Phyre^2

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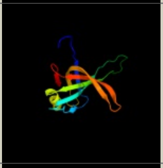
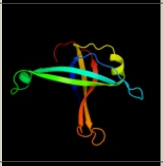
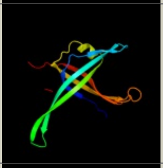
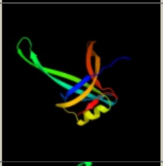
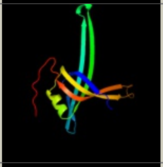
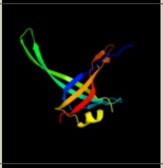
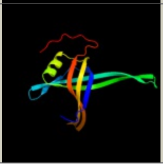
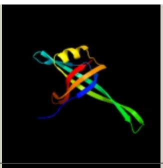
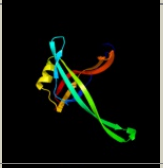
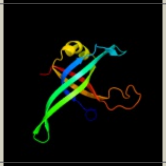
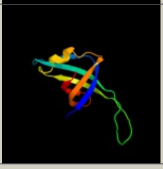
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qvca_	Alignment		100.0	100	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
2	d1eyga_	Alignment		100.0	100	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
3	c3tqyA_	Alignment		100.0	68	**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
4	c2iheA_	Alignment		100.0	32	**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
5	c1eqqD_	Alignment		100.0	100	**PDB header:**replication/rna **Chain:** D: **PDB Molecule:**single stranded dna binding protein; **PDBTitle:** single stranded dna binding protein and ssdna complex
6	c2ihfA_	Alignment		100.0	34	**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
7	c2vw9B_	Alignment		100.0	39	**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	c3pgzB_	Alignment		99.9	56	**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
9	d1ue1a_	Alignment		99.9	32	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
10	d3ulla_	Alignment		99.9	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
11	c3eivB_	Alignment		99.9	30	**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

12	c1se8A_	Alignment		99.9	35	**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
13	d1se8a_	Alignment		99.9	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
14	c1ue7A_	Alignment		99.9	33	**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
15	d1v1qa_	Alignment		99.9	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
16	c3lgjA_	Alignment		99.9	51	**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
17	c1z9fA_	Alignment		99.9	48	**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
18	c3kojA_	Alignment		99.8	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ycf41; **PDBTitle:** crystal structure of the ssb domain of q5n255_synp6 protein2 from synechococcus sp. northeast structural genomics3 consortium target snr59a.
19	c3k8aA_	Alignment		99.8	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative primosomal replication protein; **PDBTitle:** neisseria gonorrhoeae prib
20	d1txya_	Alignment		99.8	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
21	c3fhwB_	Alignment	not modelled	99.8	16	**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.
22	c3en2A_	Alignment	not modelled	99.7	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable primosomal replication protein n; **PDBTitle:** three-dimensional structure of the protein prib from2 ralstonia solanacearum at the resolution 2.3a. northeast3 structural genomics consortium target rsr213c.
23	c3stbC_	Alignment	not modelled	98.1	24	**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
24	c3k81D_	Alignment	not modelled	98.1	24	**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
25	c3e0eA_	Alignment	not modelled	96.9	19	**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
26	c3f2cA_	Alignment	not modelled	95.5	18	**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
27	c3dm3A_	Alignment	not modelled	95.4	17	**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
28	c2k50A_	Alignment	not modelled	94.5	13	**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.
29	c1ynxA_	Alignment	not modelled	93.1	21	**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)
30	c1fguA_	Alignment	not modelled	92.2	11	**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
31	d1jmca1	Alignment	not modelled	90.7	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
32	d1o7ia_	Alignment	not modelled	90.6	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
33	d1gm5a2	Alignment	not modelled	89.1	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
34	c2k75A_	Alignment	not modelled	87.9	21	**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.
35	d1jmca2	Alignment	not modelled	84.6	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
36	d1c0aa1	Alignment	not modelled	77.4	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
37	c2xgtB_	Alignment	not modelled	76.4	18	**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
38	c2hqlB_	Alignment	not modelled	76.2	24	**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
39	c3kf6A_	Alignment	not modelled	75.9	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
40	d1eova1	Alignment	not modelled	75.6	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
41	c2vl6C_	Alignment	not modelled	74.7	19	**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
42	d1b8aa1	Alignment	not modelled	74.3	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
43	d1wjja_	Alignment	not modelled	70.8	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
44	d1bbua1	Alignment	not modelled	70.2	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
45	d1e1oa1	Alignment	not modelled	66.6	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
46	d1l0wa1	Alignment	not modelled	62.6	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
47	c1ltlE_	Alignment	not modelled	61.7	22	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
48	c1eqrC_	Alignment	not modelled	53.7	19	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
49	c1gm5A_	Alignment	not modelled	52.8	12	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
50	d1ltla_	Alignment	not modelled	49.8	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
51	c3m4qA_	Alignment	not modelled	45.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
52	c1wydB_	Alignment	not modelled	45.0	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii

53	c2pi2A_	Alignment	not modelled	44.3	18	**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
54	d1vqoj1	Alignment	not modelled	41.9	25	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
55	c3d5bN_	Alignment	not modelled	41.2	42	**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.
56	c3kf8C_	Alignment	not modelled	39.8	19	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
57	d2j01n1	Alignment	not modelled	39.7	42	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
58	c3i7fA_	Alignment	not modelled	39.6	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
59	c3cf5G_	Alignment	not modelled	39.4	35	**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
60	d2zjrg1	Alignment	not modelled	39.4	35	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
61	c2zkrj_	Alignment	not modelled	38.0	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 an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
62	d1j3aa_	Alignment	not modelled	36.0	35	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
63	c4a1al_	Alignment	not modelled	34.8	25	**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.
64	c1b8aB_	Alignment	not modelled	33.8	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
65	c3izcK_	Alignment	not modelled	33.6	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
66	c2ftcH_	Alignment	not modelled	33.4	53	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**39s ribosomal protein l13, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
67	d2pi2a1	Alignment	not modelled	32.2	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
68	d1n9wa1	Alignment	not modelled	31.6	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
69	c3bjuB_	Alignment	not modelled	31.3	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
70	d1qzga_	Alignment	not modelled	30.9	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
71	c3jywM_	Alignment	not modelled	29.9	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
72	c3bboL_	Alignment	not modelled	29.6	26	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**ribosomal protein l13; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
73	c1xjvA_	Alignment	not modelled	27.2	13	**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)
74	d1krta_	Alignment	not modelled	26.5	11	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
75	c3iz5K_	Alignment	not modelled	26.4	30	**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
76	d1fnda1	Alignment	not modelled	25.7	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
77	c1e22A_	Alignment	not modelled	25.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp

78	c1jb7A_	Alignment	not modelled	25.0	10	**PDB header:**dna-binding protein/dna **Chain:** A: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
79	c1ph4A_	Alignment	not modelled	25.0	10	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggttttggcg
80	c2l3sA_	Alignment	not modelled	24.3	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**autoinhibited crk protein; **PDBTitle:** structure of the autoinhibited crk
81	d1jb7a1	Alignment	not modelled	20.4	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
82	c1asyA_	Alignment	not modelled	19.8	18	**PDB header:**complex (aminoacyl-trna synthase/trna) **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
83	d1gawa1	Alignment	not modelled	19.1	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
84	c1efwA_	Alignment	not modelled	19.1	20	**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
85	d1xjva1	Alignment	not modelled	18.7	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
86	d1htwa_	Alignment	not modelled	18.5	41	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**YjeE-like
87	d1zcea1	Alignment	not modelled	17.4	11	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
88	d1xjva2	Alignment	not modelled	17.3	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
89	d2isba1	Alignment	not modelled	17.1	30	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
90	c3f9vA_	Alignment	not modelled	16.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
91	c3e9hB_	Alignment	not modelled	15.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
92	c3kf8D_	Alignment	not modelled	14.7	26	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**protein ten1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
93	d2ar1a1	Alignment	not modelled	14.3	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
94	d2gbsa1	Alignment	not modelled	14.0	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
95	c2kenA_	Alignment	not modelled	13.8	9	**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.
96	c2wkdA_	Alignment	not modelled	13.5	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf34p2; **PDBTitle:** crystal structure of a double ile-to-met mutant of protein2 orf34 from lactococcus phage p2
97	c1s1iM_	Alignment	not modelled	13.0	30	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l16-a; **PDBTitle:** 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.
98	c3eopB_	Alignment	not modelled	13.0	11	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**thymocyte nuclear protein 1; **PDBTitle:** crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1
99	d1c3ha_	Alignment	not modelled	12.8	36	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like