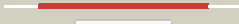

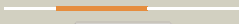


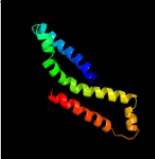

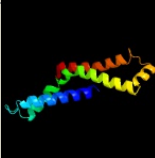







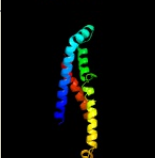

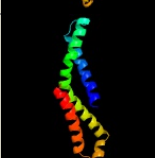

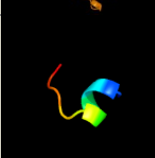

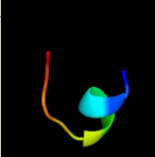


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1965_(yrbE3B)_2208515_2209330
Date	Mon Aug 5 13:25:06 BST 2019
Unique Job ID	42bb5043060defe9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4H_	 Alignment		100.0	20	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		86.1	16	PDB header: membrane protein Chain: G; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
3	c5I75F_	 Alignment		66.0	14	PDB header: transport protein Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
4	c6mjpG_	 Alignment		63.2	16	PDB header: lipid transport Chain: G; PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
5	c5I75G_	 Alignment		47.9	15	PDB header: transport protein Chain: G; PDB Molecule: fig000906: predicted permease; PDBTitle: a protein structure
6	c5x5yF_	 Alignment		35.4	19	PDB header: membrane protein Chain: F; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
7	c6qvcB_	 Alignment		30.4	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	c5xu1M_	 Alignment		26.2	12	PDB header: transport protein Chain: M; PDB Molecule: abc transporter permease; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
9	c6mjpF_	 Alignment		24.9	14	PDB header: lipid transport Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
10	c5ghaF_	 Alignment		21.9	30	PDB header: transferase/transport protein Chain: F; PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
11	d2hafa1	 Alignment		20.7	30	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like

12	c2hg5D_	Alignment		19.4	33	PDB header: membrane protein Chain: D: PDB Molecule: kcsa channel; PDBTitle: cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter
13	c2m67A_	Alignment		18.7	6	PDB header: transport protein Chain: A: PDB Molecule: merf; PDBTitle: full-length mercury transporter protein merf in lipid bilayer2 membranes
14	c2yvxD_	Alignment		16.9	9	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
15	c2hv8D_	Alignment		16.6	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
16	c2aj2A_	Alignment		16.0	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.
17	c4migC_	Alignment		14.5	19	PDB header: oxidoreductase Chain: C: PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type
18	c5sv0C_	Alignment		14.0	22	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
19	c6coyB_	Alignment		13.4	13	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, transmembrane domain
20	c1abzA_	Alignment		12.4	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
21	c6bs7A_	Alignment	not modelled	12.0	41	PDB header: ligase Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of adenylosuccinate synthetase from legionella2 pneumophila philadelphia 1
22	c3dfmA_	Alignment	not modelled	11.8	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
23	c3nd0A_	Alignment	not modelled	11.8	16	PDB header: transport protein Chain: A: PDB Molecule: sll0855 protein; PDBTitle: x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
24	d1z96a1	Alignment	not modelled	10.9	24	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
25	c1cf3A_	Alignment	not modelled	10.7	21	PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from apergillus niger
26	c3vvpA_	Alignment	not modelled	9.8	9	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of mate in complex with br-nrf
27	d1q74a_	Alignment	not modelled	9.6	40	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
28	d1g7oa1	Alignment	not modelled	9.5	12	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain

29	d2ieaa3	Alignment	not modelled	9.3	14	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
30	d2k0bx1	Alignment	not modelled	8.9	20	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
31	c1gw4A	Alignment	not modelled	8.5	36	PDB header: high density lipoproteins Chain: A: PDB Molecule: apoa-i; PDBTitle: the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
32	d1i94m	Alignment	not modelled	8.4	25	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Ribosomal protein S13
33	c6oitG	Alignment	not modelled	8.1	7	PDB header: plant protein Chain: G: PDB Molecule: protein chromatin remodeling 35; PDBTitle: cryoem structure of arabidopsis ddr' complex (drd1 peptide-dms3-rdm1)
34	d2hjqa1	Alignment	not modelled	8.0	16	Fold: LEM/SAP HeH motif Superfamily: Rho N-terminal domain-like Family: YqbF C-terminal domain-like
35	d2do8a1	Alignment	not modelled	8.0	40	Fold: VC0467-like Superfamily: VC0467-like Family: VC0467-like
36	c2m7xA	Alignment	not modelled	7.8	7	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
37	c1zaxU	Alignment	not modelled	7.6	32	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
38	c1zaxV	Alignment	not modelled	7.6	32	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
39	c1zaxW	Alignment	not modelled	7.6	32	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
40	c1zavU	Alignment	not modelled	7.6	32	PDB header: structural protein Chain: U: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
41	d1zavu1	Alignment	not modelled	7.6	32	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
42	c1zavV	Alignment	not modelled	7.6	32	PDB header: structural protein Chain: V: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
43	c1zavW	Alignment	not modelled	7.6	32	PDB header: structural protein Chain: W: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
44	c1zavY	Alignment	not modelled	7.6	32	PDB header: structural protein Chain: Y: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
45	c1zaxY	Alignment	not modelled	7.6	32	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
46	c1zavX	Alignment	not modelled	7.6	32	PDB header: structural protein Chain: X: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: ribosomal protein l10-l12(ntd) complex, space group p21
47	c1zaxX	Alignment	not modelled	7.6	32	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
48	c1vmaA	Alignment	not modelled	7.5	25	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
49	c1dd3C	Alignment	not modelled	7.4	32	PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
50	c1dd3D	Alignment	not modelled	7.4	32	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
51	c1q7tA	Alignment	not modelled	7.3	40	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein rv1170; PDBTitle: rv1170 (mshb) from mycobacterium tuberculosis
52	c2mfrA	Alignment	not modelled	7.2	12	PDB header: transferase Chain: A: PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
53	c5ehbA	Alignment	not modelled	7.2	45	PDB header: de novo protein Chain: A: PDB Molecule: phiosy;i; PDBTitle: a de novo designed hexameric coiled-coil peptide with iodotyrosine
54	c2jy8A	Alignment	not modelled	7.2	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
						PDB header: membrane protein

55	c6cfwE_	Alignment	not modelled	7.1	19	Chain: E; PDB Molecule: mbn subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
56	c5l3sF_	Alignment	not modelled	7.0	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
57	c5i34B_	Alignment	not modelled	7.0	35	PDB header: ligase Chain: B; PDB Molecule: adenylosuccinate synthetase; PDBTitle: adenylosuccinate synthetase from cryptococcus neoformans complexed2 with gdp and imp
58	c4w86B_	Alignment	not modelled	6.9	22	PDB header: hydrolase Chain: B; PDB Molecule: xyloglucan-specific endo-beta-1,4-glucanase; PDBTitle: crystal structure of xeg5a, a gh5 xyloglucan-specific endo-beta-1,4-2 glucanase from ruminal metagenomic library, in complex with glucose3 and tris
59	c4ak9A_	Alignment	not modelled	6.9	25	PDB header: protein transport Chain: A; PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
60	c3tgvD_	Alignment	not modelled	6.8	40	PDB header: heme binding protein Chain: D; PDB Molecule: heme-binding protein hutz; PDBTitle: crystal structure of hutz,the heme storsge protein from vibrio2 cholerae
61	c2j7pA_	Alignment	not modelled	6.7	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
62	c3dfiA_	Alignment	not modelled	6.6	33	PDB header: hydrolase Chain: A; PDB Molecule: pseudoaglycone deacetylase dbv21; PDBTitle: the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
63	c6cy1B_	Alignment	not modelled	6.5	33	PDB header: signaling protein Chain: B; PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
64	c2kitA_	Alignment	not modelled	6.5	15	PDB header: transferase Chain: A; PDB Molecule: serine/threonine-protein kinase tor1; PDBTitle: the solution structure of the reduced yeast tor1 fatc domain bound to2 dpc micelles at 298k
65	c1w1nA_	Alignment	not modelled	6.5	15	PDB header: transferase Chain: A; PDB Molecule: phosphatidylinositol 3-kinase tor1; PDBTitle: the solution structure of the fatc domain of the protein kinase tor12 from yeast
66	c2lxeA_	Alignment	not modelled	6.5	7	PDB header: transferase Chain: A; PDB Molecule: histone-lysine n-methyltransferase suvr4; PDBTitle: s4wyild
67	c5azcA_	Alignment	not modelled	6.4	17	PDB header: transferase Chain: A; PDB Molecule: prolipoprotein diacylglycerol transferase; PDBTitle: crystal structure of escherichia coli lgt in complex with2 phosphatidylglycerol
68	c3n4qA_	Alignment	not modelled	6.4	30	PDB header: dna binding protein Chain: A; PDB Molecule: terminase subunit ul89 protein; PDBTitle: human cytomegalovirus terminase nuclease domain, mn soaked
69	c5fiyE_	Alignment	not modelled	6.4	50	PDB header: apoptosis Chain: E; PDB Molecule: prkc apoptosis wt1 regulator protein; PDBTitle: crystal structure of coiled coil domain of pawr
70	c5d3aA_	Alignment	not modelled	6.3	44	PDB header: motor protein Chain: A; PDB Molecule: kinesin-like protein kif21a; PDBTitle: kif21a regulatory coiled coil
71	c3b9qA_	Alignment	not modelled	6.2	25	PDB header: protein transport Chain: A; PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
72	c5ehbB_	Alignment	not modelled	6.2	45	PDB header: de novo protein Chain: B; PDB Molecule: phiosyi; PDBTitle: a de novo designed hexameric coiled-coil peptide with iodotyrosine
73	c5egiB_	Alignment	not modelled	6.2	9	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+
74	c5eikA_	Alignment	not modelled	6.1	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+
75	c5l1xH_	Alignment	not modelled	6.1	37	PDB header: viral protein Chain: H; PDB Molecule: hmpv f1 subunit; PDBTitle: structure of the human metapneumovirus fusion protein in the2 postfusion conformation
76	c5nikK_	Alignment	not modelled	6.0	17	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
77	c5ch4E_	Alignment	not modelled	6.0	7	PDB header: protein transport Chain: E; PDB Molecule: protein translocase subunit sece; PDBTitle: peptide-bound state of thermus thermophilus secyeg
78	c5uyoA_	Alignment	not modelled	6.0	45	PDB header: de novo protein Chain: A; PDB Molecule: heeh_rd4_0097; PDBTitle: solution nmr structure of the de novo mini protein heeh_rd4_0097
79	d2ebfx2	Alignment	not modelled	6.0	29	Fold: EreA/ChaN-like Superfamily: EreA/ChaN-like Family: PMT domain-like
80	c3n4pA_	Alignment	not modelled	5.9	30	PDB header: dna binding protein Chain: A; PDB Molecule: terminase subunit ul89 protein; PDBTitle: human cytomegalovirus terminase nuclease domain

81	c2of5A_	Alignment	not modelled	5.8	12	PDB header: apoptosis Chain: A: PDB Molecule: death domain-containing protein cradd; PDBTitle: oligomeric death domain complex
82	c2yhsA_	Alignment	not modelled	5.8	33	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
83	d2r6gf2	Alignment	not modelled	5.8	4	Fold: MetI-like Superfamily: MetI-like Family: MetI-like
84	c2q9cA_	Alignment	not modelled	5.7	42	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmpnp with mgcl complex
85	d1zkea1	Alignment	not modelled	5.7	50	Fold: ROP-like Superfamily: HP1531-like Family: HP1531-like
86	c2og2A_	Alignment	not modelled	5.7	25	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
87	c2qy9A_	Alignment	not modelled	5.7	33	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
88	c4dagA_	Alignment	not modelled	5.7	37	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
89	c4hubG_	Alignment	not modelled	5.6	24	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l10e; PDBTitle: the re-refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution: more complete structure3 of the l7/l12 and l1 stalk, l5 and lx proteins
90	c2mgyA_	Alignment	not modelled	5.6	12	PDB header: membrane protein Chain: A: PDB Molecule: translocator protein; PDBTitle: solution structure of the mitochondrial translocator protein (tspo) in2 complex with its high-affinity ligand pk11195
91	c3ra3E_	Alignment	not modelled	5.6	86	PDB header: de novo protein Chain: E: PDB Molecule: p1c; PDBTitle: crystal structure of a section of a de novo design gigadalton protein2 fibre
92	c3dmdA_	Alignment	not modelled	5.6	33	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
93	c2cnwF_	Alignment	not modelled	5.5	42	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
94	c5il0B_	Alignment	not modelled	5.5	36	PDB header: rna binding protein Chain: B: PDB Molecule: mettl14; PDBTitle: crystal structural of the mettl3-mettl14 complex for n6-adenosine2 methylation
95	c5wb0F_	Alignment	not modelled	5.5	37	PDB header: viral protein Chain: F: PDB Molecule: fusion glycoprotein f0; PDBTitle: crystal structure of human metapneumovirus fusion glycoprotein2 stabilized in the prefusion state
96	c3ra3A_	Alignment	not modelled	5.5	86	PDB header: de novo protein Chain: A: PDB Molecule: p1c; PDBTitle: crystal structure of a section of a de novo design gigadalton protein2 fibre
97	c3lkIA_	Alignment	not modelled	5.5	20	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase with bound atp from2 xylella fastidiosa
98	c5l3qB_	Alignment	not modelled	5.5	42	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
99	c2v5hB_	Alignment	not modelled	5.4	26	PDB header: transcription Chain: B: PDB Molecule: acetylglutamate kinase; PDBTitle: controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942