

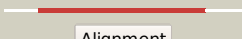

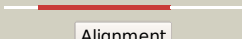



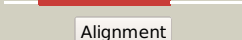



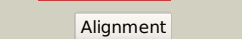

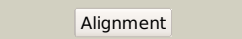

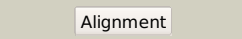

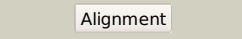

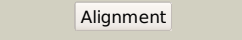
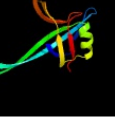











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2478c_(-)_2784133_2784618
Date	Wed Aug 7 12:50:10 BST 2019
Unique Job ID	b968ce558b510be5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1qvca_</a>	 Alignment		100.0	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
2	<a href="#">c1qvca_</a>	 Alignment		100.0	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single stranded dna binding protein monomer; <b>PDBTitle:</b> crystal structure analysis of single stranded dna binding protein2 (ssb) from e.coli
3	<a href="#">c4damA_</a>	 Alignment		99.9	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein 1; <b>PDBTitle:</b> crystal structure of small single-stranded dna-binding protein from2 streptomyces coelicolor
4	<a href="#">d1ue1a_</a>	 Alignment		99.9	31	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
5	<a href="#">c2iheA_</a>	 Alignment		99.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
6	<a href="#">c2vw9B_</a>	 Alignment		99.9	20	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> single-stranded dna binding protein; <b>PDBTitle:</b> single stranded dna binding protein complex from2 helicobacter pylori
7	<a href="#">c2ihfA_</a>	 Alignment		99.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
8	<a href="#">c3tqvA_</a>	 Alignment		99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii
9	<a href="#">c3ulpC_</a>	 Alignment		99.9	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> single-strand binding protein; <b>PDBTitle:</b> plasmodium falciparum ssb complex with ssdna
10	<a href="#">d1eyga_</a>	 Alignment		99.9	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
11	<a href="#">c3pgzB_</a>	 Alignment		99.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> crystal structure of a single strand binding protein (ssb) from2 bartonella henselae

12	<a href="#">c3eivB</a>	Alignment		99.9	40	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> single-stranded dna-binding protein 2; <b>PDBTitle:</b> crystal structure of single-stranded dna-binding protein2 from streptomyces coelicolor
13	<a href="#">c5xgtA</a>	Alignment		99.9	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of staphylococcus aureus2 single-stranded dna-binding protein ssba at 1.82 angstrom resolution
14	<a href="#">c5gqoB</a>	Alignment		99.9	68	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> structure of the second single stranded dna binding protein (ssbb)2 from mycobacterium smegmatis
15	<a href="#">c1eqqD</a>	Alignment		99.9	22	<b>PDB header:</b> replication/rna <b>Chain:</b> D: <b>PDB Molecule:</b> single stranded dna binding protein; <b>PDBTitle:</b> single stranded dna binding protein and ssdna complex
16	<a href="#">c1ue7A</a>	Alignment		99.9	32	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-strand binding protein; <b>PDBTitle:</b> crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis
17	<a href="#">c3vdyA</a>	Alignment		99.9	23	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein ssbb; <b>PDBTitle:</b> b. subtilis ssbb/ssdna
18	<a href="#">d1se8a</a>	Alignment		99.9	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
19	<a href="#">c1se8A</a>	Alignment		99.9	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-strand binding protein; <b>PDBTitle:</b> structure of single-stranded dna-binding protein (ssb) from d.2 radiodurans
20	<a href="#">c2cwaA</a>	Alignment		99.9	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-strand binding protein; <b>PDBTitle:</b> crystal structure of the single-stranded dna binding protein from2 thermus thermophilus hb8
21	<a href="#">c5odnG</a>	Alignment	not modelled	99.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> salinibacter ruber single-strand binding protein
22	<a href="#">d3ulla</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
23	<a href="#">d1v1qa</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
24	<a href="#">c1z9fA</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-strand binding protein; <b>PDBTitle:</b> crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution
25	<a href="#">c3lgjA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
26	<a href="#">c3kojA</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ycf41; <b>PDBTitle:</b> crystal structure of the ssb domain of q5n255_synp6 protein from2 synechococcus sp. northeast structural genomics consortium target3 snr59a.
27	<a href="#">c6cqoH</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> single-stranded dna-binding protein rim1, mitochondrial; <b>PDBTitle:</b> crystal structure of mitochondrial single-stranded dna binding2 proteins from s. cerevisiae (semet labeled), rim1 (form2)
28	<a href="#">c3k8aA</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative primosomal replication protein; <b>PDBTitle:</b> neisseria gonorrhoeae prib

29	<a href="#">d1txya</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
30	<a href="#">c3fhwB</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> primosomal replication protein n; <b>PDBTitle:</b> crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
31	<a href="#">c3en2A</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable primosomal replication protein n; <b>PDBTitle:</b> three-dimensional structure of the protein prib from ralstonia2 solanacearum at the resolution 2.3a. northeast structural genomics3 consortium target rsr213c.
32	<a href="#">c4dniA</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> protein binding, rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fusion protein of rna-editing complex proteins mp42 and <b>PDBTitle:</b> structure of editosome protein
33	<a href="#">c3stbC</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> rna binding protein/immune system <b>Chain:</b> C: <b>PDB Molecule:</b> rna-editing complex protein mp42; <b>PDBTitle:</b> a complex of two editosome proteins and two nanobodies
34	<a href="#">c3k81D</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> immune system, rna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> mp18 rna editing complex protein; <b>PDBTitle:</b> structure of the central interaction protein from the trypanosoma2 brucei editosome in complex with single domain antibodies
35	<a href="#">c3e0eA</a>	Alignment	not modelled	93.8	18	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a; <b>PDBTitle:</b> crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 target mrr110b
36	<a href="#">c2hqlB</a>	Alignment	not modelled	89.3	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein mg376 homolog; <b>PDBTitle:</b> crystal structure of a small single-stranded dna binding2 protein from mycoplasma pneumoniae
37	<a href="#">c2vl6C</a>	Alignment	not modelled	79.8	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> minichromosome maintenance protein mcm; <b>PDBTitle:</b> structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
38	<a href="#">c5fkvA</a>	Alignment	not modelled	78.9	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit alpha; <b>PDBTitle:</b> cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
39	<a href="#">c4pogC</a>	Alignment	not modelled	76.3	22	<b>PDB header:</b> replication, dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> cell division control protein 21; <b>PDBTitle:</b> mcm-ssdna co-crystal structure
40	<a href="#">d1gm5a2</a>	Alignment	not modelled	76.2	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> RecG "wedge" domain
41	<a href="#">c4hspA</a>	Alignment	not modelled	71.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf3299 family protein (pa4066) from2 pseudomonas aeruginosa pao1 at 2.45 a resolution
42	<a href="#">c1ynxA</a>	Alignment	not modelled	71.5	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> replication factor-a protein 1; <b>PDBTitle:</b> solution structure of dna binding domain a (dbd-a) of2 s.cerevisiae replication protein a (rpa)
43	<a href="#">c4dk6D</a>	Alignment	not modelled	69.5	22	<b>PDB header:</b> rna binding protein/immune system <b>Chain:</b> D: <b>PDB Molecule:</b> rna-editing complex protein mp81; <b>PDBTitle:</b> structure of editosome protein
44	<a href="#">c2k50A</a>	Alignment	not modelled	67.6	6	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> replication factor a related protein; <b>PDBTitle:</b> solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
45	<a href="#">c4gs3A</a>	Alignment	not modelled	66.3	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna-binding protein; <b>PDBTitle:</b> dimeric structure of the n-terminal domain of prib protein from2 thermoanaerobacter tencongensis solved ab initio
46	<a href="#">c4ywkA</a>	Alignment	not modelled	63.4	15	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 21; <b>PDBTitle:</b> pyrococcus furiosus mcm n-terminal domain with zinc-binding subdomain2 b deleted
47	<a href="#">c4owxB</a>	Alignment	not modelled	61.5	19	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> soSS complex subunit b1; <b>PDBTitle:</b> structural basis of soSS1 in complex with a 12nt ssdna
48	<a href="#">c1fguA</a>	Alignment	not modelled	59.8	6	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replication protein a 70 kda dna-binding subunit; <b>PDBTitle:</b> ssdna-binding domain of the large subunit of replication2 protein a
49	<a href="#">d1o7ia</a>	Alignment	not modelled	59.6	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
50	<a href="#">c4me3A</a>	Alignment	not modelled	53.8	25	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna replication licensing factor mcm related protein; <b>PDBTitle:</b> 1.8 angstrom crystal structure of the n-terminal domain of an archaeal2 mcm
51	<a href="#">d1jmca1</a>	Alignment	not modelled	52.1	9	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
52	<a href="#">d1vqoj1</a>	Alignment	not modelled	50.7	35	<b>Fold:</b> Ribosomal protein L13 <b>Superfamily:</b> Ribosomal protein L13 <b>Family:</b> Ribosomal protein L13

53	<a href="#">c4gn5A_</a>	Alignment	not modelled	50.3	21	<b>PDB header:</b> de novo protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> obody am3l15; <b>PDBTitle:</b> obody am3l15 bound to hen egg-white lysozyme
54	<a href="#">c1vw4H_</a>	Alignment	not modelled	50.3	33	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 54s ribosomal protein l23, mitochondrial; <b>PDBTitle:</b> structure of the yeast mitochondrial large ribosomal subunit
55	<a href="#">d1c0aa1</a>	Alignment	not modelled	50.2	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Anticodon-binding domain
56	<a href="#">c5groA_</a>	Alignment	not modelled	48.1	8	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate--trna(asp/asn) ligase; <b>PDBTitle:</b> crystal structure of the n-terminal anticodon-binding domain of non-2 discriminating aspartyl-trna synthetase from helicobacter pylori
57	<a href="#">d1jmca2</a>	Alignment	not modelled	47.2	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
58	<a href="#">c3dm3A_</a>	Alignment	not modelled	46.7	28	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replication factor a; <b>PDBTitle:</b> crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjrl118e
59	<a href="#">c4wfaG_</a>	Alignment	not modelled	45.9	50	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 50s ribosomal protein l13; <b>PDBTitle:</b> the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with linezolid
60	<a href="#">c5o60K_</a>	Alignment	not modelled	45.7	45	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 50s ribosomal protein l13; <b>PDBTitle:</b> structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
61	<a href="#">d1l0wa1</a>	Alignment	not modelled	45.4	8	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Anticodon-binding domain
62	<a href="#">c1lttE_</a>	Alignment	not modelled	44.9	25	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> dna replication initiator (cdc21/cdc54); <b>PDBTitle:</b> the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
63	<a href="#">c4gopC_</a>	Alignment	not modelled	44.6	7	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
64	<a href="#">c3j3bO_</a>	Alignment	not modelled	44.5	40	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l13a; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
65	<a href="#">c4a1a1_</a>	Alignment	not modelled	44.3	40	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 60s ribosomal protein l13a; <b>PDBTitle:</b> 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.
66	<a href="#">d1j3aa_</a>	Alignment	not modelled	43.9	40	<b>Fold:</b> Ribosomal protein L13 <b>Superfamily:</b> Ribosomal protein L13 <b>Family:</b> Ribosomal protein L13
67	<a href="#">c3cf5G_</a>	Alignment	not modelled	43.6	40	<b>PDB header:</b> ribosome/antibiotic <b>Chain:</b> G: <b>PDB Molecule:</b> 50s ribosomal protein l13; <b>PDBTitle:</b> thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
68	<a href="#">d2zjrg1</a>	Alignment	not modelled	43.6	40	<b>Fold:</b> Ribosomal protein L13 <b>Superfamily:</b> Ribosomal protein L13 <b>Family:</b> Ribosomal protein L13
69	<a href="#">d1ltia_</a>	Alignment	not modelled	43.2	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA replication initiator (cdc21/cdc54) N-terminal domain
70	<a href="#">c3j3wj_</a>	Alignment	not modelled	43.0	53	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 50s ribosomal protein l13; <b>PDBTitle:</b> atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
71	<a href="#">c3d5bN_</a>	Alignment	not modelled	42.6	47	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 50s ribosomal protein l13; <b>PDBTitle:</b> 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.
72	<a href="#">c2zkrj_</a>	Alignment	not modelled	42.4	40	<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> J: <b>PDB Molecule:</b> rna expansion segment es15 part ii; <b>PDBTitle:</b> 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
73	<a href="#">c3izcK_</a>	Alignment	not modelled	42.4	40	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 60s ribosomal protein rpl16 (l13p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
74	<a href="#">c6hv93_</a>	Alignment	not modelled	39.8	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> 3: <b>PDB Molecule:</b> dna replication licensing factor mcm3; <b>PDBTitle:</b> s. cerevisiae cmg-pol epsilon-dna
75	<a href="#">d2j01n1</a>	Alignment	not modelled	39.7	47	<b>Fold:</b> Ribosomal protein L13 <b>Superfamily:</b> Ribosomal protein L13 <b>Family:</b> Ribosomal protein L13
76	<a href="#">c5bmqa_</a>	Alignment	not modelled	38.5	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> erfk/ybis/ycfs/ynhg family protein; <b>PDBTitle:</b> crystal structure of l,d-transpeptidase (yku) from stackebrandtia2 nassauensis
77	<a href="#">c3jywM_</a>	Alignment	not modelled	38.2	40	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l16(a); <b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome

						based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
78	<a href="#">c3j39O_</a>	Alignment	not modelled	37.7	45	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l13a; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
79	<a href="#">c3f2cA_</a>	Alignment	not modelled	37.6	18	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> geobacillus kaustophilus dna polc; <b>PDBTitle:</b> dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
80	<a href="#">c5m1cL_</a>	Alignment	not modelled	37.0	45	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 50s ribosomal protein l13, chloroplastic; <b>PDBTitle:</b> cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
81	<a href="#">c4hikA_</a>	Alignment	not modelled	34.0	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protection of telomeres protein 1; <b>PDBTitle:</b> crystal structure of schizosaccharomyces pombe pot1pc bound to ssdna2 (ggttacggt)
82	<a href="#">c3iz5K_</a>	Alignment	not modelled	33.7	45	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> 60s ribosomal protein l13a (l13p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
83	<a href="#">c5mvrA_</a>	Alignment	not modelled	33.1	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna threonylcarbamoyladenosine biosynthesis protein tsae; <b>PDBTitle:</b> crystal structure of bacillus subtilus ydib
84	<a href="#">c3zf7O_</a>	Alignment	not modelled	31.6	35	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l13a, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
85	<a href="#">c3jc72_</a>	Alignment	not modelled	31.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> 2: <b>PDB Molecule:</b> dna replication licensing factor mcm2; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
86	<a href="#">c2ftcH_</a>	Alignment	not modelled	30.8	32	<b>PDB header:</b> ribosome <b>Chain:</b> H: <b>PDB Molecule:</b> 39s ribosomal protein l13, mitochondrial; <b>PDBTitle:</b> structural model for the large subunit of the mammalian mitochondrial2 ribosome
87	<a href="#">d1bbua1</a>	Alignment	not modelled	30.0	14	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Anticodon-binding domain
88	<a href="#">c4v19N_</a>	Alignment	not modelled	29.2	30	<b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> mitoribosomal protein ul13m, mrpl13; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
89	<a href="#">d1b8aa1</a>	Alignment	not modelled	27.8	13	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Anticodon-binding domain
90	<a href="#">c3bboL_</a>	Alignment	not modelled	26.1	42	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> ribosomal protein l13; <b>PDBTitle:</b> homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
91	<a href="#">d1fnda1</a>	Alignment	not modelled	24.8	21	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
92	<a href="#">c2k75A_</a>	Alignment	not modelled	24.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ta0387; <b>PDBTitle:</b> solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
93	<a href="#">c3f9vA_</a>	Alignment	not modelled	22.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> minichromosome maintenance protein mcm; <b>PDBTitle:</b> crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
94	<a href="#">c4xvoB_</a>	Alignment	not modelled	22.1	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> l,d-transpeptidase; <b>PDBTitle:</b> l,d-transpeptidase from mycobacterium smegmatis
95	<a href="#">c2xgtB_</a>	Alignment	not modelled	21.4	17	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> asparaginyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
96	<a href="#">c6fpeE_</a>	Alignment	not modelled	21.4	32	<b>PDB header:</b> rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> atpase yjee, predicted to have essential role in cell wall <b>PDBTitle:</b> bacterial protein complex
97	<a href="#">c3jc57_</a>	Alignment	not modelled	21.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> 7: <b>PDB Molecule:</b> dna replication licensing factor mcm7; <b>PDBTitle:</b> structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
98	<a href="#">c1gm5A_</a>	Alignment	not modelled	21.0	16	<b>PDB header:</b> helicase <b>Chain:</b> A: <b>PDB Molecule:</b> recg; <b>PDBTitle:</b> structure of recg bound to three-way dna junction
99	<a href="#">c4glaD_</a>	Alignment	not modelled	20.8	23	<b>PDB header:</b> hydrolase/de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> obody n18; <b>PDBTitle:</b> obody n18 bound to hen egg-white lysozyme