Phyre2

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Description	P0AFG0
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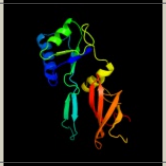
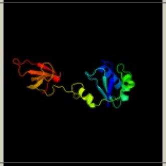
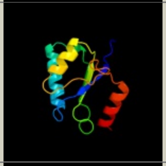
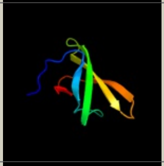
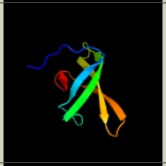
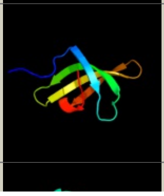
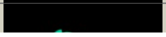
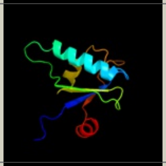
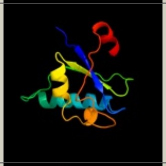
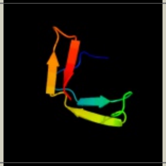
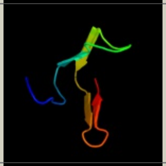
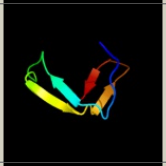
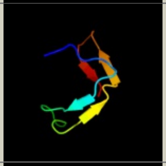
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m1gB_	Alignment		100.0	42	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
2	c2xhcA_	Alignment		100.0	53	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
3	c2ougC_	Alignment		100.0	18	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional activator rfah; **PDBTitle:** crystal structure of the rfah transcription factor at 2.1a2 resolution
4	c2k06A_	Alignment		100.0	100	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of the aminoterminal domain of e. coli2 nusg
5	c3p8bB_	Alignment		100.0	20	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
6	d1nz8a_	Alignment		99.9	39	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
7	d1m1ha2	Alignment		99.9	31	**Fold:**Ferredoxin-like **Superfamily:**N-utilization substance G protein NusG, N-terminal domain **Family:**N-utilization substance G protein NusG, N-terminal domain
8	d1nz9a_	Alignment		99.6	62	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
9	c2jvvA_	Alignment		99.6	100	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
10	c2kvqG_	Alignment		99.6	100	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
11	d1nppa2	Alignment		99.5	63	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
						

12	c3ewgA_	Alignment		98.3	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription antitermination protein nusg; **PDBTitle:** crystal structure of the n-terminal domain of nusg (ngn) from2 methanocaldococcus jannaschii
13	c2exuA_	Alignment		98.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation protein spt4/spt5; **PDBTitle:** crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
14	c3h7hB_	Alignment		98.2	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
15	c2e6zA_	Alignment		97.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
16	d1vqot1	Alignment		96.9	33	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
17	c4a1cS_	Alignment		96.8	22	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rpl26; **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 4.
18	c3iz5Y_	Alignment		96.7	19	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l26 (l24p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
19	c2zkrt_	Alignment		96.7	19	**PDB header:**ribosomal protein/rna **Chain:** T: **PDB Molecule:**rna expansion segment es39 part iii; **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
20	c2ckkA_	Alignment		96.6	13	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**kin17; **PDBTitle:** high resolution crystal structure of the human kin172 c-terminal domain containing a kow motif3 kin17.
21	c2e70A_	Alignment	not modelled	96.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the fifth kow motif of human2 transcription elongation factor spt5
22	d2zjrr1	Alignment	not modelled	96.4	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
23	d2do3a1	Alignment	not modelled	96.3	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
24	c1s1iU_	Alignment	not modelled	94.8	21	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l26-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.
25	d2gycs1	Alignment	not modelled	94.4	22	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
26	c3bboW_	Alignment	not modelled	93.9	18	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**ribosomal protein l24; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
27	d1ib8a1	Alignment	not modelled	93.1	24	**Fold:**Sm-like fold **Superfamily:**YhbC-like, C-terminal domain **Family:**YhbC-like, C-terminal domain
28	d2j01y1	Alignment	not modelled	92.7	30	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
						PDB header:ribosome

29	c2ftcN_	Alignment	not modelled	89.8	27	**Chain:** N: **PDB Molecule:**mitochondrial ribosomal protein l24; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
30	c2jz2A_	Alignment	not modelled	85.7	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
31	c3iz5N_	Alignment	not modelled	76.7	27	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
32	c4a19F_	Alignment	not modelled	74.6	18	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl14; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
33	d2joya1	Alignment	not modelled	70.3	17	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L14e
34	c4a18N_	Alignment	not modelled	70.1	21	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**rpl27; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
35	c3izcN_	Alignment	not modelled	66.8	17	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein rpl14 (l14e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
36	c3kbgA_	Alignment	not modelled	64.4	13	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s4e; **PDBTitle:** crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
37	d1vqoq1	Alignment	not modelled	57.3	26	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
38	c2xzmW_	Alignment	not modelled	51.4	15	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**40s ribosomal protein s4; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
39	c3iz6D_	Alignment	not modelled	51.2	23	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
40	d1nxza1	Alignment	not modelled	45.3	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
41	d2vv5a1	Alignment	not modelled	44.4	32	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
42	d1vhka1	Alignment	not modelled	43.0	11	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
43	c1ib8A_	Alignment	not modelled	39.7	24	**PDB header:**nucleic acid binding protein **Chain:** A: **PDB Molecule:**conserved protein sp14.3; **PDBTitle:** solution structure and function of a conserved protein2 sp14.3 encoded by an essential streptococcus pneumoniae3 gene
44	d2pu9b1	Alignment	not modelled	36.1	33	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
45	c2pmzV_	Alignment	not modelled	35.1	17	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
46	c3qz9D_	Alignment	not modelled	31.2	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**co-type nitrile hydratase beta subunit; **PDBTitle:** crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
47	c2eqmA_	Alignment	not modelled	29.0	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
48	c3izbD_	Alignment	not modelled	26.8	18	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein rps4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
49	c3kw2A_	Alignment	not modelled	25.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
50	d1psea_	Alignment	not modelled	23.6	22	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
51	d2coya1	Alignment	not modelled	22.6	14	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
52	d1a8pa1	Alignment	not modelled	22.5	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
53	d2hqha1	Alignment	not modelled	22.3	16	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain

54	d1qp3a_	Alignment	not modelled	21.7	24	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
55	d1ixda_	Alignment	not modelled	21.4	14	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
56	c3izca_	Alignment	not modelled	20.3	23	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**60s ribosomal protein rpl1 (l1p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
57	c2dxcG_	Alignment	not modelled	19.7	30	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**thiocyanate hydrolase subunit alpha; **PDBTitle:** recombinant thiocyanate hydrolase, fully-matured form
58	c3q1jA_	Alignment	not modelled	19.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 1 of human phd finger protein 20
59	d1h3ga1	Alignment	not modelled	18.9	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
60	c2eqjA_	Alignment	not modelled	17.8	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
61	d1ugpb_	Alignment	not modelled	17.8	12	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
62	c2y35A_	Alignment	not modelled	17.8	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ld22664p; **PDBTitle:** crystal structure of xrn1-substrate complex
63	c3iz5a_	Alignment	not modelled	17.5	33	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**60s ribosomal protein l1 (l1p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
64	d2cowa1	Alignment	not modelled	17.5	17	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
65	c3cgnA_	Alignment	not modelled	17.2	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
66	d2zjrm1	Alignment	not modelled	17.0	25	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
67	d1dzfa2	Alignment	not modelled	15.8	19	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
68	c2kr7A_	Alignment	not modelled	15.5	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
69	d1v29b_	Alignment	not modelled	15.4	15	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
70	c3pifD_	Alignment	not modelled	15.2	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**5'->3' exoribonuclease (xrn1); **PDBTitle:** crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
71	c2zkrq_	Alignment	not modelled	15.1	13	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 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
72	c3izcG_	Alignment	not modelled	14.3	19	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**60s ribosomal protein rpl6 (l6e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
73	d1eika_	Alignment	not modelled	13.2	14	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
74	d2zgwa1	Alignment	not modelled	12.8	38	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Biotin repressor (BirA)
75	d1efca1	Alignment	not modelled	12.6	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
76	c2kfwA_	Alignment	not modelled	12.1	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
77	d2gycn1	Alignment	not modelled	11.8	31	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
78	c2k8iA_	Alignment	not modelled	11.4	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
79	d1gxie_	Alignment	not modelled	11.4	22	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)

80	c1nwxN_	Alignment	not modelled	11.1	30	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**ribosomal protein l19; **PDBTitle:** complex of the large ribosomal subunit from deinococcus2 radiodurans with abt-773
81	d2j01t1	Alignment	not modelled	10.9	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal protein L19
82	c3izcU_	Alignment	not modelled	10.7	17	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein rpl21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
83	d1gawa1	Alignment	not modelled	10.7	38	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
84	c2vv5D_	Alignment	not modelled	10.6	20	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**small-conductance mechanosensitive channel; **PDBTitle:** the open structure of mscs
85	d1fr3a_	Alignment	not modelled	10.4	14	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**Molybdate/tungstate binding protein MOP
86	c1z85B_	Alignment	not modelled	10.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein tm1380; **PDBTitle:** crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
87	c2k5hA_	Alignment	not modelled	10.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
88	c2e5pA_	Alignment	not modelled	10.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
89	d2ahob2	Alignment	not modelled	9.8	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
90	d1jb0e_	Alignment	not modelled	9.0	22	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
91	d1wjqa_	Alignment	not modelled	8.6	23	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
92	d1whka_	Alignment	not modelled	8.5	9	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
93	c2k52A_	Alignment	not modelled	8.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1198; **PDBTitle:** structure of uncharacterized protein mj1198 from2 methanocaldococcus jannaschii. northeast structural3 genomics target mjr117b
94	d1fdra1	Alignment	not modelled	8.2	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
95	c2khjA_	Alignment	not modelled	8.2	17	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
96	d1hmja_	Alignment	not modelled	8.1	24	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
97	d1fnda1	Alignment	not modelled	8.0	38	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
98	d1mhna_	Alignment	not modelled	7.9	15	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
99	c2vc8A_	Alignment	not modelled	7.7	20	**PDB header:**protein-binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of the lsm domain of human edc3 (enhancer2 of decapping 3)