
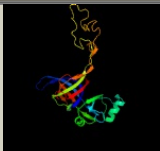

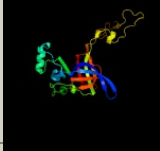

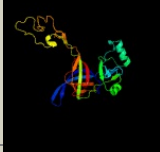

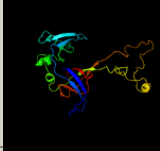









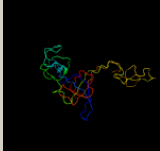

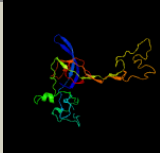




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0701_(rplC)_800812_801465
Date	Fri Jul 26 01:50:27 BST 2019
Unique Job ID	7913027477ab57a3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5o60D_	Alignment 		100.0	88	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l3; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
2	c1vw3C_	Alignment 		100.0	41	PDB header: ribosome Chain: C: PDB Molecule: 54s ribosomal protein l9, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
3	c4v19E_	Alignment 		100.0	30	PDB header: ribosome Chain: E: PDB Molecule: mitoribosomal protein ul3m, mrpl3; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
4	d2gycb1	Alignment 		100.0	51	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Ribosomal protein L3
5	c3j3vD_	Alignment 		100.0	53	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l3; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
6	c4wfbB_	Alignment 		100.0	52	PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein l3; PDBTitle: the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with bc-3205
7	d2zjrb1	Alignment 		100.0	53	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Ribosomal protein L3
8	c5mlcE_	Alignment 		100.0	43	PDB header: ribosome Chain: E: PDB Molecule: 50s ribosomal protein l3, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
9	c2ftcC_	Alignment 		100.0	33	PDB header: ribosome Chain: C: PDB Molecule: mitochondrial 39s ribosomal protein l3; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
10	d2j01e1	Alignment 		100.0	56	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Ribosomal protein L3
11	d1vqob1	Alignment 		100.0	35	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Ribosomal protein L3

12	c3jywC_	Alignment		100.0	27	PDB header: ribosome Chain: C: PDB Molecule: 60s ribosomal protein I3; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
13	c3j21C_	Alignment		100.0	30	PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein I3p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
14	c3u5iB_	Alignment		100.0	27	PDB header: ribosome Chain: B: PDB Molecule: 60s ribosomal protein I3; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome b
15	c1s1iC_	Alignment		100.0	27	PDB header: ribosome Chain: C: PDB Molecule: 60s ribosomal protein I3; 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.
16	c3iz5C_	Alignment		100.0	26	PDB header: ribosome Chain: C: PDB Molecule: 60s ribosomal protein I3 (I3p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
17	c4a1aB_	Alignment		100.0	27	PDB header: ribosome Chain: B: PDB Molecule: ribosomal protein I3; 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 3.
18	c3j39B_	Alignment		100.0	24	PDB header: ribosome Chain: B: PDB Molecule: 60s ribosomal protein I3; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
19	c2zkrb_	Alignment		100.0	26	PDB header: ribosomal protein/rna Chain: B: PDB Molecule: rna expansion segment es4; 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
20	c3zf7f_	Alignment		100.0	25	PDB header: ribosome Chain: F: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
21	c5ancA_	Alignment	not modelled	100.0	26	PDB header: translation Chain: A: PDB Molecule: 60s ribosomal protein I3; PDBTitle: mechanism of eif6 release from the nascent 60s ribosomal subunit
22	c3bboF_	Alignment	not modelled	100.0	42	PDB header: ribosome Chain: F: PDB Molecule: ribosomal protein I3; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
23	d1qfja1	Alignment	not modelled	33.0	18	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
24	c1a8pA_	Alignment	not modelled	25.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nahp\;ferredoxin oxidoreductase; PDBTitle: ferredoxin reductase from azotobacter vinelandii
25	c3j21R_	Alignment	not modelled	23.6	33	PDB header: ribosome Chain: R: PDB Molecule: 50s ribosomal protein I21e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
26	d1vqqo1	Alignment	not modelled	22.7	44	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
27	c1a3qA_	Alignment	not modelled	20.0	15	PDB header: transcription/dna Chain: A: PDB Molecule: protein (nuclear factor kappa-b p52); PDBTitle: human nf-kappa-b p52 bound to dna
28	c4p6vF_	Alignment	not modelled	19.6	28	PDB header: oxidoreductase Chain: F: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit f; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae PDB header: ribosomal protein/rna

29	c2zkrq_	Alignment	not modelled	18.9	33	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
30	d1fdra1	Alignment	not modelled	18.2	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
31	c2bruC_	Alignment	not modelled	17.7	50	PDB header: oxidoreductase Chain: C: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
32	d1d4oa_	Alignment	not modelled	16.7	50	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
33	c2I55A_	Alignment	not modelled	16.3	8	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
34	d1pnoa_	Alignment	not modelled	15.9	67	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Transhydrogenase domain III (dIII)
35	c1pt9B_	Alignment	not modelled	15.5	50	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase, mitochondrial; PDBTitle: crystal structure analysis of the dii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
36	c3zf7U_	Alignment	not modelled	13.8	67	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein I21e, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
37	d1r4ya_	Alignment	not modelled	13.8	23	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Ribotoxin
38	d1de3a_	Alignment	not modelled	13.7	24	Fold: Microbial ribonucleases Superfamily: Microbial ribonucleases Family: Ribotoxin
39	c3j3bT_	Alignment	not modelled	13.4	40	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein I21; PDBTitle: structure of the human 60s ribosomal proteins
40	d1qcsa1	Alignment	not modelled	13.3	19	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Cdc48 N-terminal domain-like
41	c1sliQ_	Alignment	not modelled	13.2	33	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein I21-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.
42	c5ogxA_	Alignment	not modelled	13.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 reductase; PDBTitle: crystal structure of amycolatopsis cytochrome p450 reductase gcob.
43	c3izcU_	Alignment	not modelled	12.9	30	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein rpl21 (I21e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
44	c4a1aP_	Alignment	not modelled	12.8	40	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein I21; 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.
45	c1le5E_	Alignment	not modelled	12.5	26	PDB header: transcription/dna Chain: E: PDB Molecule: nuclear factor nf-kappa-b p65 subunit; PDBTitle: crystal structure of a nf-kb heterodimer bound to an ifnb-kb
46	d2i6va1	Alignment	not modelled	12.4	20	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: EpsC C-terminal domain-like
47	c3iz5U_	Alignment	not modelled	12.4	40	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein I21 (I21e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
48	c4o9uB_	Alignment	not modelled	12.3	67	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
49	c4arpB_	Alignment	not modelled	12.2	29	PDB header: hydrolase Chain: B: PDB Molecule: pesticin; PDBTitle: structure of the inactive pesticin e178a mutant
50	c3a98A_	Alignment	not modelled	12.1	18	PDB header: signaling protein Chain: A: PDB Molecule: dedicator of cytokinesis protein 2; PDBTitle: crystal structure of the complex of the interacting regions of dock22 and elmo1
51	c2hdeA_	Alignment	not modelled	12.1	40	PDB header: transcription Chain: A: PDB Molecule: histone deacetylase complex subunit sap18; PDBTitle: solution structure of human sap18
52	c4bg7A_	Alignment	not modelled	12.0	24	PDB header: replication Chain: A: PDB Molecule: putative transcriptional coactivator p15; PDBTitle: bacteriophage t5 homolog of the eukaryotic transcription coactivator2 pc4 implicated in recombination-dependent dna replication
53	c1qfjD_	Alignment	not modelled	11.3	18	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (flavin reductase); PDBTitle: crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli

54	d2do3a1	Alignment	not modelled	11.3	29	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
55	d1a8pa1	Alignment	not modelled	11.3	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
56	c4wqmA_	Alignment	not modelled	11.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene-4-monooxygenase electron transfer component; PDBTitle: structure of the toluene 4-monooxygenase nadh oxidoreductase t4mof,2 k270s k271s variant
57	c6i52B_	Alignment	not modelled	11.2	33	PDB header: dna binding protein Chain: B: PDB Molecule: replication factor a protein 2; PDBTitle: yeast rpa bound to ssdna
58	c4ytbB_	Alignment	not modelled	11.0	33	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
59	c1nfiC_	Alignment	not modelled	10.8	26	PDB header: complex (transcription reg/ank repeat) Chain: C: PDB Molecule: nf-kappa-b p65; PDBTitle: i-kappa-b-alpha/nf-kappa-b complex
60	c1zeqX_	Alignment	not modelled	10.8	8	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
61	d1ikna2	Alignment	not modelled	10.6	27	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: Rel/Dorsal transcription factors, DNA-binding domain
62	c1yb2A_	Alignment	not modelled	10.4	0	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0852; PDBTitle: structure of a putative methyltransferase from thermoplasma2 acidophilum.
63	d1yb2a1	Alignment	not modelled	10.4	0	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like
64	c5ccbB_	Alignment	not modelled	10.4	31	PDB header: transferase/rna Chain: B: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase non-catalytic PDBTitle: crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah
65	c1zuyB_	Alignment	not modelled	10.3	12	PDB header: contractile protein Chain: B: PDB Molecule: myosin-5 isoform; PDBTitle: high-resolution structure of yeast myo5 sh3 domain
66	c5o60V_	Alignment	not modelled	10.0	19	PDB header: ribosome Chain: V: PDB Molecule: 50s ribosomal protein l24; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
67	d1uwfa1	Alignment	not modelled	9.7	13	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
68	c4b4dA_	Alignment	not modelled	9.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-nadp reductase; PDBTitle: crystal structure of fad-containing ferredoxin-nadp reductase from2 xanthomonas axonopodis pv. citri
69	d1vqot1	Alignment	not modelled	9.4	25	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
70	c4z89J_	Alignment	not modelled	9.3	21	PDB header: rim-binding protein Chain: J: PDB Molecule: rim-binding protein, isoform f; PDBTitle: sh3-ii of drosophila rim-binding protein bound to a cacophony derived2 peptide
71	c1v1cA_	Alignment	not modelled	8.9	35	PDB header: sh3-domain Chain: A: PDB Molecule: obscurin; PDBTitle: solution structure of the sh3 domain of obscurin
72	c2kjpA_	Alignment	not modelled	8.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ylbj; PDBTitle: solution structure of protein ylbj (bsu15050) from bacillus2 subtilis, northeast structural genomics consortium target3 sr713a
73	d1opka1	Alignment	not modelled	8.6	12	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
74	c5mmiV_	Alignment	not modelled	8.6	25	PDB header: ribosome Chain: V: PDB Molecule: plastid ribosomal protein ul24c; PDBTitle: structure of the large subunit of the chloroplast ribosome
75	c5ergA_	Alignment	not modelled	8.6	19	PDB header: transferase Chain: A: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase non-catalytic PDBTitle: crystal structure of the two-subunit trna m1a58 methyltransferase2 trm6-trm61 in complex with sam
76	d2zjrr1	Alignment	not modelled	8.5	13	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
77	c3iz5Y_	Alignment	not modelled	8.5	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
78	c3j21U_	Alignment	not modelled	8.2	25	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)
						Fold: mRNA decapping enzyme DcpS N-terminal domain

79	d1vira2	Alignment	not modelled	8.2	16	Superfamily: mRNA decapping enzyme Dcp5 N-terminal domain Family: mRNA decapping enzyme Dcp5 N-terminal domain
80	c1cqxB	Alignment	not modelled	8.1	13	PDB header: lipid binding protein Chain: B: PDB Molecule: flavo-hemoglobin; PDBTitle: crystal structure of the flavo-hemoglobin from <i>Alcaligenes eutrophus</i> at 2.175 Å resolution
81	c2i0nA	Alignment	not modelled	8.1	9	PDB header: structural protein Chain: A: PDB Molecule: class VII unconventional myosin; PDBTitle: structure of dictyostelium discoideum myosin VII SH3 domain2 with adjacent proline-rich region
82	c4a1cS	Alignment	not modelled	8.0	13	PDB header: ribosome Chain: S: PDB Molecule: rpl26; PDBTitle: <i>Thermophila</i> 60S ribosomal subunit in complex with initiation factor 6. This file contains 5S rRNA, 3.5S rRNA and proteins of molecule 4.
83	c4tu3X	Alignment	not modelled	8.0	32	PDB header: hydrolase/protein transport Chain: X: PDB Molecule: phosphoinositide phosphatase Sac1; PDBTitle: crystal structure of yeast Sac1/Vps74 complex
84	c1qgyA	Alignment	not modelled	7.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin-NADP+ reductase; PDBTitle: ferredoxin:NADP+ reductase mutant with Lys 75 replaced by Glu (K75E)
85	c3iuwA	Alignment	not modelled	7.5	38	PDB header: RNA binding protein Chain: A: PDB Molecule: activating signal co-integrator; PDBTitle: crystal structure of activating signal co-integrator (np_814290.1) from <i>Enterococcus faecalis</i> V583 at 1.58 Å resolution
86	c2lj0A	Alignment	not modelled	7.2	29	PDB header: signaling protein Chain: A: PDB Molecule: sorbin and SH3 domain-containing protein 1; PDBTitle: the third SH3 domain of R85fl
87	d1ra0a1	Alignment	not modelled	7.1	26	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Cytosine deaminase
88	c3x2dM	Alignment	not modelled	7.1	50	PDB header: viral protein/immune system Chain: M: PDB Molecule: envelope glycoprotein gp1; PDBTitle: crystal structure of Marburg virus gp in complex with the human2 survivor antibody Mr78
89	d1sm4a1	Alignment	not modelled	6.9	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
90	c1vpzB	Alignment	not modelled	6.9	36	PDB header: RNA binding protein Chain: B: PDB Molecule: carbon storage regulator homolog; PDBTitle: crystal structure of a putative carbon storage regulator protein2 (CSRA, PA0905) from <i>Pseudomonas aeruginosa</i> at 2.05 Å resolution
91	c4pogC	Alignment	not modelled	6.8	33	PDB header: replication, DNA binding protein/DNA Chain: C: PDB Molecule: cell division control protein 21; PDBTitle: MCM-SSDNA co-crystal structure
92	c5o0xA	Alignment	not modelled	6.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative ferric reductase; PDBTitle: crystal structure of dehydrogenase domain of <i>Cylindrospermum stagnale</i> 2 NADPH-oxidase 5 (NOX5)
93	c2rqrA	Alignment	not modelled	6.7	17	PDB header: protein binding Chain: A: PDB Molecule: engulfment and cell motility protein 1, linker, dedicatior PDBTitle: the solution structure of human Dock2 SH3 domain - Elmo1 peptide2 chimera complex
94	c4y6tD	Alignment	not modelled	6.7	23	PDB header: structural protein Chain: D: PDB Molecule: coat protein; PDBTitle: structure of tobacco streak virus coat protein dimer at 2.4 Å resolution
95	c3s88I	Alignment	not modelled	6.7	63	PDB header: immune system/viral protein Chain: I: PDB Molecule: envelope glycoprotein; PDBTitle: crystal structure of Sudan ebolavirus glycoprotein (strain Gulu) bound2 to 16f6
96	c1krhA	Alignment	not modelled	6.6	32	PDB header: oxidoreductase Chain: A: PDB Molecule: benzoate 1,2-dioxygenase reductase; PDBTitle: X-ray structure of benzoate dioxygenase reductase
97	c2v6cC	Alignment	not modelled	6.4	33	PDB header: DNA binding protein Chain: C: PDB Molecule: minichromosome maintenance protein MCM; PDBTitle: structural analysis of the <i>Sulfolobus solfataricus</i> MCM2 protein N-terminal domain
98	c4g1bB	Alignment	not modelled	6.3	30	PDB header: oxidoreductase Chain: B: PDB Molecule: flavo-hemoglobin; PDBTitle: X-ray structure of yeast flavo-hemoglobin in complex with econazole
99	c5j21C	Alignment	not modelled	6.2	20	PDB header: hydrolase Chain: C: PDB Molecule: bifunctional oligoribonuclease and PAP phosphatase NRNA; PDBTitle: structure of <i>Bacillus nanornase</i> A (wt)