





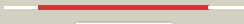


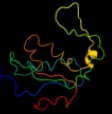




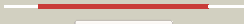















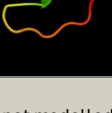


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2j01n1</a>	 Alignment		100.0	56	<b>Fold:</b> Ribosomal protein L13 <b>Superfamily:</b> Ribosomal protein L13 <b>Family:</b> Ribosomal protein L13
2	<a href="#">d2zjrg1</a>	 Alignment		100.0	55	<b>Fold:</b> Ribosomal protein L13 <b>Superfamily:</b> Ribosomal protein L13 <b>Family:</b> Ribosomal protein L13
3	<a href="#">c3d5bN_</a>	 Alignment		100.0	55	<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.
4	<a href="#">c3cf5G_</a>	 Alignment		100.0	55	<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
5	<a href="#">d2gych1</a>	 Alignment		100.0	100	<b>Fold:</b> Ribosomal protein L13 <b>Superfamily:</b> Ribosomal protein L13 <b>Family:</b> Ribosomal protein L13
6	<a href="#">c2ftcH_</a>	 Alignment		100.0	33	<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
7	<a href="#">c3bboL_</a>	 Alignment		100.0	59	<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 subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
8	<a href="#">c1sliM_</a>	 Alignment		100.0	27	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l16-a; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
9	<a href="#">c3iz5K_</a>	 Alignment		100.0	23	<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
10	<a href="#">c2zkrj_</a>	 Alignment		100.0	27	<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 an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
11	<a href="#">c3izcK_</a>	 Alignment		100.0	27	<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

12	<a href="#">c4a1a1_</a>	Alignment		100.0	29	<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.
13	<a href="#">c3jywM_</a>	Alignment		100.0	28	<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
14	<a href="#">dlj3aa_</a>	Alignment		100.0	33	<b>Fold:</b> Ribosomal protein L13 <b>Superfamily:</b> Ribosomal protein L13 <b>Family:</b> Ribosomal protein L13
15	<a href="#">dlvqoj1</a>	Alignment		100.0	26	<b>Fold:</b> Ribosomal protein L13 <b>Superfamily:</b> Ribosomal protein L13 <b>Family:</b> Ribosomal protein L13
16	<a href="#">dlqvca_</a>	Alignment		34.0	30	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
17	<a href="#">c3kojA_</a>	Alignment		31.5	35	<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 protein2 from synechococcus sp. northeast structural genomics3 consortium target snr59a.
18	<a href="#">clz9fA_</a>	Alignment		26.8	42	<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
19	<a href="#">c3fmaD_</a>	Alignment		24.2	29	<b>PDB header:</b> protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> protein smy2; <b>PDBTitle:</b> crystal structure of the gyf domain of smy2 in complex with a proline-2 rich peptide from bbp/scsf1
20	<a href="#">c2vw9B_</a>	Alignment		23.6	25	<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
21	<a href="#">c2ra9A_</a>	Alignment	not modelled	23.2	33	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein duf1285; <b>PDBTitle:</b> crystal structure of a duf1285 family protein (sbal_2486) from2 shewanella baltica os155 at 1.40 a resolution
22	<a href="#">d2pstx1</a>	Alignment	not modelled	22.0	23	<b>Fold:</b> Mbth/L9 domain-like <b>Superfamily:</b> Mbth-like <b>Family:</b> Mbth-like
23	<a href="#">cleqqD_</a>	Alignment	not modelled	21.6	32	<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
24	<a href="#">dltzaa_</a>	Alignment	not modelled	18.1	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ApaG-like <b>Family:</b> ApaG-like
25	<a href="#">dlxq4a_</a>	Alignment	not modelled	17.8	21	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ApaG-like <b>Family:</b> ApaG-like
26	<a href="#">d2gpfa1</a>	Alignment	not modelled	17.4	23	<b>Fold:</b> Mbth/L9 domain-like <b>Superfamily:</b> Mbth-like <b>Family:</b> Mbth-like
27	<a href="#">d2q07a1</a>	Alignment	not modelled	17.1	10	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> PUA domain
28	<a href="#">c2fleA_</a>	Alignment	not modelled	17.0	43	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein apag; <b>PDBTitle:</b> solution structure of apag protein
29	<a href="#">dlpuja_</a>	Alignment	not modelled	17.0	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins

30	<a href="#">d1xvsa_</a>	Alignment	not modelled	16.9	43	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> ApaG-like <b>Family:</b> ApaG-like
31	<a href="#">c2khrA_</a>	Alignment	not modelled	15.3	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein mbth; <b>PDBTitle:</b> solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
32	<a href="#">d1eyga_</a>	Alignment	not modelled	15.0	30	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
33	<a href="#">d2bm8a1</a>	Alignment	not modelled	13.5	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Cmcl-like
34	<a href="#">c2p8tA_</a>	Alignment	not modelled	13.1	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph0730; <b>PDBTitle:</b> hypothetical protein ph0730 from pyrococcus horikoshii ot3
35	<a href="#">d1ue1a_</a>	Alignment	not modelled	13.0	35	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
36	<a href="#">d2d7na1</a>	Alignment	not modelled	12.7	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
37	<a href="#">c2q07A_</a>	Alignment	not modelled	12.2	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein af0587; <b>PDBTitle:</b> crystal structure of af0587, a protein of unknown function
38	<a href="#">c3tqyA_</a>	Alignment	not modelled	12.1	35	<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
39	<a href="#">c2ihfA_</a>	Alignment	not modelled	11.2	37	<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
40	<a href="#">c3eivB_</a>	Alignment	not modelled	11.1	32	<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
41	<a href="#">c2e6zA_</a>	Alignment	not modelled	10.3	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> solution structure of the second kow motif of human2 transcription elongation factor spt5
42	<a href="#">c3rhfB_</a>	Alignment	not modelled	10.2	44	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyphosphate kinase 2 family protein; <b>PDBTitle:</b> crystal structure of polyphosphate kinase 2 from arthrobacter2 aurescens tc1
43	<a href="#">c3pgzB_</a>	Alignment	not modelled	10.2	27	<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
44	<a href="#">c3czqA_</a>	Alignment	not modelled	9.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyphosphate kinase 2; <b>PDBTitle:</b> crystal structure of putative polyphosphate kinase 2 from2 sinorhizobium meliloti
45	<a href="#">c1ue7A_</a>	Alignment	not modelled	9.8	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-binding2 protein from mycobacterium tuberculosis
46	<a href="#">d1v1qa_</a>	Alignment	not modelled	9.0	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
47	<a href="#">c3czpA_</a>	Alignment	not modelled	8.8	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative polyphosphate kinase 2; <b>PDBTitle:</b> crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
48	<a href="#">c2iheA_</a>	Alignment	not modelled	8.6	36	<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
49	<a href="#">c2l9dA_</a>	Alignment	not modelled	8.5	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of the protein yp_546394.1, the first structural2 representative of the pfam family pf12112
50	<a href="#">c2rndA_</a>	Alignment	not modelled	8.4	29	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> myc box-dependent-interacting protein 1; <b>PDBTitle:</b> structure of the n-terminal barpeptide in dpc micelles
51	<a href="#">c1is7F_</a>	Alignment	not modelled	8.2	14	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> gtp cyclohydrolase i; <b>PDBTitle:</b> crystal structure of rat gtpchi/grp stimulatory complex
52	<a href="#">d1a8ra_</a>	Alignment	not modelled	8.1	17	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> GTP cyclohydrolase I
53	<a href="#">d2d7pa1</a>	Alignment	not modelled	8.1	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
54	<a href="#">d2d7ma1</a>	Alignment	not modelled	7.6	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
55	<a href="#">c3iswA_</a>	Alignment	not modelled	7.4	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> filamin-a; <b>PDBTitle:</b> crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cfr
						<b>PDB header:</b> apoptosis

56	<a href="#">c3mx7A_</a>	Alignment	not modelled	7.1	19	<b>Chain:</b> A: <b>PDB Molecule:</b> fas apoptotic inhibitory molecule 1; <b>PDBTitle:</b> crystal structure analysis of human faim-ntd
57	<a href="#">d2w0pa1</a>	Alignment	not modelled	6.9	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
58	<a href="#">d2ntka1</a>	Alignment	not modelled	6.9	26	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> Archaeal IMP cyclohydrolase PurO <b>Family:</b> Archaeal IMP cyclohydrolase PurO
59	<a href="#">d2do3a1</a>	Alignment	not modelled	6.7	25	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> SPT5 KOW domain-like
60	<a href="#">c2l8kA_</a>	Alignment	not modelled	6.6	31	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> non-structural protein 7; <b>PDBTitle:</b> nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
61	<a href="#">d1txya_</a>	Alignment	not modelled	6.6	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Single strand DNA-binding domain, SSB
62	<a href="#">d2exna1</a>	Alignment	not modelled	6.4	31	<b>Fold:</b> MOSC N-terminal domain-like <b>Superfamily:</b> MOSC N-terminal domain-like <b>Family:</b> MOSC N-terminal domain-like
63	<a href="#">c3ec1A_</a>	Alignment	not modelled	6.4	23	<b>PDB header:</b> hydrolase, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> yqeh gtpase; <b>PDBTitle:</b> structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnol1 / atnol1 ortholog)
64	<a href="#">c2wojD_</a>	Alignment	not modelled	6.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> adp-alf4 complex of s. cerevisiae get3
65	<a href="#">c3iswB_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> filamin-a; <b>PDBTitle:</b> crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cfr
66	<a href="#">c2brqA_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> filamin a; <b>PDBTitle:</b> crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
67	<a href="#">c2w0pB_</a>	Alignment	not modelled	6.3	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> filamin-a; <b>PDBTitle:</b> crystal structure of the filamin a repeat 21 complexed with2 the migfilin peptide
68	<a href="#">d1wp1a_</a>	Alignment	not modelled	6.2	14	<b>Fold:</b> T-fold <b>Superfamily:</b> Tetrahydrobiopterin biosynthesis enzymes-like <b>Family:</b> GTP cyclohydrolase I
69	<a href="#">c3k6qB_</a>	Alignment	not modelled	6.2	11	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative ligand binding protein; <b>PDBTitle:</b> crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
70	<a href="#">d1a9xa3</a>	Alignment	not modelled	6.1	19	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
71	<a href="#">d1v5pa_</a>	Alignment	not modelled	6.1	21	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Pleckstrin-homology domain (PH domain)
72	<a href="#">c3cf4A_</a>	Alignment	not modelled	5.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase alpha subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex
73	<a href="#">c3bjoA_</a>	Alignment	not modelled	5.8	19	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized atp-binding protein mj1010; <b>PDBTitle:</b> crystal structure of the c-terminal domain of a possible atp-binding2 protein from methanocaldococcus jannaschii dsm 2661
74	<a href="#">c2k7qA_</a>	Alignment	not modelled	5.6	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> filamin-a; <b>PDBTitle:</b> filamin a ig-like domains 18-19
75	<a href="#">c2r37A_</a>	Alignment	not modelled	5.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 3; <b>PDBTitle:</b> crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
76	<a href="#">d2bp3a1</a>	Alignment	not modelled	5.5	31	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Filamin repeat (rod domain)
77	<a href="#">d2h9fa2</a>	Alignment	not modelled	5.5	19	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PA0793-like