kif21a; <b>PDBTitle:</b> kif21a regulatory coiled coil
76	<a href="#">c3dfiA_</a>	Alignment	not modelled	5.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pseudoaglycone deacetylase dbv21; <b>PDBTitle:</b> the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
77	<a href="#">d1tc3c_</a>	Alignment	not modelled	5.1	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Recombinase DNA-binding domain