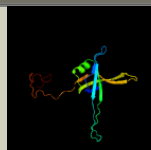
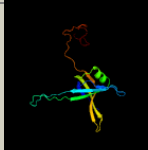
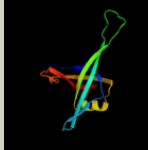
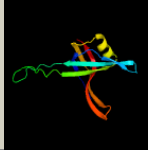
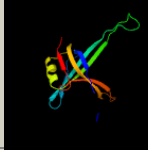
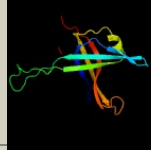
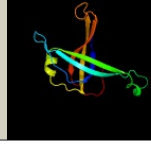
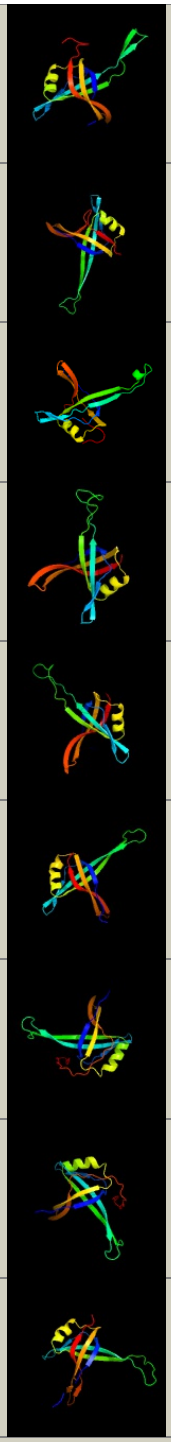
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0054_(ssb)_58583_59077
Date	Tue Jul 23 14:50:08 BST 2019
Unique Job ID	fb2fbec35595cd3f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qvcA_	Alignment		100.0	30	**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
2	d1qvca_	Alignment		100.0	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
3	d1ue1a_	Alignment		99.9	98	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
4	c3tqyA_	Alignment		99.9	34	**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
5	c3eivB_	Alignment		99.9	75	**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
6	d1eyga_	Alignment		99.9	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
7	c2vw9B_	Alignment		99.9	26	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**single-stranded dna binding protein; **PDBTitle:** single stranded dna binding protein complex from2 helicobacter pylori
8	c3ulpC_	Alignment		99.9	22	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**single-strand binding protein; **PDBTitle:** plasmodium falciparum ssb complex with ssdna
9	c2ihfA_	Alignment		99.9	29	**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
10	c5xgtA_	Alignment		99.9	40	**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
11	c2iheA_	Alignment		99.9	27	**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

12	c4damA_	Alignment		99.9	36	**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
13	c3pgzB_	Alignment		99.9	28	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of a single strand binding protein (ssb) from2 bartonella henselae
14	c1eqqD_	Alignment		99.9	33	**PDB header:**replication/rna **Chain:** D: **PDB Molecule:**single stranded dna binding protein; **PDBTitle:** single stranded dna binding protein and ssdna complex
15	c3vdyA_	Alignment		99.9	39	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein ssbb; **PDBTitle:** b. subtilis ssbb/ssdna
16	c5odnG_	Alignment		99.9	34	**PDB header:**dna binding protein **Chain:** G: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** salinibacter ruber single-strand binding protein
17	c2cwaA_	Alignment		99.9	37	**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
18	d1se8a_	Alignment		99.9	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
19	c1se8A_	Alignment		99.9	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** structure of single-stranded dna-binding protein (ssb) from d.2 radiodurans
20	d3ulla_	Alignment		99.9	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
21	c1ue7A_	Alignment	not modelled	99.9	99	**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
22	c1z9fA_	Alignment	not modelled	99.9	33	**PDB header:**dna binding protein **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
23	c5gqoB_	Alignment	not modelled	99.9	32	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** structure of the second single stranded dna binding protein (ssbb)2 from mycobacterium smegmatis
24	d1v1qa_	Alignment	not modelled	99.9	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
25	c3lgjA_	Alignment	not modelled	99.8	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
26	c3kojA_	Alignment	not modelled	99.8	21	**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.
27	c3k8aA_	Alignment	not modelled	99.8	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative primosomal replication protein; **PDBTitle:** neisseria gonorrhoeae prib
28	c6cqoH_	Alignment	not modelled	99.8	20	**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)
29	d1txya_	Alignment	not modelled	99.8	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
30	c3fhwB_	Alignment	not modelled	99.7	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**primosomal replication protein n; **PDBTitle:** crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
31	c3en2A_	Alignment	not modelled	99.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable primosomal replication protein n; **PDBTitle:** three-dimensional structure of the protein prib from ralstonia2 solanacearum at the resolution 2.3a. northeast structural genomics3 consortium target rsr213c.
32	c4dniA_	Alignment	not modelled	97.9	20	**PDB header:**protein binding, rna binding protein **Chain:** A: **PDB Molecule:**fusion protein of rna-editing complex proteins mp42 and **PDBTitle:** structure of editosome protein
33	c3stbC_	Alignment	not modelled	97.9	20	**PDB header:**rna binding protein/immune system **Chain:** C: **PDB Molecule:**rna-editing complex protein mp42; **PDBTitle:** a complex of two editosome proteins and two nanobodies
34	c3k81D_	Alignment	not modelled	97.6	23	**PDB header:**immune system, rna binding protein **Chain:** D: **PDB Molecule:**mp18 rna editing complex protein; **PDBTitle:** structure of the central interaction protein from the trypanosoma2 brucei editosome in complex with single domain antibodies
35	c3e0eA_	Alignment	not modelled	96.9	20	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein a; **PDBTitle:** crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
36	c4gs3A_	Alignment	not modelled	96.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** dimeric structure of the n-terminal domain of prib protein from2 thermoanaerobacter tencongensis solved ab initio
37	c4owxB_	Alignment	not modelled	96.3	14	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**soss complex subunit b1; **PDBTitle:** structural basis of soss1 in complex with a 12nt ssdna
38	c2k50A_	Alignment	not modelled	95.6	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
39	c3dm3A_	Alignment	not modelled	95.3	18	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor a; **PDBTitle:** crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
40	c3f2cA_	Alignment	not modelled	95.0	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
41	c1fguA_	Alignment	not modelled	93.7	12	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein a 70 kda dna-binding subunit; **PDBTitle:** ssdna-binding domain of the large subunit of replication2 protein a
42	d1o7ia_	Alignment	not modelled	92.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
43	c5fkvA_	Alignment	not modelled	92.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
44	c1ynxA_	Alignment	not modelled	92.3	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication factor-a protein 1; **PDBTitle:** solution structure of dna binding domain a (dbd-a) of2 s.cerevisiae replication protein a (rpa)
45	c4gopC_	Alignment	not modelled	91.0	12	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure and conformational change of a replication protein a2 heterotrimer bound to ssdna
46	d1jmca1	Alignment	not modelled	90.6	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
47	c2k75A_	Alignment	not modelled	88.6	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ta0387; **PDBTitle:** solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
48	d1gm5a2	Alignment	not modelled	88.0	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
49	d1jmca2	Alignment	not modelled	85.2	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
50	c5groA_	Alignment	not modelled	78.4	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartate--trna(asp/asn) ligase; **PDBTitle:** crystal structure of the n-terminal anticodon-binding domain of non-2 discriminating aspartyl-trna synthetase from helicobacter pylori
51	c2vl6C_	Alignment	not modelled	78.1	25	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
						PDB header:replication, dna binding protein/dna

52	c4pogC_	Alignment	not modelled	76.4	28	**Chain:** C: **PDB Molecule:**cell division control protein 21; **PDBTitle:** mcm-ssdna co-crystal structure
53	d1c0aa1	Alignment	not modelled	73.7	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
54	d1wjja_	Alignment	not modelled	72.0	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
55	d1l0wa1	Alignment	not modelled	71.9	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
56	c2xgtB_	Alignment	not modelled	71.3	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic; **PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
57	c4ywkA_	Alignment	not modelled	70.9	33	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division control protein 21; **PDBTitle:** pyrococcus furiosus mcm n-terminal domain with zinc-binding subdomain2 b deleted
58	d1b8aa1	Alignment	not modelled	68.5	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
59	c3kf6A_	Alignment	not modelled	67.6	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
60	c4gopB_	Alignment	not modelled	66.8	25	**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
61	d1eova1	Alignment	not modelled	64.3	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
62	c4gn5A_	Alignment	not modelled	63.8	21	**PDB header:**de novo protein/hydrolase **Chain:** A: **PDB Molecule:**obody am3l15; **PDBTitle:** obody am3l15 bound to hen egg-white lysozyme
63	d1bbua1	Alignment	not modelled	63.4	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
64	c6i52B_	Alignment	not modelled	62.1	26	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**replication factor a protein 2; **PDBTitle:** yeast rpa bound to ssdna
65	c2hqlB_	Alignment	not modelled	60.9	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hypothetical protein mg376 homolog; **PDBTitle:** crystal structure of a small single-stranded dna binding2 protein from mycoplasma pneumoniae
66	c4hspA_	Alignment	not modelled	60.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a duf3299 family protein (pa4066) from2 pseudomonas aeruginosa pao1 at 2.45 a resolution
67	c1eqrC_	Alignment	not modelled	59.5	18	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
68	c1ltlE_	Alignment	not modelled	57.8	20	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
69	d1e1oa1	Alignment	not modelled	56.3	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
70	c4wj4A_	Alignment	not modelled	55.4	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**aspartate--trna(asp/asn) ligase; **PDBTitle:** crystal structure of non-discriminating aspartyl-trna synthetase from2 pseudomonas aeruginosa complexed with trna(asn) and aspartic acid
71	c4dk6D_	Alignment	not modelled	54.2	19	**PDB header:**rna binding protein/immune system **Chain:** D: **PDB Molecule:**rna-editing complex protein mp81; **PDBTitle:** structure of editosome protein
72	c4glaD_	Alignment	not modelled	53.3	18	**PDB header:**hydrolase/de novo protein **Chain:** D: **PDB Molecule:**obody nl8; **PDBTitle:** obody nl8 bound to hen egg-white lysozyme
73	c6bwyA_	Alignment	not modelled	53.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protection of telomeres protein 1, dna dc->du-editing **PDBTitle:** dna substrate selection by apobec3g
74	c4hikA_	Alignment	not modelled	52.2	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protection of telomeres protein 1; **PDBTitle:** crystal structure of schizosaccharomyces pombe pot1pc bound to ssdna2 (ggttacggt)
75	d1vqoj1	Alignment	not modelled	51.2	35	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
76	c4joiA_	Alignment	not modelled	49.6	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cst complex subunit stn1; **PDBTitle:** crystal structure of the human telomeric stn1-ten1 complex
77	c1vw4H_	Alignment	not modelled	48.0	30	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**54s ribosomal protein l23, mitochondrial; **PDBTitle:** structure of the yeast mitochondrial large ribosomal subunit
78	c1xjvA_	Alignment	not modelled	47.9	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protection of telomeres 1; **PDBTitle:** crystal structure of human pot1 bound to telomeric single-2 stranded dna (ttagggttag)

79	c3j3wJ_	Alignment	not modelled	47.4	42	**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)
80	d1ltla_	Alignment	not modelled	47.3	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
81	c4wfaG_	Alignment	not modelled	47.1	45	**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
82	c5bmqA_	Alignment	not modelled	46.7	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**erfk/ybis/ycfs/ynhg family protein; **PDBTitle:** crystal structure of l,d-transpeptidase (yku) from stackebrandtia2 nassauensis
83	c5o60K_	Alignment	not modelled	46.5	45	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
84	c5mvrA_	Alignment	not modelled	45.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna threonylcarbamoyladenosine biosynthesis protein tsae; **PDBTitle:** crystal structure of bacillus subtilus ydib
85	c6hv93_	Alignment	not modelled	45.6	13	**PDB header:**dna binding protein **Chain:** 3: **PDB Molecule:**dna replication licensing factor mcm3; **PDBTitle:** s. cerevisiae cmg-pol epsilon-dna
86	c3cf5G_	Alignment	not modelled	45.0	30	**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
87	d2zjrg1	Alignment	not modelled	45.0	30	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
88	c4a1aI_	Alignment	not modelled	45.0	35	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l13a; **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.
89	d1j3aa_	Alignment	not modelled	44.7	30	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
90	c3j3bO_	Alignment	not modelled	44.7	30	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**60s ribosomal protein l13a; **PDBTitle:** structure of the human 60s ribosomal proteins
91	c2kenA_	Alignment	not modelled	44.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazei. northeast structural3 genomics consortium target mar214a.
92	c3izcK_	Alignment	not modelled	43.5	30	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein rpl16 (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
93	c1gm5A_	Alignment	not modelled	43.5	12	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
94	c3d5bN_	Alignment	not modelled	43.4	37	**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.
95	c2zkrj_	Alignment	not modelled	42.6	30	**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
96	d2j01n1	Alignment	not modelled	42.2	37	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
97	c4me3A_	Alignment	not modelled	41.8	20	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication licensing factor mcm related protein; **PDBTitle:** 1.8 angstrom crystal structure of the n-terminal domain of an archaeal2 mcm
98	c3jywM_	Alignment	not modelled	39.0	30	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l16(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
99	c1b8aB_	Alignment	not modelled	38.9	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
100	d1xjva2	Alignment	not modelled	38.8	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
101	c5mlcL_	Alignment	not modelled	38.5	40	**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
102	c3j39O_	Alignment	not modelled	38.5	35	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**60s ribosomal protein l13a; **PDBTitle:** structure of the d. melanogaster 60s ribosomal proteins
						Fold:OB-fold

103	d1krta_	Alignment	not modelled	38.0	25	**Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
104	c1wydB_	Alignment	not modelled	37.8	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
105	c6fpeE_	Alignment	not modelled	37.8	41	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**atpase yjee, predicted to have essential role in cell wall **PDBTitle:** bacterial protein complex
106	c3jc72_	Alignment	not modelled	36.5	15	**PDB header:**hydrolase **Chain:** 2: **PDB Molecule:**dna replication licensing factor mcm2; **PDBTitle:** structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
107	c4o2dB_	Alignment	not modelled	36.5	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**aspartate--trna ligase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid
108	c3iz5K_	Alignment	not modelled	35.1	40	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l13a (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
109	d1xjva1	Alignment	not modelled	34.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
110	c2ftcH_	Alignment	not modelled	34.6	21	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**39s ribosomal protein l13, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
111	c2pi2A_	Alignment	not modelled	33.0	21	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
112	c3zf7O_	Alignment	not modelled	32.6	35	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**60s ribosomal protein l13a, putative; **PDBTitle:** high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
113	c4kkpA_	Alignment	not modelled	32.4	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rbma protein; **PDBTitle:** crystal structure of vibrio cholerae rbma (crystal form 2)
114	c5hgqD_	Alignment	not modelled	31.9	22	**PDB header:**ligase/ligase inhibitor **Chain:** D: **PDB Molecule:**lysine--trna ligase; **PDBTitle:** loa loa lysyl-trna synthetase in complex with cladosporin.
115	c4j15A_	Alignment	not modelled	31.4	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartate--trna ligase, cytoplasmic; **PDBTitle:** crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex
116	c3bboL_	Alignment	not modelled	30.6	42	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**ribosomal protein l13; **PDBTitle:** homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
117	c4v19N_	Alignment	not modelled	29.8	20	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**mitoribosomal protein ul13m, mrpl13; **PDBTitle:** structure of the large subunit of the mammalian mitoribosome, part 12 of 2
118	c3i7fA_	Alignment	not modelled	28.7	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
119	d1fnda1	Alignment	not modelled	28.4	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
120	c1efwA_	Alignment	not modelled	28.3	17	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli