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Description	P0A7J7
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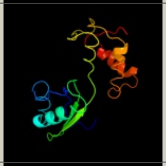
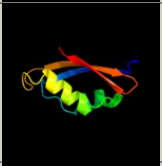
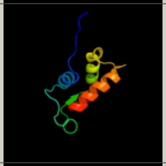
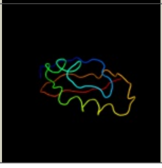
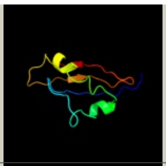
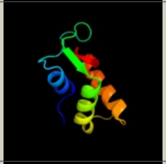
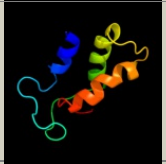
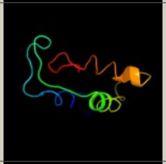
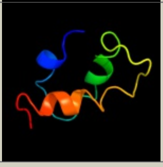
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bboK_	Alignment		100.0	54	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**ribosomal protein l11; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
2	c2vhml_	Alignment		100.0	100	**PDB header:**ribosome **Chain:** l: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** structure of pdf binding helix in complex with the ribosome2 (part 1 of 4)
3	c1jqmA_	Alignment		100.0	61	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** fitting of l11 protein and elongation factor g (ef-g) in2 the cryo-em map of e. coli 70s ribosome bound with ef-g,3 gdp and fusidic acid
4	c2ftcG_	Alignment		100.0	40	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**39s ribosomal protein l11, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
5	c1s1iK_	Alignment		100.0	21	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l12; **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.
6	c3iz5J_	Alignment		100.0	26	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l12 (l11p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
7	c3cjtP_	Alignment		100.0	70	**PDB header:**transferase/ribosomal protein **Chain:** P: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11
8	d3cjsb1	Alignment		100.0	70	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
9	d1wiba_	Alignment		100.0	23	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
10	d1hc8a_	Alignment		100.0	68	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
11	d2gycg2	Alignment		100.0	100	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain

12	d1xbpg2	Alignment		100.0	69	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
13	d1mmsa2	Alignment		100.0	67	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
14	c1vq8l_	Alignment		99.9	36	**PDB header:**ribosome **Chain:** l: **PDB Molecule:**50s ribosomal protein l11p; **PDBTitle:** the structure of ccda-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
15	d1mmsa1	Alignment		99.9	54	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
16	d1vqoi1	Alignment		99.9	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
17	d1xbpg1	Alignment		99.9	51	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
18	c2zkri_	Alignment		99.9	26	**PDB header:**ribosomal protein/rna **Chain:** I: **PDB Molecule:**rna expansion segment es15 part i; **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
19	d2gycg1	Alignment		99.9	100	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
20	d3cjrb1	Alignment		99.5	40	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
21	d1iwga2	Alignment	not modelled	28.9	22	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
22	c3bboD_	Alignment	not modelled	18.7	16	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein l1; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
23	c2jwlB_	Alignment	not modelled	18.4	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
24	c3r2cJ_	Alignment	not modelled	18.2	20	**PDB header:**transcription/rna **Chain:** J: **PDB Molecule:**30s ribosomal protein s10; **PDBTitle:** crystal structure of antitermination factors nusb and nuse in complex2 with boxa rna
25	c3qoyA_	Alignment	not modelled	15.2	14	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**50s ribosomal protein l1; **PDBTitle:** crystal structure of ribosomal protein l1 from aquifex aeolicus
26	c1nohB_	Alignment	not modelled	13.9	38	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**head morphogenesis protein; **PDBTitle:** the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
27	c2asbA_	Alignment	not modelled	13.1	14	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** structure of a mycobacterium tuberculosis nusa-rna complex
28	d1hh2p2	Alignment	not modelled	12.1	29	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)

29	c1lshB_	Alignment	not modelled	12.0	20	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**lipovitellin (lv-2); **PDBTitle:** lipid-protein interactions in lipovitellin
30	d1lshb_	Alignment	not modelled	12.0	20	**Fold:**Lipovitellin-phosvitin complex; beta-sheet shell regions **Superfamily:**Lipovitellin-phosvitin complex; beta-sheet shell regions **Family:**Lipovitellin-phosvitin complex; beta-sheet shell regions
31	d2qalj1	Alignment	not modelled	11.2	33	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S10 **Family:**Ribosomal protein S10
32	c1s1hJ_	Alignment	not modelled	11.2	24	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**40s ribosomal protein s20; **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, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
33	c2zkqj_	Alignment	not modelled	11.1	19	**PDB header:**ribosomal protein/rna **Chain:** J: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
34	c3bbnJ_	Alignment	not modelled	9.8	26	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**ribosomal protein s10; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
35	d2uubj1	Alignment	not modelled	9.6	29	**Fold:**Ferredoxin-like **Superfamily:**Ribosomal protein S10 **Family:**Ribosomal protein S10
36	d1i94m_	Alignment	not modelled	9.3	12	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
37	c3iz6J_	Alignment	not modelled	9.2	19	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**40s ribosomal protein s20 (s10p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
38	d1ny711	Alignment	not modelled	8.9	30	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
39	d2hfha_	Alignment	not modelled	8.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
40	c2k53A_	Alignment	not modelled	8.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a3dk08 protein; **PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
41	d2ftxb1	Alignment	not modelled	8.0	38	**Fold:**Kinetochore globular domain-like **Superfamily:**Kinetochore globular domain **Family:**Spc24-like
42	d2asba2	Alignment	not modelled	7.5	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
43	c1hh2P_	Alignment	not modelled	7.4	24	**PDB header:**transcription regulation **Chain:** P: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima
44	c1l2fA_	Alignment	not modelled	7.3	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n utilization substance protein a; **PDBTitle:** crystal structure of nusa from thermotoga maritima: a2 structure-based role of the n-terminal domain
45	c3mtuE_	Alignment	not modelled	7.1	32	**PDB header:**contractile protein **Chain:** E: **PDB Molecule:**head morphogenesis protein, tropomyosin alpha-1 chain; **PDBTitle:** structure of the tropomyosin overlap complex from chicken smooth2 muscle
46	d2d9ra1	Alignment	not modelled	7.1	20	**Fold:**Double-split beta-barrel **Superfamily:**AF2212/PG0164-like **Family:**PG0164-like
47	d1k1sa1	Alignment	not modelled	7.0	24	**Fold:**Lesion bypass DNA polymerase (Y-family), little finger domain **Superfamily:**Lesion bypass DNA polymerase (Y-family), little finger domain **Family:**Lesion bypass DNA polymerase (Y-family), little finger domain
48	c2cazB_	Alignment	not modelled	6.8	25	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein **PDBTitle:** escrt-i core
49	d2cazb1	Alignment	not modelled	6.8	25	**Fold:**Long alpha-hairpin **Superfamily:**Endosomal sorting complex assembly domain **Family:**VPS28 N-terminal domain
50	c2khvA_	Alignment	not modelled	6.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage integrase; **PDBTitle:** solution nmr structure of protein nmul_a0922 from2 nitrosospira multiformis. northeast structural genomics3 consortium target nmr38b.
51	d1pgl11	Alignment	not modelled	6.3	23	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
52	d2j01c1	Alignment	not modelled	6.2	36	**Fold:**Ribosomal protein L1 **Superfamily:**Ribosomal protein L1 **Family:**Ribosomal protein L1
53	c4a18U_	Alignment	not modelled	5.7	44	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**rpl13; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with

						initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
54	c2vohB_	Alignment	not modelled	5.7	25	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bcl-2 homologous antagonist/killer; **PDBTitle:** structure of mouse a1 bound to the bak bh3-domain
55	d1iwga6	Alignment	not modelled	5.7	16	**Fold:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Superfamily:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains **Family:**Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
56	c2a03A_	Alignment	not modelled	5.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fe-superoxide dismutase homolog; **PDBTitle:** superoxide dismutase protein from plasmodium berghei
57	d1vqod1	Alignment	not modelled	5.4	30	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**Ribosomal protein L5
58	d1k1ga_	Alignment	not modelled	5.3	19	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)