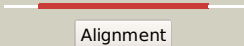
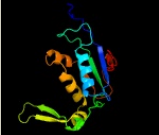
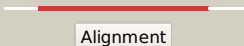

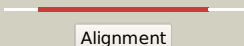




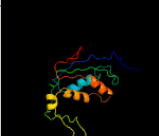


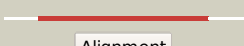




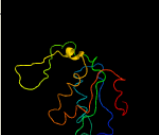















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3443c_(rpM)_3862127_3862570
Date	Fri Aug 9 18:20:11 BST 2019
Unique Job ID	7f101e89b9fa8f29

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60K_			100.0	81	PDB header: ribosome Chain: K; PDB Molecule: 50s ribosomal protein l13; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	c4wfaG_			100.0	50	PDB header: ribosome Chain: G; PDB Molecule: 50s ribosomal protein l13; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with linezolid
3	c5mlcL_			100.0	52	PDB header: ribosome Chain: L; PDB Molecule: 50s ribosomal protein l13, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
4	c3j3wj_			100.0	51	PDB header: ribosome Chain: J; PDB Molecule: 50s ribosomal protein l13; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
5	d2j01n1			100.0	51	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
6	d2zjrg1			100.0	49	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
7	c3cf5G_			100.0	49	PDB header: ribosome/antibiotic Chain: G; PDB Molecule: 50s ribosomal protein l13; PDBTitle: thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
8	c3d5bN_			100.0	52	PDB header: ribosome Chain: N; PDB Molecule: 50s ribosomal protein l13; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
9	d2gych1			100.0	51	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
10	c4v19N_			100.0	33	PDB header: ribosome Chain: N; PDB Molecule: mitoribosomal protein ul13m, mrp113; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
11	c2ftcH_			100.0	33	PDB header: ribosome Chain: H; PDB Molecule: 39s ribosomal protein l13, mitochondrial; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome

12	c3bboL_	Alignment		100.0	54	PDB header: ribosome Chain: L: PDB Molecule: ribosomal protein I13; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
13	c1vw4H_	Alignment		100.0	36	PDB header: ribosome Chain: H: PDB Molecule: 54s ribosomal protein I23, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
14	c3j39O_	Alignment		100.0	27	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein I13a; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
15	c1s1iM_	Alignment		100.0	28	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein I16-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.
16	c2zkrj_	Alignment		100.0	25	PDB header: ribosomal protein/rna Chain: J: PDB Molecule: rna expansion segment es15 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
17	c3j3bO_	Alignment		100.0	24	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein I13a; PDBTitle: structure of the human 60s ribosomal proteins
18	c3iz5K_	Alignment		100.0	25	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein I13a (I13p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
19	c3izcK_	Alignment		100.0	27	PDB header: ribosome Chain: K: PDB Molecule: 60s ribosomal protein rpl16 (I13p); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
20	c4a1aI_	Alignment		100.0	25	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein I13a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
21	c3zf7O_	Alignment	not modelled	100.0	26	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein I13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
22	c3jywM_	Alignment	not modelled	100.0	28	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein I16(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
23	d1j3aa_	Alignment	not modelled	100.0	33	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
24	d1vqoj1	Alignment	not modelled	100.0	26	Fold: Ribosomal protein L13 Superfamily: Ribosomal protein L13 Family: Ribosomal protein L13
25	d1qvca_	Alignment	not modelled	32.5	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
26	c1qvca_	Alignment	not modelled	32.5	40	PDB header: dna binding protein Chain: A: PDB Molecule: single stranded dna binding protein monomer; PDBTitle: crystal structure analysis of single stranded dna binding protein2 (ssb) from e.coli
27	c3kojA_	Alignment	not modelled	30.5	25	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein ycf41; PDBTitle: crystal structure of the ssb domain of q5n255_synp6 protein from2 synechococcus sp. northeast structural genomics consortium target3 snr59a.
28	c5gqaB	Alignment	not modelled	28.8	45	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein;

28	c3gqub	Alignment	not modelled	28.8	43	PDBTitle: structure of the second single stranded dna binding protein (ssbb)2 from mycobacterium smegmatis PDB header: dna binding protein
29	c1z9fA	Alignment	not modelled	27.0	53	Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution
30	c4damA	Alignment	not modelled	26.3	45	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein 1; PDBTitle: crystal structure of small single-stranded dna-binding protein from2 streptomyces coelicolor
31	c5odnG	Alignment	not modelled	25.2	35	PDB header: dna binding protein Chain: G: PDB Molecule: single-stranded dna-binding protein; PDBTitle: salinibacter ruber single-strand binding protein
32	c2ra9A	Alignment	not modelled	24.3	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein duf1285; PDBTitle: crystal structure of a duf1285 family protein (sba1_2486) from2 shewanella baltica os155 at 1.40 a resolution
33	c2vw9B	Alignment	not modelled	22.1	35	PDB header: dna-binding protein Chain: B: PDB Molecule: single-stranded dna binding protein; PDBTitle: single stranded dna binding protein complex from2 helicobacter pylori
34	c1eqqD	Alignment	not modelled	20.4	42	PDB header: replication/rna Chain: D: PDB Molecule: single stranded dna binding protein; PDBTitle: single stranded dna binding protein and ssdna complex
35	d2pstx1	Alignment	not modelled	20.1	31	Fold: Mbth/L9 domain-like Superfamily: Mbth-like Family: Mbth-like
36	c5hdwA	Alignment	not modelled	18.4	29	PDB header: protein binding Chain: A: PDB Molecule: f-box only protein 3; PDBTitle: apag domain of fbxo3
37	d1tzaa	Alignment	not modelled	17.2	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
38	c5ld1D	Alignment	not modelled	17.1	29	PDB header: transferase Chain: D: PDB Molecule: polyphosphate:amp phosphotransferase; PDBTitle: crystal structure of polyphosphate kinase from meiothermus ruber bound2 to atp
39	d1xq4a	Alignment	not modelled	17.0	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
40	c3fmaD	Alignment	not modelled	16.9	29	PDB header: protein binding Chain: D: PDB Molecule: protein smy2; PDBTitle: crystal structure of the gyf domain of smy2 in complex with a proline-2 rich peptide from bbp/scsf1
41	c3vdyA	Alignment	not modelled	16.8	26	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded dna-binding protein ssbb; PDBTitle: b. subtilis ssbb/ssdna
42	c2f1eA	Alignment	not modelled	16.5	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein apag; PDBTitle: solution structure of apag protein
43	d1xvsa	Alignment	not modelled	16.3	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
44	d2gpfa1	Alignment	not modelled	16.0	31	Fold: Mbth/L9 domain-like Superfamily: Mbth-like Family: Mbth-like
45	d1puja	Alignment	not modelled	14.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
46	c5wmmB	Alignment	not modelled	14.6	23	PDB header: biosynthetic protein Chain: B: PDB Molecule: mbth homologue; PDBTitle: crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
47	c5ja1B	Alignment	not modelled	14.5	38	PDB header: ligase Chain: B: PDB Molecule: enterobactin biosynthesis protein ybdz; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 mbth-like protein ybdz
48	c2wojD	Alignment	not modelled	14.4	23	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
49	d1evga	Alignment	not modelled	14.1	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
50	c2khrA	Alignment	not modelled	13.6	31	PDB header: biosynthetic protein Chain: A: PDB Molecule: protein mbth; PDBTitle: solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
51	d2q07a1	Alignment	not modelled	13.2	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
52	c5xgtA	Alignment	not modelled	12.9	25	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of the n-terminal domain of staphylococcus aureus2 single-stranded dna-binding protein ssba at 1.82 angstrom resolution
53	d2bm8a1	Alignment	not modelled	12.1	27	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Cmcl-like
54	d1ue1a	Alignment	not modelled	11.8	40	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB

55	c2ihfA	Alignment	not modelled	11.5	30	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
56	c2lpdA	Alignment	not modelled	11.3	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a mbth-like protein from burkholderia2 pseudomallei, the etiological agent responsible for melioidosis,3 seattle structural genomics center for infectious disease target4 bupsa.13472.b
57	c5u89B	Alignment	not modelled	10.8	23	PDB header: hydrolase/inhibitor Chain: B: PDB Molecule: mbth domain protein; PDBTitle: crystal structure of a cross-module fragment from the dimodular nrps2 dxbf
58	c3tqyA	Alignment	not modelled	10.8	30	PDB header: transferase Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii
59	c2p8tA	Alignment	not modelled	10.6	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph0730; PDBTitle: hypothetical protein ph0730 from pyrococcus horikoshii ot3
60	c3eivB	Alignment	not modelled	10.3	37	PDB header: dna binding protein Chain: B: PDB Molecule: single-stranded dna-binding protein 2; PDBTitle: crystal structure of single-stranded dna-binding protein2 from streptomyces coelicolor
61	c1is7F	Alignment	not modelled	10.0	23	PDB header: hydrolase/protein binding Chain: F: PDB Molecule: gtp cyclohydrolase i; PDBTitle: crystal structure of rat gtpchi/gfrp stimulatory complex
62	c3rhfB	Alignment	not modelled	10.0	38	PDB header: transferase Chain: B: PDB Molecule: putative polyphosphate kinase 2 family protein; PDBTitle: crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1
63	c3czqA	Alignment	not modelled	9.8	35	PDB header: transferase Chain: A: PDB Molecule: putative polyphosphate kinase 2; PDBTitle: crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti
64	c2q07A	Alignment	not modelled	9.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein af0587; PDBTitle: crystal structure of af0587, a protein of unknown function
65	c2e6zA	Alignment	not modelled	9.7	22	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
66	c6aqeB	Alignment	not modelled	9.1	31	PDB header: transferase Chain: B: PDB Molecule: molecule a; PDBTitle: crystal structure of ppk2 in complex with mg atp
67	d2exna1	Alignment	not modelled	9.0	21	Fold: MOSC N-terminal domain-like Superfamily: MOSC N-terminal domain-like Family: MOSC N-terminal domain-like
68	c2rndA	Alignment	not modelled	8.7	24	PDB header: endocytosis Chain: A: PDB Molecule: myc box-dependent-interacting protein 1; PDBTitle: structure of the n-terminal barpeptide in dpc micelles
69	c2iheA	Alignment	not modelled	8.7	29	PDB header: dna binding protein Chain: A: PDB Molecule: single-stranded dna-binding protein; PDBTitle: crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
70	c3czpA	Alignment	not modelled	8.4	38	PDB header: transferase Chain: A: PDB Molecule: putative polyphosphate kinase 2; PDBTitle: crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
71	c4xz7A	Alignment	not modelled	8.3	33	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a tgase
72	c4yegA	Alignment	not modelled	8.3	25	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase 2; PDBTitle: characterisation of polyphosphate kinase 2 from the intracellular2 pathogen francisella tularensis
73	d1a8ra	Alignment	not modelled	8.2	17	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
74	d1wpla	Alignment	not modelled	7.8	23	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: GTP cyclohydrolase I
75	d1v5pa	Alignment	not modelled	7.6	21	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
76	d2d7na1	Alignment	not modelled	7.4	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
77	c2mlgA	Alignment	not modelled	7.4	21	PDB header: dna binding protein Chain: A: PDB Molecule: sulfolobus transcription factor 76 aminoacid protein, PDBTitle: stf76 from the sulfolobus islandicus plasmid-virus pssvx
78	d1v1qa	Alignment	not modelled	7.1	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
79	c5n0IC	Alignment	not modelled	7.0	32	PDB header: transcription Chain: C: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: the structure of the cofactor binding gaf domain of the nutrient2 sensor cody from clostridium difficile
80	d2uubp1	Aliagment	not modelled	6.6	33	Fold: Ribosomal protein S16 Superfamily: Ribosomal protein S16

						Family: Ribosomal protein S16
81	c1ue7A_	Alignment	not modelled	6.5	26	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis
82	d1a9xa3	Alignment	not modelled	6.5	24	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
83	c5v6xB_	Alignment	not modelled	6.3	31	PDB header: ligase/rna Chain: B: PDB Molecule: pyrrolysine--trna ligase; PDBTitle: crystal structure of the trna binding domain of pyrrolysyl-trna2 synthetase mutant (32a ntd) bound to trna(pyl)
84	c2cwaA_	Alignment	not modelled	6.3	45	PDB header: dna binding protein Chain: A: PDB Molecule: single-strand binding protein; PDBTitle: crystal structure of the single-stranded dna binding protein from2 thermus thermophilus hb8
85	d2do3a1	Alignment	not modelled	6.0	30	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
86	c4nwyA_	Alignment	not modelled	6.0	12	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase-like protein of the testis; PDBTitle: crystal structure of the b' domain of human protein disulfide2 isomerase-like protein of the testis (pdilt)
87	d2ntka1	Alignment	not modelled	5.8	21	Fold: Ntn hydrolase-like Superfamily: Archaeal IMP cyclohydrolase PurO Family: Archaeal IMP cyclohydrolase PurO
88	c6au0A_	Alignment	not modelled	5.7	44	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: polyphosphate:amp phosphotransferase; PDBTitle: crystal structure of ppk2 (class iii) in complex with bisphosphonate2 inhibitor (2-((3,5-dichlorophenyl)amino)ethane-1,1-diyl)diphosphonic3 acid
89	c2l8kA_	Alignment	not modelled	5.5	46	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 7; PDBTitle: nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
90	c2r37A_	Alignment	not modelled	5.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 3; PDBTitle: crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
91	c6r7tB_	Alignment	not modelled	5.1	33	PDB header: immune system Chain: B: PDB Molecule: melanoma-associated antigen b1; PDBTitle: crystal structure of human melanoma-associated antigen b1 (mageb1) in2 complex with nanobody
92	c6cqoH_	Alignment	not modelled	5.1	24	PDB header: dna binding protein Chain: H: PDB Molecule: single-stranded dna-binding protein rim1, mitochondrial; PDBTitle: crystal structure of mitochondrial single-stranded dna binding2 proteins from s. cerevisiae (semet labeled), rim1 (form2)
93	d1txya_	Alignment	not modelled	5.0	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB