


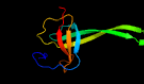





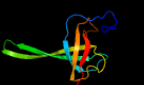

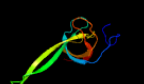







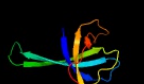

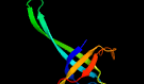
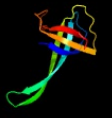
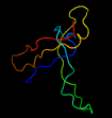
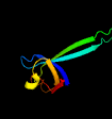


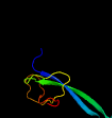

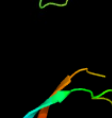
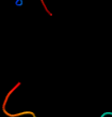


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0710_(rpsQ)_805759_806169
 Date Fri Jul 26 01:50:28 BST 2019
 Unique Job ID e484dd3c782e40fd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o5jQ_	 Alignment		100.0	88	PDB header: ribosome Chain: Q; PDB Molecule: 30s ribosomal protein s17; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
2	c3zeyE_	 Alignment		100.0	24	PDB header: ribosome Chain: E; PDB Molecule: 40s ribosomal proteins s11, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
3	c3u5gL_	 Alignment		100.0	32	PDB header: ribosome Chain: L; PDB Molecule: 40s ribosomal protein s11-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
4	c3j3aL_	 Alignment		100.0	30	PDB header: ribosome Chain: L; PDB Molecule: 40s ribosomal protein s11; PDBTitle: structure of the human 40s ribosomal proteins
5	c3j20R_	 Alignment		100.0	34	PDB header: ribosome Chain: R; PDB Molecule: 30s ribosomal protein s17p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
6	c2xznQ_	 Alignment		100.0	22	PDB header: ribosome Chain: Q; PDB Molecule: ribosomal protein s17 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
7	c5xyiL_	 Alignment		100.0	28	PDB header: ribosome Chain: L; PDB Molecule: uncharacterized protein; PDBTitle: small subunit of trichomonas vaginalis ribosome
8	d2uubq1	 Alignment		100.0	46	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
9	d1i94q_	 Alignment		100.0	46	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
10	c3bbnQ_	 Alignment		100.0	38	PDB header: ribosome Chain: Q; PDB Molecule: ribosomal protein s17; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
11	d2gy9q1	 Alignment		100.0	55	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like

12	c1s1hQ_	Alignment		100.0	32	PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein s11; 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, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
13	d1ripa_	Alignment		100.0	63	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
14	c2zkqg_	Alignment		100.0	28	PDB header: ribosomal protein/rna Chain: Q: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
15	c3j6vQ_	Alignment		100.0	28	PDB header: ribosome Chain: Q: PDB Molecule: 28s ribosomal protein s17, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
16	c3izbP_	Alignment		99.9	33	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein rps11 (s17p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
17	c3iz6P_	Alignment		99.9	25	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein s11 (s17p); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
18	d1t9ha1	Alignment		46.6	18	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
19	c6gmaA_	Alignment		34.8	32	PDB header: protein binding Chain: A: PDB Molecule: rb1-inducible coiled-coil protein 1; PDBTitle: crystal structure of the fip200 c-terminal region
20	c2xzm1_	Alignment		25.3	42	PDB header: ribosome Chain: 1: PDB Molecule: ribosomal protein s28e containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
21	d1ne3a_	Alignment	not modelled	24.6	33	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
22	c3zeyZ_	Alignment	not modelled	22.6	58	PDB header: ribosome Chain: Z: PDB Molecule: 40s ribosomal protein s33, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
23	d1ny4a_	Alignment	not modelled	22.1	42	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
24	d1u0la1	Alignment	not modelled	18.8	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
25	d1e32a1	Alignment	not modelled	18.1	25	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
26	c4i7aD_	Alignment	not modelled	16.7	24	PDB header: structural protein Chain: D: PDB Molecule: ethanolamine utilization protein eutn/carboxysome PDBTitle: grpn pentameric microcompartment shell protein from rhodospirillum2 rubrum
27	c5ly5A_	Alignment	not modelled	15.7	14	PDB header: unknown function Chain: A: PDB Molecule: arcadin-1; PDBTitle: arcadin-1 from pyrobaculum calidifontis
28	c2yv5A_	Alignment	not modelled	15.6	25	PDB header: hydrolase Chain: A: PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus
						PDB header: protein binding

29	c2rqra_	Alignment	not modelled	15.1	25	Chain: A: PDB Molecule: engulfment and cell motility protein 1, linker, dedicator PDBTitle: the solution structure of human dock2 sh3 domain - elmo1 peptide2 chimera complex
30	c5uvnA_	Alignment	not modelled	14.5	12	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
31	c5uvnC_	Alignment	not modelled	14.5	12	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
32	c5uvnD_	Alignment	not modelled	14.5	12	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
33	c5uvnE_	Alignment	not modelled	14.5	12	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
34	c5uvnF_	Alignment	not modelled	14.5	12	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
35	c5uvnB_	Alignment	not modelled	14.5	12	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
36	d2hd3a1	Alignment	not modelled	14.2	16	Fold: OB-fold Superfamily: EutN/CcmL-like Family: EutN/CcmL-like
37	c3iz6Y_	Alignment	not modelled	14.2	33	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s28 (s28e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
38	c4n8xB_	Alignment	not modelled	13.8	18	PDB header: structural protein Chain: B: PDB Molecule: carbon dioxide concentrating mechanism protein; PDBTitle: the structure of nostoc sp. pcc 7120 ccml
39	c4ytIB_	Alignment	not modelled	13.1	17	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
40	c4k73A_	Alignment	not modelled	13.1	38	PDB header: transferase Chain: A: PDB Molecule: l,d-transpeptidase; PDBTitle: x-ray crystal structure of an l,d-transpeptidase from mycobacterium2 tuberculosis h37rv
41	d1udxa3	Alignment	not modelled	12.6	33	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
42	c2yupA_	Alignment	not modelled	12.3	20	PDB header: cell adhesion Chain: A: PDB Molecule: vinexin; PDBTitle: solution structure of the second sh3 domain of human vinexin
43	c4tseA_	Alignment	not modelled	12.3	23	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mib1; PDBTitle: crystal structure of the mib repeat domain of mind bomb 1
44	c5uz4Z_	Alignment	not modelled	12.2	19	PDB header: ribosome/hydrolase Chain: Z: PDB Molecule: small ribosomal subunit biogenesis gtpase rsga; PDBTitle: the cryo-em structure of yjeq bound to the 30s subunit suggests a2 fidelity checkpoint function for this protein in ribosome assembly
45	c5ohoB_	Alignment	not modelled	12.2	16	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: crystal structure of the kowx-kow4 domain of human dsif
46	c2dbkA_	Alignment	not modelled	12.1	25	PDB header: signaling protein Chain: A: PDB Molecule: crk-like protein; PDBTitle: solution structures of the sh3 domain of human crk-like2 protein
47	c5znpB_	Alignment	not modelled	11.9	14	PDB header: gene regulation Chain: B: PDB Molecule: short life family protein; PDBTitle: crystal structure of ptshl in complex with an h3k4me3 peptide
48	c3d0fA_	Alignment	not modelled	11.7	12	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
49	d1grja2	Alignment	not modelled	11.5	14	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
50	c3nmzD_	Alignment	not modelled	11.3	20	PDB header: cell adhesion/cell cycle Chain: D: PDB Molecule: rho guanine nucleotide exchange factor 4; PDBTitle: crystal structure of apc complexed with asef
51	d1ue9a_	Alignment	not modelled	11.3	17	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
52	c2d8jA_	Alignment	not modelled	10.8	14	PDB header: transferase Chain: A: PDB Molecule: fyn-related kinase; PDBTitle: solution structure of the sh3 domain of fyn-related kinase
53	d1grja2	Alignment	not modelled	10.7	12	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
54	c2e6zA_	Alignment	not modelled	10.6	17	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the second kow motif of human2 transcription elongation factor spt5

55	c1negA	Alignment	not modelled	9.5	13	PDB header: structural protein Chain: A: PDB Molecule: spectrin alpha chain, brain; PDBTitle: crystal structure analysis of n-and c-terminal labeled sh3-domain of2 alpha-chicken spectrin
56	d1nega	Alignment	not modelled	9.5	13	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
57	d2b1ya1	Alignment	not modelled	9.4	11	Fold: Atu1913-like Superfamily: Atu1913-like Family: Atu1913-like
58	c2dl8A	Alignment	not modelled	8.6	10	PDB header: signaling protein Chain: A: PDB Molecule: slit-robo rho gtpase-activating protein 2; PDBTitle: solution structure of the sh3 domain of human slit-robo rho2 gtpase-activating protein 2
59	c1grjA	Alignment	not modelled	8.5	12	PDB header: transcription regulation Chain: A: PDB Molecule: grea protein; PDBTitle: grea transcript cleavage factor from escherichia coli
60	c2dmoA	Alignment	not modelled	8.5	14	PDB header: signaling protein Chain: A: PDB Molecule: neutrophil cytosol factor 2; PDBTitle: refined solution structure of the 1st sh3 domain from human2 neutrophil cytosol factor 2 (ncf-2)
61	d1h8ka	Alignment	not modelled	8.5	14	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
62	c3plxB	Alignment	not modelled	8.1	50	PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
63	c4gopB	Alignment	not modelled	7.9	18	PDB header: dna binding protein/dna Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
64	c1x2pA	Alignment	not modelled	7.8	17	PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 2; PDBTitle: solution structure of the sh3 domain of the protein2 arginine n-methyltransferase 2
65	c2mi6A	Alignment	not modelled	7.8	25	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusg; PDBTitle: solution structure of the carboxy terminal domain of nusg from2 mycobacterium tuberculosis
66	d1nz9a	Alignment	not modelled	7.6	27	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
67	c1uheA	Alignment	not modelled	7.6	40	PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase alpha chain; PDBTitle: crystal structure of aspartate decarboxylase, isoasparagine complex
68	c2egcA	Alignment	not modelled	7.6	15	PDB header: signaling protein Chain: A: PDB Molecule: sh3 and px domain-containing protein 2a; PDBTitle: solution structure of the fifth sh3 domain from human2 kiaa0418 protein
69	c5ounA	Alignment	not modelled	7.4	25	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like protein 2; PDBTitle: nmr solution structure of the external dii domain of rvb2 from2 saccharomyces cerevisiae
70	c2jvvA	Alignment	not modelled	7.3	13	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
71	c2kvqG	Alignment	not modelled	7.3	13	PDB header: transcription Chain: G: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
72	c1vc3B	Alignment	not modelled	7.3	40	PDB header: lyase Chain: B: PDB Molecule: l-aspartate-alpha-decarboxylase heavy chain; PDBTitle: crystal structure of l-aspartate-alpha-decarboxylase
73	c2d7gD	Alignment	not modelled	7.3	58	PDB header: hydrolase Chain: D: PDB Molecule: primosomal protein n'; PDBTitle: crystal structure of the aa complex of the n-terminal domain of pria
74	c2ekhA	Alignment	not modelled	7.2	15	PDB header: signaling protein Chain: A: PDB Molecule: sh3 and px domain-containing protein 2a; PDBTitle: solution structures of the sh3 domain of human kiaa0418
75	c1pyuD	Alignment	not modelled	7.1	40	PDB header: lyase Chain: D: PDB Molecule: aspartate 1-decarboxylase alfa chain; PDBTitle: processed aspartate decarboxylase mutant with ser25 mutated to cys
76	d1oe1a2	Alignment	not modelled	7.0	21	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
77	c4xi7A	Alignment	not modelled	6.8	22	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mib1; PDBTitle: crystal structure of the mzm-rep domains of mind bomb 1 in complex2 with jagged1 n-box peptide
78	d1e6ga	Alignment	not modelled	6.7	10	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
79	c1wxbA	Alignment	not modelled	6.7	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: epidermal growth factor receptor pathway PDBTitle: solution structure of the sh3 domain from human epidermal2 growth factor receptor pathway substrate 8-like protein
80	d1arka	Alignment	not modelled	6.7	31	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
						Fold: Double psi beta-barrel

81	d1ppya_	Alignment	not modelled	6.7	36	Superfamily: ADC-like Family: Pyruvoyl dependent aspartate decarboxylase, ADC
82	c2ct4A_	Alignment	not modelled	6.6	29	PDB header: signaling protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: solution strutcure of the sh3 domain of the cdc42-2 interacting protein 4
83	d1nppa2	Alignment	not modelled	6.5	36	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
84	d1uffa_	Alignment	not modelled	6.5	25	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
85	c5utvA_	Alignment	not modelled	6.4	24	PDB header: viral protein Chain: A: PDB Molecule: papain-like proteinase; PDBTitle: sars-unique fold in the rousettus bat coronavirus hku9
86	c2moxA_	Alignment	not modelled	6.3	14	PDB header: signaling protein Chain: A: PDB Molecule: sorbin and sh3 domain-containing protein 1; PDBTitle: solution structure of tandem sh3 domain of sorbin and sh3 domain-2 containing protein 1
87	d1uuea_	Alignment	not modelled	6.2	14	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
88	c2ed0A_	Alignment	not modelled	6.2	13	PDB header: signaling protein Chain: A: PDB Molecule: abl interactor 2; PDBTitle: solution structure of the sh3 domain of abl interactor 22 (abelson interactor 2)
89	c2c45F_	Alignment	not modelled	6.1	36	PDB header: lyase Chain: F: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: native precursor of pyruvoyl dependent aspartate decarboxylase
90	c1pt1B_	Alignment	not modelled	6.1	36	PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
91	c3ougA_	Alignment	not modelled	6.1	27	PDB header: lyase Chain: A: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
92	c2pqhA_	Alignment	not modelled	6.1	13	PDB header: structural protein Chain: A: PDB Molecule: spectrin alpha chain, brain; PDBTitle: structure of sh3 chimera with a type ii ligand linked to the chain c-2 terminal
93	d1i07a_	Alignment	not modelled	6.1	10	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
94	d1uwva1	Alignment	not modelled	6.0	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain
95	d1g2ba_	Alignment	not modelled	6.0	13	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
96	d1j3ta_	Alignment	not modelled	5.9	15	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
97	c4he5A_	Alignment	not modelled	5.9	20	PDB header: unknown function Chain: A: PDB Molecule: peptidase family u32; PDBTitle: crystal structure of the selenomethionine variant of the c-terminal2 domain of geobacillus thermoleovorans putative u32 peptidase
98	c2crvA_	Alignment	not modelled	5.8	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
99	c2hj1A_	Alignment	not modelled	5.8	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae