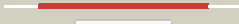
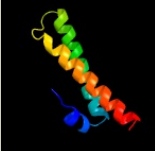


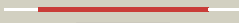




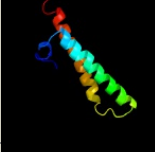

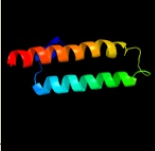



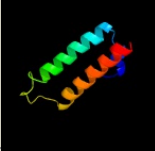

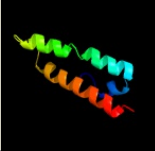

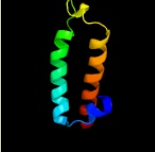

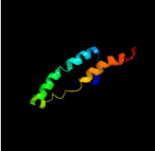

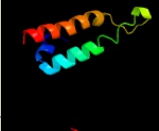
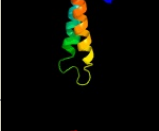
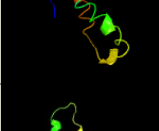


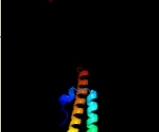
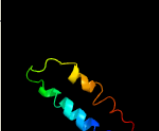
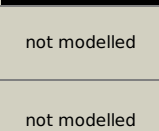


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0709_rpmC_805529_805762
 Date Fri Jul 26 01:50:28 BST 2019
 Unique Job ID 5808d7afd6369f51

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60Z_	 Alignment		99.9	88	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l29; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	c3izrc_	 Alignment		99.9	29	PDB header: ribosome Chain: C: PDB Molecule: 60s ribosomal protein l3 (l3p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
3	c3j21W_	 Alignment		99.9	31	PDB header: ribosome Chain: W: PDB Molecule: 50s ribosomal protein l29p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
4	d1r73a_	 Alignment		99.9	50	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
5	d2zjrv1	 Alignment		99.9	37	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
6	d2hgq11	 Alignment		99.9	42	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
7	c2j375_	 Alignment		99.9	32	PDB header: ribosome Chain: 5: PDB Molecule: ribosomal protein l35; PDBTitle: model of mammalian srp bound to 80s rncs
8	d1vqov1	 Alignment		99.9	37	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
9	c3bboZ_	 Alignment		99.8	34	PDB header: ribosome Chain: Z: PDB Molecule: ribosomal protein l29; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
10	c3j3wX_	 Alignment		99.8	56	PDB header: ribosome Chain: X: PDB Molecule: 50s ribosomal protein l29; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
11	c3jywX_	 Alignment		99.8	32	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l35; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution

12	c2zkrv	Alignment		99.8	36	PDB header: ribosomal protein/rna Chain: V: PDB Molecule: rna expansion segment es9 part2; 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
13	d2gycw1	Alignment		99.8	43	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
14	c5mlcZ	Alignment		99.8	37	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l29, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
15	c1s1iX	Alignment		99.8	38	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l35; 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.
16	c3j39h	Alignment		99.7	32	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l9; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
17	c3j3bh	Alignment		99.7	28	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l9; PDBTitle: structure of the human 60s ribosomal proteins
18	c4a1eU	Alignment		99.7	28	PDB header: ribosome Chain: U: PDB Molecule: rpl35; 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
19	c3u5eh	Alignment		99.6	30	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l9-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
20	d2j0121	Alignment		99.1	45	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
21	c4ce42	Alignment	not modelled	99.0	23	PDB header: ribosome Chain: 2: PDB Molecule: mrpl47; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
22	c4v192	Alignment	not modelled	98.9	23	PDB header: ribosome Chain: 2: PDB Molecule: mitoribosomal protein ul29m, mrpl47; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
23	c1vw4T	Alignment	not modelled	98.7	22	PDB header: ribosome Chain: T: PDB Molecule: 54s ribosomal protein l4, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
24	c3zf7k	Alignment	not modelled	97.2	38	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein l10, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
25	c4uzxA	Alignment	not modelled	45.8	19	PDB header: rna binding protein Chain: A: PDB Molecule: protein tho1; PDBTitle: high-resolution nmr structures of the domains of saccharomyces2 cerevisiae tho1
26	c2o1sC	Alignment	not modelled	40.9	33	PDB header: transferase Chain: C: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from2 escherichia coli
27	c6ouwA	Alignment	not modelled	35.6	26	PDB header: transferase Chain: A: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxps) from deinococcus2 radiodurans with enamine intermediate bound
28	c2o1xA	Alignment	not modelled	27.5	26	PDB header: transferase Chain: A: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate synthase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate synthase (dxs) from deinococcus2 radiodurans
						PDB header: protein transport

29	c2hv8D_	Alignment	not modelled	26.2	26	Chain: D: PDB Molecule: rab11 family-interacting protein 3; PDBTitle: crystal structure of gtp-bound rab11 in complex with fip3
30	c3j38P_	Alignment	not modelled	22.1	26	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein s15, isoform a; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
31	d1qjja2	Alignment	not modelled	21.1	38	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
32	c4y66D_	Alignment	not modelled	19.8	15	PDB header: cell cycle Chain: D: PDB Molecule: putative tbpip family protein; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex
33	c5i0qA_	Alignment	not modelled	18.4	45	PDB header: immune system Chain: A: PDB Molecule: m protein, serotype 2.1; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of mutant group a3 streptococcus m2 (k65a, n66a) protein
34	c5hyuA_	Alignment	not modelled	15.7	45	PDB header: immune system Chain: A: PDB Molecule: m protein, serotype 2.1; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m23 protein
35	d2hjqa1	Alignment	not modelled	13.8	20	Fold: LEM/SAP HeH motif Superfamily: Rho N-terminal domain-like Family: YqbF C-terminal domain-like
36	c1sy9B_	Alignment	not modelled	12.4	58	PDB header: calcium-binding protein Chain: B: PDB Molecule: cyclic-nucleotide-gated olfactory channel; PDBTitle: structure of calmodulin complexed with a fragment of the2 olfactory cng channel
37	c1j1eB_	Alignment	not modelled	12.4	22	PDB header: contractile protein Chain: B: PDB Molecule: troponin t; PDBTitle: crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
38	d1jeia_	Alignment	not modelled	12.4	36	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
39	c5xyiP_	Alignment	not modelled	11.6	26	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein s19, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
40	c5j5vC_	Alignment	not modelled	11.5	19	PDB header: toxin Chain: C: PDB Molecule: immunity protein cdii; PDBTitle: cdia-ct from uropathogenic escherichia coli in complex with cognate2 immunity protein and cysk
41	c6c48E_	Alignment	not modelled	11.5	33	PDB header: cell cycle/dna binding Chain: E: PDB Molecule: protein lin-52 homolog; PDBTitle: crystal structure of b-myb-lin9-lin52 complex
42	c6f1ux_	Alignment	not modelled	10.5	18	PDB header: motor protein Chain: X: PDB Molecule: bicd family-like cargo adapter 1; PDBTitle: n terminal region of dynein tail domains in complex with dynactin2 filament and bicdr-1
43	c3layF_	Alignment	not modelled	10.3	13	PDB header: metal binding protein Chain: F: PDB Molecule: zinc resistance-associated protein; PDBTitle: alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
44	c3j20T_	Alignment	not modelled	10.1	28	PDB header: ribosome Chain: T: PDB Molecule: 30s ribosomal protein s19p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
45	c5lj3R_	Alignment	not modelled	9.8	20	PDB header: splicing Chain: R: PDB Molecule: pre-mrna-splicing factor cwc21; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
46	d2odgc1	Alignment	not modelled	9.8	43	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
47	d1h1js_	Alignment	not modelled	9.7	22	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
48	c3zeyl_	Alignment	not modelled	9.3	19	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s15, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
49	d1xwya1	Alignment	not modelled	9.3	22	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: TatD Mg-dependent DNase-like
50	c2kveA_	Alignment	not modelled	9.1	30	PDB header: hormone Chain: A: PDB Molecule: mesencephalic astrocyte-derived neurotrophic factor; PDBTitle: c-terminal domain of mesencephalic astrocyte-derived neurotrophic2 factor (manf)
51	c6bk8K_	Alignment	not modelled	9.1	21	PDB header: rna binding protein Chain: K: PDB Molecule: pre-mrna-splicing factor cwc21; PDBTitle: s. cerevisiae spliceosomal post-catalytic p complex
52	c1gcmC_	Alignment	not modelled	9.1	35	PDB header: transcription regulation Chain: C: PDB Molecule: gcn4p-ii; PDBTitle: gcn4 leucine zipper core mutant p-li
53	c4ps2A_	Alignment	not modelled	9.0	17	PDB header: contractile protein Chain: A: PDB Molecule: putative type vi secretion protein; PDBTitle: structure of the c-terminal fragment (87-165) of e.coli eaec tssb2 molecule
54	c4auvG_	Alignment	not modelled	8.9	39	PDB header: apoptosis Chain: G: PDB Molecule: breast cancer metastasis suppressor 1; PDBTitle: crystal structure of the brms1 n-terminal region

55	c3tweB	Alignment	not modelled	8.8	35	PDB header: unknown function Chain: B: PDB Molecule: alpha4h; PDBTitle: crystal structure of the de novo designed peptide alpha4h
56	c3tsoC	Alignment	not modelled	8.7	36	PDB header: protein transport Chain: C: PDB Molecule: rab11 family-interacting protein 2; PDBTitle: structure of the cancer associated rab25 protein in complex with fip2
57	c1zrjA	Alignment	not modelled	8.7	35	PDB header: dna binding protein Chain: A: PDB Molecule: e1b-55kda-associated protein 5 isoform c; PDBTitle: solution structure of the sap domain of human e1b-55kda-2 associated protein 5 isoform c
58	c6bn1A	Alignment	not modelled	7.8	35	PDB header: signaling protein Chain: A: PDB Molecule: serine/threonine-protein kinase hippo; PDBTitle: salvador hippo sarah domain complex
59	c4by7X	Alignment	not modelled	7.5	28	PDB header: transcription Chain: X: PDB Molecule: transcription factor bye1; PDBTitle: elongating rna polymerase ii-bye1 tld complex
60	c2n64B	Alignment	not modelled	7.2	26	PDB header: signaling protein Chain: B: PDB Molecule: sh3 domain-containing kinase-binding protein 1; PDBTitle: nmr structure of the c-terminal coiled-coil domain of cin85
61	c5x9xB	Alignment	not modelled	7.2	45	PDB header: signaling protein Chain: B: PDB Molecule: metabotropic gaba-b receptor subtype 2; PDBTitle: solution structure of heterodimeric coiled-coil domain of drosophila2 gabab receptor 1 and 2
62	c2vdaA	Alignment	not modelled	7.1	33	PDB header: protein transport Chain: A: PDB Molecule: translocase subunit seca; PDBTitle: solution structure of the seca-signal peptide complex
63	c1yv0T	Alignment	not modelled	7.1	21	PDB header: contractile protein Chain: T: PDB Molecule: troponin t, fast skeletal muscle isoforms; PDBTitle: crystal structure of skeletal muscle troponin in the ca2+-free state
64	c5xxuP	Alignment	not modelled	7.0	33	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein us19; PDBTitle: small subunit of toxoplasma gondii ribosome
65	d1ov9a	Alignment	not modelled	7.0	47	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
66	d1qoja	Alignment	not modelled	6.9	22	Fold: Long alpha-hairpin Superfamily: C-terminal UvrC-binding domain of UvrB Family: C-terminal UvrC-binding domain of UvrB
67	c1envA	Alignment	not modelled	6.9	32	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 envelope protein chimera consisting of a fragment of PDBTitle: atomic structure of the ectodomain from hiv-1 gp41
68	c4u5tB	Alignment	not modelled	6.6	18	PDB header: transcription/transcription inhibitor Chain: B: PDB Molecule: vbp leucine zipper; PDBTitle: crystal structure of vbp leucine zipper with bound arylstibonic acid
69	d1r8ja1	Alignment	not modelled	6.6	20	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
70	c2rg8A	Alignment	not modelled	6.5	21	PDB header: apoptosis, translation Chain: A: PDB Molecule: programmed cell death protein 4; PDBTitle: crystal structure of programmed for cell death 4 middle ma3 domain
71	c2e8mA	Alignment	not modelled	6.5	20	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
72	c2do1A	Alignment	not modelled	6.4	30	PDB header: gene regulation Chain: A: PDB Molecule: nuclear protein hcc-1; PDBTitle: solution structure of the sap domain of human nuclear2 protein hcc-1
73	c2xusa	Alignment	not modelled	6.2	30	PDB header: protein binding Chain: A: PDB Molecule: breast cancer metastasis-suppressor 1; PDBTitle: crystal structure of the brms1 n-terminal region
74	d1h9fa	Alignment	not modelled	6.1	35	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
75	d1sv1a	Alignment	not modelled	6.0	10	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
76	d1fs1b1	Alignment	not modelled	6.0	21	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
77	c2q6qB	Alignment	not modelled	5.7	42	PDB header: cell cycle Chain: B: PDB Molecule: spindle pole body component spc42; PDBTitle: crystal structure of spc42p, a critical component of spindle pole body2 in budding yeast
78	c5z6nA	Alignment	not modelled	5.7	19	PDB header: transferase Chain: A: PDB Molecule: protein elaa; PDBTitle: crystal structure of escherichia coli elaa
79	c3ggzC	Alignment	not modelled	5.7	13	PDB header: protein transport, endocytosis Chain: C: PDB Molecule: increased sodium tolerance protein 1; PDBTitle: crystal structure of s.cerevisiae ist1 n-terminal domain in complex2 with did2 mim motif
80	d1dd3a1	Alignment	not modelled	5.6	27	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 PDB header: transcription

81	c4udeA	Alignment	not modelled	5.6	25	Chain: A: PDB Molecule: ginlly protein; PDBTitle: an oligomerization domain confers pioneer properties to the2 leafy master floral regulator
82	c1nl3B	Alignment	not modelled	5.5	36	PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase seca 1 subunit; PDBTitle: crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
83	c1kddD	Alignment	not modelled	5.4	26	PDB header: de novo protein Chain: D: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
84	c2outA	Alignment	not modelled	5.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mu-like prophage flumu protein gp35, protein PDBTitle: solution structure of hi1506, a novel two domain protein2 from haemophilus influenzae
85	d1hf8a1	Alignment	not modelled	5.4	17	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: Phosphoinositide-binding clathrin adaptor, domain 2
86	c2d9mA	Alignment	not modelled	5.4	24	PDB header: rna binding protein Chain: A: PDB Molecule: zinc finger ccch-type domain containing protein PDBTitle: solution structure of ccch type zinc-finger domain 3 in2 zinc finger ccch-type domain containing 7a
87	c3frrA	Alignment	not modelled	5.1	29	PDB header: protein binding Chain: A: PDB Molecule: uncharacterized protein kiaa0174; PDBTitle: structure of human ist1(ntd) - (residues 1-189)(p21)
88	c4ehsB	Alignment	not modelled	5.1	20	PDB header: transferase Chain: B: PDB Molecule: dna primase; PDBTitle: crystal structure of helicobacter pylori dnag primase c terminal2 domain
89	c2a8vA	Alignment	not modelled	5.1	19	PDB header: protein/rna Chain: A: PDB Molecule: rna binding domain of rho transcription PDBTitle: rho transcription termination factor/rna complex
90	c4dzlL	Alignment	not modelled	5.1	27	PDB header: de novo protein Chain: L: PDB Molecule: coiled-coil peptide cc-tri; PDBTitle: a de novo designed coiled coil cc-tri
91	c1kd8E	Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: E: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l
92	c1kd9D	Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: D: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
93	c1kd9E	Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: E: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l
94	c1kddE	Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: E: PDB Molecule: gcn4 acid base heterodimer base-d12la16l; PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12la16l base-d12la16l