



















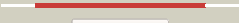



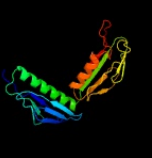



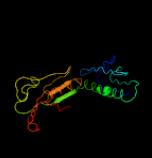
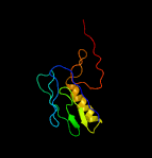
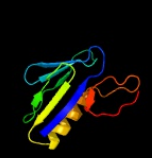


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0719_(rplF)_813401_813940
Date	Fri Jul 26 01:50:29 BST 2019
Unique Job ID	8cdcd5ecff074a7d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60G_	 Alignment		100.0	87	PDB header: ribosome Chain: G; PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	c3bboI_	 Alignment		100.0	47	PDB header: ribosome Chain: I; PDB Molecule: ribosomal protein l6; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
3	c1vw4F_	 Alignment		100.0	35	PDB header: ribosome Chain: F; PDB Molecule: 54s ribosomal protein l6, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
4	c1sm1E_	 Alignment		100.0	55	PDB header: ribosome/antibiotic Chain: E; PDB Molecule: 50s ribosomal protein l6; PDBTitle: complex of the large ribosomal subunit from deinococcus radiodurans2 with quinupristin and dalfopristin
5	c2hguH_	 Alignment		100.0	55	PDB header: ribosome Chain: H; PDB Molecule: 50s ribosomal protein l6; PDBTitle: 70s t.th. ribosome functional complex with mrna and e- and p-site2 trnas at 4.5a. this entry 2hgu contains 50s ribosomal subunit. the3 30s ribosomal subunit can be found in pdb entry 2hgr.
6	c2i2vG_	 Alignment		100.0	43	PDB header: ribosome Chain: G; PDB Molecule: 50s ribosomal protein l6; PDBTitle: crystal structure of ribosome with messenger rna and the anticodon2 stem-loop of p-site trna. this file contains the 50s subunit of one3 70s ribosome. the entire crystal structure contains two 70s ribosomes4 and is described in remark 400.
7	c1pnuE_	 Alignment		100.0	55	PDB header: ribosome Chain: E; PDB Molecule: 50s ribosomal protein l6; PDBTitle: crystal structure of a streptomycin dependent ribosome from2 escherichia coli, 50s subunit of 70s ribosome. this file, 1pnu,3 contains only molecules of the 50s ribosomal subunit. the 30s4 subunit, mrna, p-site trna, and a-site trna are in the pdb file 1pns.
8	c487dI_	 Alignment		100.0	51	PDB header: ribosome Chain: J; PDB Molecule: protein (50s l6 ribosomal protein); PDBTitle: seven ribosomal proteins fitted to a cryo-electron2 microscopic map of the large 50s subunit at 7.5 angstroms3 resolution
9	c3j21F_	 Alignment		100.0	31	PDB header: ribosome Chain: F; PDB Molecule: 50s ribosomal protein l6p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
10	c3ccmE_	 Alignment		100.0	27	PDB header: ribosome Chain: E; PDB Molecule: 50s ribosomal protein l6p; PDBTitle: structure of anisomycin resistant 50s ribosomal subunit: 23s rna2 mutation g2611u
11	c2zkre_	 Alignment		100.0	22	PDB header: ribosomal protein/rna Chain: E; PDB Molecule: rna expansion segment es7 part ii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map

12	c3j39H_	Alignment		100.0	20	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein I9; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
13	c4a1eE_	Alignment		100.0	25	PDB header: ribosome Chain: E: PDB Molecule: 60s ribosomal protein I9; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
14	c5an9B_	Alignment		100.0	23	PDB header: translation Chain: B: PDB Molecule: 60s ribosomal protein I9; PDBTitle: mechanism of eif6 release from the nascent 60s ribosomal subunit
15	c3zf7y_	Alignment		100.0	22	PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein I24, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
16	c3iz5F_	Alignment		100.0	25	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein I9 (I6p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
17	c4wf9E_	Alignment		100.0	49	PDB header: ribosome Chain: E: PDB Molecule: 50s ribosomal protein I6; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with telithromycin
18	c1s1iH_	Alignment		100.0	25	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein I9-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
19	d2qamg2	Alignment		100.0	48	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
20	d1rl6a2	Alignment		100.0	54	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
21	d2zjre1	Alignment	not modelled	100.0	61	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
22	d2j01h2	Alignment	not modelled	100.0	58	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
23	d2qamg1	Alignment	not modelled	99.9	38	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
24	d1vqoe1	Alignment	not modelled	99.9	23	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
25	d1rl6a1	Alignment	not modelled	99.9	47	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
26	d2cqla1	Alignment	not modelled	99.9	28	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
27	d2zjre2	Alignment	not modelled	99.9	47	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
28	d2j01h1	Alignment	not modelled	99.8	48	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
29	d1vqoe2	Alignment	not modelled	99.7	31	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6

						Family: Ribosomal protein L6
30	c2bolA_	Alignment	not modelled	61.5	18	PDB header: heat shock protein Chain: A: PDB Molecule: small heat shock protein; PDBTitle: crystal structure and assembly of tsp36, a metazoan small heat shock2 protein
31	c3q9qB_	Alignment	not modelled	36.8	18	PDB header: chaperone Chain: B: PDB Molecule: heat shock protein beta-1; PDBTitle: hspb1 fragment second crystal form
32	c2wj7D_	Alignment	not modelled	35.5	35	PDB header: chaperone Chain: D: PDB Molecule: alpha-crystallin b chain; PDBTitle: human alphab crystallin
33	d1a0ia1	Alignment	not modelled	35.4	12	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
34	c6f2rA_	Alignment	not modelled	34.4	24	PDB header: chaperone Chain: A: PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
35	c6f2rE_	Alignment	not modelled	34.4	24	PDB header: chaperone Chain: E: PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
36	c4pbdA_	Alignment	not modelled	33.1	27	PDB header: protein binding Chain: A: PDB Molecule: protein shq1 homolog; PDBTitle: crystal structure of the n-terminal cs domain of human shq1
37	c6f2rI_	Alignment	not modelled	31.6	24	PDB header: chaperone Chain: I: PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
38	c5ltwK_	Alignment	not modelled	29.7	19	PDB header: protein binding Chain: K: PDB Molecule: heat shock protein beta-6; PDBTitle: complex of human 14-3-3 sigma clu1 mutant with phosphorylated heat2 shock protein b6
39	c6f2rK_	Alignment	not modelled	29.3	24	PDB header: chaperone Chain: K: PDB Molecule: hspb2,heat shock protein beta-2,heat shock protein beta-2, PDBTitle: a hetrotetramer of human hspb2 and hspb3
40	c6ghsA_	Alignment	not modelled	26.7	26	PDB header: hydrolase Chain: A: PDB Molecule: tagi restriction endonuclease; PDBTitle: modification dependent tagi restriction endonuclease
41	c2jugB_	Alignment	not modelled	25.6	29	PDB header: biosynthetic protein Chain: B: PDB Molecule: stbc protein; PDBTitle: multienzyme docking in hybrid megasynthetases
42	c6f2rT_	Alignment	not modelled	24.5	12	PDB header: chaperone Chain: T: PDB Molecule: heat shock protein beta-3,heat shock protein beta-3,heat PDBTitle: a hetrotetramer of human hspb2 and hspb3
43	c2klrA_	Alignment	not modelled	23.3	35	PDB header: chaperone Chain: A: PDB Molecule: alpha-crystallin b chain; PDBTitle: solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
44	c5y82B_	Alignment	not modelled	22.7	19	PDB header: transport protein Chain: B: PDB Molecule: membrane protein insertase yidc; PDBTitle: crystal structure of the periplasmic domain of the thermotoga maritima2 yidc
45	d1oopc_	Alignment	not modelled	21.1	18	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
46	c2ygdV_	Alignment	not modelled	20.5	35	PDB header: chaperone Chain: V: PDB Molecule: PDBTitle: molecular architectures of the 24meric eye lens chaperone alphab-2 crystallin elucidated by a triple hybrid approach
47	d1eah3_	Alignment	not modelled	20.4	16	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
48	c2wzr3_	Alignment	not modelled	20.1	7	PDB header: virus Chain: 3: PDB Molecule: polyprotein; PDB Fragment: residues 285-503; PDBTitle: the structure of foot and mouth disease virus serotype sat1
49	d2mev3_	Alignment	not modelled	20.1	13	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
50	d1ncqc_	Alignment	not modelled	19.7	13	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
51	c4ydzA_	Alignment	not modelled	17.2	29	PDB header: chaperone Chain: A: PDB Molecule: stress-induced protein 1; PDBTitle: stress-induced protein 1 from caenorhabditis elegans
52	c5mquC_	Alignment	not modelled	16.5	9	PDB header: virus Chain: C: PDB Molecule: vp3; PDBTitle: crystal structure of bovine enterovirus 2 determined with serial2 femtosecond x-ray crystallography
53	c3vbhC_	Alignment	not modelled	16.1	13	PDB header: virus Chain: C: PDB Molecule: genome polyprotein, vapsid protein vp3; PDBTitle: crystal structure of formaldehyde treated human enterovirus 71 (space2 group r32)
54	c2wj5A_	Alignment	not modelled	15.8	24	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein beta-6; PDBTitle: rat alpha crystallin domain
55	d1v5ma_	Alignment	not modelled	15.4	25	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
						Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins)

56	d1aym3_	Alignment	not modelled	15.4	22	Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
57	c6dv5T_	Alignment	not modelled	15.2	18	PDB header: chaperone Chain: T; PDB Molecule: heat shock protein beta-1; PDBTitle: oligomeric complex of a hsp27 24-mer at 3.6 a resolution
58	c3nicA_	Alignment	not modelled	15.2	31	PDB header: hydrolase/dna Chain: A; PDB Molecule: eco29kir; PDBTitle: dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
59	c2gh8B_	Alignment	not modelled	14.8	13	PDB header: virus Chain: B; PDB Molecule: capsid protein; PDBTitle: x-ray structure of a native calicivirus
60	c2mbIA_	Alignment	not modelled	14.7	22	PDB header: de novo protein Chain: A; PDB Molecule: top7 fold protein top7m13; PDBTitle: solution nmr structure of de novo designed top7 fold protein top7m13,2 northeast structural genomics consortium (nesg) target or33
61	d1j5pa3	Alignment	not modelled	14.6	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
62	c4imyG_	Alignment	not modelled	14.5	44	PDB header: transferase Chain: G; PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
63	c4imyl_	Alignment	not modelled	14.5	44	PDB header: transferase Chain: I; PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
64	d1bev3_	Alignment	not modelled	13.9	15	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
65	d2gv8a2	Alignment	not modelled	13.7	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
66	d1omwg_	Alignment	not modelled	13.0	38	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Transducin (heterotrimeric G protein), gamma chain Family: Transducin (heterotrimeric G protein), gamma chain
67	d1fpn3_	Alignment	not modelled	12.9	18	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
68	c2wff3_	Alignment	not modelled	12.9	14	PDB header: virus Chain: 3; PDB Molecule: p1; PDB Fragment: capsid protein vp3, residues 311-536; PDBTitle: equine rhinitis a virus
69	c4imyH_	Alignment	not modelled	12.8	44	PDB header: transferase Chain: H; PDB Molecule: af4/fmr2 family member 4; PDBTitle: the aff4 scaffold binds human p-tefb adjacent to hiv tat
70	c31eA_	Alignment	not modelled	12.2	18	PDB header: chaperone Chain: A; PDB Molecule: alpha-crystallin a chain; PDBTitle: bovine alphaa crystallin zinc bound
71	c3kd4A_	Alignment	not modelled	12.1	17	PDB header: hydrolase Chain: A; PDB Molecule: putative protease; PDBTitle: crystal structure of a putative protease (bdj_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
72	c2gjhA_	Alignment	not modelled	11.4	28	PDB header: de novo protein Chain: A; PDB Molecule: designed protein; PDBTitle: nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
73	d1cov3_	Alignment	not modelled	10.9	16	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
74	c3cjb_	Alignment	not modelled	10.4	9	PDB header: virus Chain: B; PDB Molecule: polyprotein; PDBTitle: structure of seneca valley virus-001
75	c2ktsA_	Alignment	not modelled	9.4	19	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hslj; PDBTitle: nmr structure of the protein np_415897.1
76	c3i38E_	Alignment	not modelled	9.3	33	PDB header: chaperone Chain: E; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
77	c3i38C_	Alignment	not modelled	9.3	33	PDB header: chaperone Chain: C; PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
78	c5j4aA_	Alignment	not modelled	9.2	53	PDB header: toxin Chain: A; PDB Molecule: trna nuclease cdia; PDBTitle: cdia-ct toxin from burkholderia pseudomallei e479 in complex with2 cognate cdii immunity protein
79	c2n3jA_	Alignment	not modelled	9.0	18	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein beta-1; PDBTitle: solution structure of the alpha-crystallin domain from the redox-2 sensitive chaperone, hspb1
80	d1hxs3_	Alignment	not modelled	8.7	18	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
81	d1rhi3_	Alignment	not modelled	8.3	16	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
82	c5cupB_	Alignment	not modelled	8.2	46	PDB header: transferase Chain: B; PDB Molecule: phosphate propanoyltransferase; PDBTitle: structure of rhodopseudomonas palustris pdul - phosphate bound form

83	c4zjdF_	Alignment	not modelled	7.9	11	PDB header: chaperone Chain: F: PDB Molecule: aggregation suppressing protein; PDBTitle: small heat shock protein agsa from salmonella typhimurium: truncations2 at n- and c- termini
84	c3glaA_	Alignment	not modelled	7.8	24	PDB header: chaperone Chain: A: PDB Molecule: low molecular weight heat shock protein; PDBTitle: crystal structure of the hspa from xanthomonas axonopodis
85	c2d2fA_	Alignment	not modelled	7.6	17	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
86	c5mb8J_	Alignment	not modelled	7.4	21	PDB header: chaperone Chain: J: PDB Molecule: 25.3 kda heat shock protein, chloroplastic; PDBTitle: hsp21 dodecamer, structural model based on cryo-em and homology2 modelling
87	d1aqtA2	Alignment	not modelled	7.2	14	Fold: Epsilon subunit of F1F0-ATP synthase N-terminal domain Superfamily: Epsilon subunit of F1F0-ATP synthase N-terminal domain Family: Epsilon subunit of F1F0-ATP synthase N-terminal domain
88	d1r1a3_	Alignment	not modelled	7.2	15	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
89	c2mmvA_	Alignment	not modelled	7.0	32	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein zapa; PDBTitle: zapa mutant dimer from geobacillus stearothermophilus
90	d2z0sa2	Alignment	not modelled	6.9	6	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
91	d1cuka3	Alignment	not modelled	6.8	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
92	c4qeoA_	Alignment	not modelled	6.7	20	PDB header: transcription/dna Chain: A: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-9 specific PDBTitle: crystal structure of kryptonite in complex with mchh dna, h3(1-15)2 peptide and sah
93	d1fmd3_	Alignment	not modelled	6.6	13	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
94	d1ev13_	Alignment	not modelled	6.6	15	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
95	c3zueB_	Alignment	not modelled	6.5	19	PDB header: virus Chain: B: PDB Molecule: capsid structural protein vp60; PDBTitle: rabbit hemorrhagic disease virus (rhdv)capsid protein
96	c4nj5A_	Alignment	not modelled	6.3	20	PDB header: metal binding protein Chain: A: PDB Molecule: probable histone-lysine n-methyltransferase, h3 lysine-9 PDBTitle: crystal structure of suvh9
97	c5aca3_	Alignment	not modelled	6.2	9	PDB header: virus Chain: 3: PDB Molecule: vp3; PDBTitle: structure-based energetics of protein interfaces guide foot-and-mouth2 disease virus vaccine design
98	c3w1zD_	Alignment	not modelled	6.2	18	PDB header: chaperone Chain: D: PDB Molecule: heat shock protein 16; PDBTitle: heat shock protein 16.0 from schizosaccharomyces pombe
99	c6fkhe_	Alignment	not modelled	6.1	15	PDB header: membrane protein Chain: E: PDB Molecule: atp synthase subunit alpha, chloroplastic; PDBTitle: chloroplast f1fo conformation 2