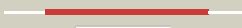






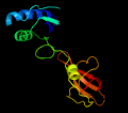















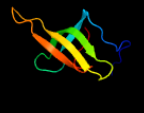


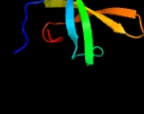
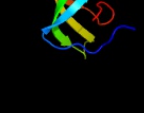


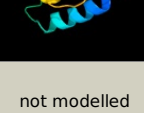


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0639_(nusG)_734257_734973
 Date Fri Jul 26 01:50:20 BST 2019
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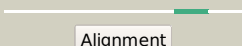
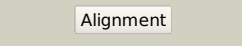
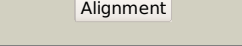

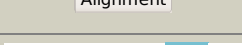



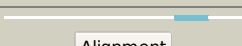
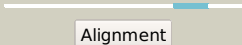
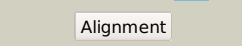
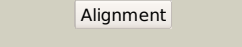
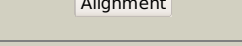
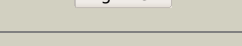
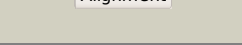
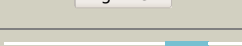




Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m1gB_	 Alignment		100.0	39	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	49	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
3	c2lq8A_	 Alignment		100.0	34	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: domain interaction in thermotoga maritima nusg
4	c5tbzK_	 Alignment		100.0	43	PDB header: transcription/rna Chain: K: PDB Molecule: transcription termination/antitermination protein nusg; PDBTitle: e. coli rna polymerase complexed with nusg
5	c4zn3A_	 Alignment		100.0	21	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: crystal structure of mjspt4:spt5 complex conformation b
6	c2ougC_	 Alignment		100.0	23	PDB header: transcription Chain: C: PDB Molecule: transcriptional activator rfah; PDBTitle: crystal structure of the rfah transcription factor at 2.1a resolution
7	c3p8bB_	 Alignment		100.0	23	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
8	c2k06A_	 Alignment		100.0	37	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of the aminoterminal domain of e. coli nusg
9	d1nz8a_	 Alignment		100.0	49	Fold: Ferredoxin-like Superfamily: N-utilization substance G protein NusG, N-terminal domain Family: N-utilization substance G protein NusG, N-terminal domain
10	d1m1ha2	 Alignment		100.0	28	Fold: Ferredoxin-like Superfamily: N-utilization substance G protein NusG, N-terminal domain Family: N-utilization substance G protein NusG, N-terminal domain
11	c5oikZ_	 Alignment		99.9	17	PDB header: transcription Chain: Z: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of an rna polymerase ii-dsif transcription elongation2 complex

12	c5xonW_	Alignment		99.8	18	PDB header: transcription/rna Chain: W: PDB Molecule: protein that forms a complex with spt4p; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
13	c2mi6A_	Alignment		99.8	98	PDB header: transcription Chain: A: PDB Molecule: transcription termination/antitermination protein nusg; PDBTitle: solution structure of the carboxy terminal domain of nusg from2 mycobacterium tuberculosis
14	d1nppa2	Alignment		99.8	52	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
15	d1nz9a_	Alignment		99.8	53	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
16	c2jvvA_	Alignment		99.7	53	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
17	c2kvqG_	Alignment		99.7	53	PDB header: transcription Chain: G: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
18	c2lcIA_	Alignment		99.6	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator rfah; PDBTitle: solution structure of rfah carboxyterminal domain
19	c6ir9W_	Alignment		99.5	19	PDB header: transcription/rna/dna Chain: W: PDB Molecule: spt5; PDBTitle: rna polymerase ii elongation complex bound with elf1 and spt4/5,2 stalled at shl(-1) of the nucleosome
20	c3ewgA_	Alignment		98.4	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
21	c2exuA_	Alignment	not modelled	97.7	18	PDB header: transcription Chain: A: PDB Molecule: transcription initiation protein spt4/spt5; PDBTitle: crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
22	c3h7hB_	Alignment	not modelled	97.6	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)
23	c3j21U_	Alignment	not modelled	97.5	22	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l24p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
24	c4ytIB_	Alignment	not modelled	97.3	16	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
25	d1vqot1	Alignment	not modelled	97.3	30	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
26	c3iz5Y_	Alignment	not modelled	97.3	15	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
27	c4a1cS_	Alignment	not modelled	97.2	14	PDB header: ribosome Chain: S: PDB Molecule: rpl26; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rna,3 5.8s rna and proteins of molecule 4.
28	c2e6zA_	Alignment	not modelled	97.1	18	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
29	c3zf7Z_	Alignment	not modelled	97.1	11	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein l26, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
30	c2ckkA_	Alignment	not modelled	97.1	13	PDB header: nuclear protein Chain: A: PDB Molecule: kin17; PDBTitle: high resolution crystal structure of the human kin17 c-terminal domain2 containing a kow motif
31	c2zkrt_	Alignment	not modelled	97.0	11	PDB header: ribosomal protein/rna Chain: T: PDB Molecule: rna expansion segment es39 part iii; 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
32	d2zjrr1	Alignment	not modelled	97.0	21	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
33	c4v19Y_	Alignment	not modelled	97.0	18	PDB header: ribosome Chain: Y: PDB Molecule: mitoribosomal protein ul24m, mrpl24; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
34	c5mmiV_	Alignment	not modelled	96.9	21	PDB header: ribosome Chain: V: PDB Molecule: plastid ribosomal protein ul24c; PDBTitle: structure of the large subunit of the chloroplast ribosome
35	c1vw4Q_	Alignment	not modelled	96.9	18	PDB header: ribosome Chain: Q: PDB Molecule: 54s ribosomal protein l40, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
36	c5o60V_	Alignment	not modelled	96.8	17	PDB header: ribosome Chain: V: PDB Molecule: 50s ribosomal protein l24; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
37	d2do3a1	Alignment	not modelled	96.7	21	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
38	c2e70A_	Alignment	not modelled	96.6	15	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
39	c1s1iU_	Alignment	not modelled	96.2	20	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein l26-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
40	d2gycs1	Alignment	not modelled	95.7	19	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
41	c5ohoB_	Alignment	not modelled	95.5	25	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: crystal structure of the kowx-kow4 domain of human dsif
42	c3bboW_	Alignment	not modelled	95.3	21	PDB header: ribosome Chain: W: PDB Molecule: ribosomal protein l24; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
43	d2j01y1	Alignment	not modelled	95.1	21	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
44	c2ftcN_	Alignment	not modelled	94.0	20	PDB header: ribosome Chain: N: PDB Molecule: mitochondrial ribosomal protein l24; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
45	c3j3vU_	Alignment	not modelled	93.9	20	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l24; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
46	c4ytkA_	Alignment	not modelled	93.6	14	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow1-linker1 domain of transcription elongation2 factor spt5
47	c5ohqA_	Alignment	not modelled	93.3	13	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: crystal structure of the kow6-kow7 domain of human dsif
48	d1ib8a1	Alignment	not modelled	92.0	20	Fold: Sm-like fold Superfamily: YhbC-like, C-terminal domain Family: YhbC-like, C-terminal domain
49	c4aukB_	Alignment	not modelled	85.9	23	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase m; PDBTitle: crystal structure of c2498 2'-o-ribose methyltransferase rlm from2 escherichia coli
50	d1vqoq1	Alignment	not modelled	85.6	25	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
51	c2jz2A_	Alignment	not modelled	83.8	17	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
52	c3j21R_	Alignment	not modelled	77.7	19	PDB header: ribosome Chain: R: PDB Molecule: 50s ribosomal protein l21e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
53	c3iz5N_	Alignment	not modelled	77.1	22	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
54	d2joya1	Alignment	not modelled	74.6	20	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L14e
55	c4pl6A	Alignment	not modelled	73.7	23	PDB header: transcription Chain: A: PDB Molecule: at1g02740; PDBTitle: structure of the chromodomain of mrg2 in complex with h3k4me3
56	c3izcN	Alignment	not modelled	73.5	34	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
57	c4a19F	Alignment	not modelled	73.1	22	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.
58	c3j39M	Alignment	not modelled	70.0	22	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l14; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
59	c3kbgA	Alignment	not modelled	69.1	19	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: crystal structure of the 30s ribosomal protein s4e from thermoplasma2 acidophilum. northeast structural genomics consortium target tar28.
60	c3j3bM	Alignment	not modelled	68.8	32	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l14; PDBTitle: structure of the human 60s ribosomal proteins
61	c2lrqA	Alignment	not modelled	67.1	16	PDB header: transcription Chain: A: PDB Molecule: nua4 complex subunit eaf3 homolog; PDBTitle: chemical shift assignment and solution structure of fr822a from2 drosophila melanogaster. northeast structural genomics consortium3 target fr822a
62	c4tseA	Alignment	not modelled	64.2	24	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mib1; PDBTitle: crystal structure of the mib repeat domain of mind bomb 1
63	c3j215	Alignment	not modelled	64.2	19	PDB header: ribosome Chain: 5: PDB Molecule: 50s ribosomal protein l14e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
64	c2eqmA	Alignment	not modelled	60.7	15	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]
65	c3q1jA	Alignment	not modelled	60.5	22	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 1 of human phd finger protein 20
66	c3zf7v	Alignment	not modelled	60.4	19	PDB header: ribosome Chain: V: PDB Molecule: 60s ribosomal protein l22, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
67	d1luta	Alignment	not modelled	60.2	13	Fold: Ferredoxin-like Superfamily: Sporulation related repeat Family: Sporulation related repeat
68	d1nxza1	Alignment	not modelled	59.2	25	Fold: PUA domain-like Superfamily: PUA domain-like Family: Yggj N-terminal domain-like
69	d2vv5a1	Alignment	not modelled	56.3	21	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
70	d2f5ka1	Alignment	not modelled	55.1	21	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
71	c2dxcG	Alignment	not modelled	55.0	26	PDB header: hydrolase Chain: G: PDB Molecule: thiocyanate hydrolase subunit alpha; PDBTitle: recombinant thiocyanate hydrolase, fully-matured form
72	c5in1A	Alignment	not modelled	51.6	21	PDB header: transcription Chain: A: PDB Molecule: mrg701; PDBTitle: crystal structure of the mrg701 chromodomain
73	d2j01t1	Alignment	not modelled	51.0	14	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L19
74	c5xyiE	Alignment	not modelled	48.0	14	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s4; PDBTitle: small subunit of trichomonas vaginalis ribosome
75	d1vhka1	Alignment	not modelled	47.4	15	Fold: PUA domain-like Superfamily: PUA domain-like Family: Yggj N-terminal domain-like
76	d1h3ga1	Alignment	not modelled	46.3	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
77	c2xzmW	Alignment	not modelled	45.8	13	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
78	d2zgw1	Alignment	not modelled	45.2	21	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Biotin repressor (BirA)

79	c3zey1	 Alignment	not modelled	44.8	16	PDB header: ribosome Chain: 1: PDB Molecule: 40s ribosomal protein s4, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
80	c3qz9D	 Alignment	not modelled	44.3	26	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.
81	c5xxuE	 Alignment	not modelled	44.2	15	PDB header: ribosome Chain: E: PDB Molecule: ribosomal protein es4; PDBTitle: small subunit of toxoplasma gondii ribosome
82	c3iz6D	 Alignment	not modelled	43.7	20	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
83	c2eqjA	 Alignment	not modelled	42.9	24	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
84	c5dmaA	 Alignment	not modelled	42.3	12	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pcrA; PDBTitle: crystal structure of c-terminal tudor domain in pcrA/uvrd helicase
85	d1ugpb	 Alignment	not modelled	39.0	15	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
86	c2y35A	 Alignment	not modelled	38.9	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: ld22664p; PDBTitle: crystal structure of xrn1-substrate complex
87	c3j20E	 Alignment	not modelled	37.9	24	PDB header: ribosome Chain: E: PDB Molecule: 30s ribosomal protein s4e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
88	d2zjrm1	 Alignment	not modelled	37.2	16	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal protein L19
89	c4fm4D	 Alignment	not modelled	36.5	17	PDB header: lyase Chain: D: PDB Molecule: nitrile hydratase beta subunit; PDBTitle: wild type fe-type nitrile hydratase from comamonas testosteroni ni1
90	d1v29b	 Alignment	not modelled	35.6	30	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
91	c5znpB	 Alignment	not modelled	35.6	16	PDB header: gene regulation Chain: B: PDB Molecule: short life family protein; PDBTitle: crystal structure of ptshl in complex with an h3k4me3 peptide
92	d2pu9b1	 Alignment	not modelled	35.4	25	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
93	c3j3bZ	 Alignment	not modelled	34.6	21	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein l27; PDBTitle: structure of the human 60s ribosomal proteins
94	c4v19T	 Alignment	not modelled	34.5	12	PDB header: ribosome Chain: T: PDB Molecule: mitoribosomal protein bl19m, mrpl19; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
95	c1ib8A	 Alignment	not modelled	32.8	20	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
96	c3j1wU	 Alignment	not modelled	32.8	8	PDB header: cell invasion Chain: U: PDB Molecule: protein prgh; PDBTitle: a refined model of the prototypical salmonella typhimurium t3ss basal2 body reveals the molecular basis for its assembly
97	c4hw9E	 Alignment	not modelled	32.7	15	PDB header: membrane protein Chain: E: PDB Molecule: mechanosensitive channel mscs; PDBTitle: crystal structure of helicobacter pylori mscs (closed state)
98	c3t9nG	 Alignment	not modelled	32.1	18	PDB header: membrane protein Chain: G: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: crystal structure of a membrane protein
99	d1mhna	 Alignment	not modelled	32.0	24	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
100	c3j39Z	 Alignment	not modelled	31.9	26	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein l27; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
101	c2zkrq	 Alignment	not modelled	31.2	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 an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
102	c3u5cE	 Alignment	not modelled	30.6	19	PDB header: ribosome Chain: E: PDB Molecule: 40s ribosomal protein s4-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
103	c3zf7a	 Alignment	not modelled	30.6	21	PDB header: ribosome Chain: A: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

104	d1s7ia_	Alignment	not modelled	29.9	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: DGPF domain (Pfam 04946)
105	c5ha0A_	Alignment	not modelled	28.7	55	PDB header: transport protein Chain: A: PDB Molecule: lipocalin ai-4; PDBTitle: crystal structure of the ltbp1 leukotriene d4 complex
106	d2qdyb1	Alignment	not modelled	27.9	27	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
107	c4a4fA_	Alignment	not modelled	27.3	12	PDB header: rna binding protein Chain: A: PDB Molecule: survival of motor neuron-related-splicing factor 30; PDBTitle: solution structure of spf30 tudor domain in complex with symmetrically2 dimethylated arginine
108	c5o60Q_	Alignment	not modelled	27.1	16	PDB header: ribosome Chain: Q: PDB Molecule: 50s ribosomal protein l19; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
109	c4a18N_	Alignment	not modelled	27.0	19	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
110	c3u5eZ_	Alignment	not modelled	26.8	17	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein l27-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
111	c3izcU_	Alignment	not modelled	26.2	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
112	c4nnkA_	Alignment	not modelled	25.3	15	PDB header: ribosomal protein Chain: A: PDB Molecule: 30s ribosomal protein s1; PDBTitle: structural basis for targeting the ribosomal protein s1 of2 mycobacterium tuberculosis by pyrazinamide
113	c1x60A_	Alignment	not modelled	24.3	15	PDB header: hydrolase Chain: A: PDB Molecule: sporulation-specific n-acetylmuramoyl-l-alanine PDBTitle: solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
114	c4tvrA_	Alignment	not modelled	23.7	21	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase uhrf2; PDBTitle: tandem tudor and phd domains of uhrf2
115	d2ahob2	Alignment	not modelled	23.2	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
116	d1q46a2	Alignment	not modelled	22.9	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
117	d1pm1x_	Alignment	not modelled	22.6	50	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
118	c3pifD_	Alignment	not modelled	22.5	18	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
119	c2ml6A_	Alignment	not modelled	22.4	45	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein zp_02069618.1 from bacteroides uniformis atcc2 8492
120	d1e0ta3	Alignment	not modelled	22.4	13	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain