










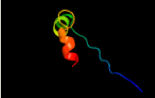
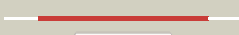

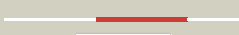
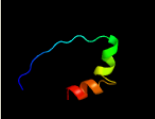





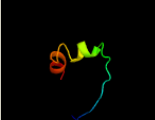


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2908c (-)_3216915_3217157
Date	Thu Aug 8 16:20:06 BST 2019
Unique Job ID	2903a8fc791b6ddf

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pt7G_	 Alignment		97.5	16	PDB header: hydrolase/protein binding Chain: G; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of cag virb11 (hp0525) and an inhibitory protein2 (hp1451)
2	c3gkuB_	 Alignment		97.4	21	PDB header: rna binding protein Chain: B; PDB Molecule: probable rna-binding protein; PDBTitle: crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
3	c2cy1A_	 Alignment		97.3	21	PDB header: transcription Chain: A; PDB Molecule: nusa protein homolog; PDBTitle: crystal structure of ape1850
4	c2jzxA_	 Alignment		96.2	23	PDB header: rna binding protein Chain: A; PDB Molecule: poly(rc)-binding protein 2; PDBTitle: pcbp2 kh1-kh2 domains
5	c2hh2A_	 Alignment		96.1	31	PDB header: rna binding protein Chain: A; PDB Molecule: kh-type splicing regulatory protein; PDBTitle: solution structure of the fourth kh domain of ksrp
6	d1x4ma1	 Alignment		96.0	28	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)
7	d1wh9a_	 Alignment		95.8	15	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
8	c2anrA_	 Alignment		95.8	26	PDB header: rna-binding protein/rna Chain: A; PDB Molecule: neuro-oncological ventral antigen 1; PDBTitle: crystal structure (ii) of nova-1 kh1/kh2 domain tandem with 25nt rna2 hairpin
9	d2axya1	 Alignment		95.7	25	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)
10	d1j4wa2	 Alignment		95.6	26	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)
11	d1we8a_	 Alignment		95.6	26	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)

12	c1ztgD_	Alignment		95.5	25	PDB header: dna, rna binding protein/dna Chain: D: PDB Molecule: poly(rc)-binding protein 1; PDBTitle: human alpha polyc binding protein kh1
13	d1wvna1	Alignment		95.5	29	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)
14	d1j4wa1	Alignment		95.5	23	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)
15	c2jvza_	Alignment		95.4	34	PDB header: splicing Chain: A: PDB Molecule: far upstream element-binding protein 2; PDBTitle: solution nmr structure of the second and third kh domains2 of ksrp
16	d1khma_	Alignment		95.4	25	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)
17	c2qndA_	Alignment		95.3	27	PDB header: rna binding protein Chain: A: PDB Molecule: fmr1 protein; PDBTitle: crystal structure of the kh1-kh2 domains from human fragile x mental2 retardation protein
18	d1ec6a_	Alignment		95.3	30	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)
19	d1zzka1	Alignment		95.2	29	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)
20	c2hh3A_	Alignment		95.0	31	PDB header: rna binding protein Chain: A: PDB Molecule: kh-type splicing regulatory protein; PDBTitle: solution structure of the third kh domain of ksrp
21	c4b8tA_	Alignment	not modelled	94.8	31	PDB header: transcription/rna Chain: A: PDB Molecule: kh-type splicing regulatory protein; PDBTitle: rna binding protein solution structure of the third kh2 domain of ksrp in complex with the g-rich target sequence.
22	d1x4na1	Alignment	not modelled	94.8	30	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)
23	d2asba3	Alignment	not modelled	94.7	22	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
24	d1viga_	Alignment	not modelled	94.7	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)
25	d2ba0a3	Alignment	not modelled	94.7	27	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)
26	d1dtja_	Alignment	not modelled	94.7	29	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)
27	d1tuaa1	Alignment	not modelled	94.6	35	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)
28	c1j4wA_	Alignment	not modelled	94.6	23	PDB header: transcription/dna Chain: A: PDB Molecule: fuse binding protein; PDBTitle: complex of the kh3 and kh4 domains of fbp with a2 single stranded 29mer dna oligonucleotide from the fuse3 element of the c-myc oncogene
						Fold: Alpha-lytic protease prodomain-like

29	d1hh2p3	Alignment	not modelled	94.6	27	Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
30	c2dgrA	Alignment	not modelled	94.5	28	PDB header: rna binding protein Chain: A: PDB Molecule: ring finger and kh domain-containing protein 1; PDBTitle: solution structure of the second kh domain in ring finger2 and kh domain containing protein 1
31	d2qalc1	Alignment	not modelled	94.5	22	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
32	c2n8IA	Alignment	not modelled	94.4	26	PDB header: rna binding protein/rna Chain: A: PDB Molecule: insulin-like growth factor 2 mrna-binding protein 1; PDBTitle: zipcode-binding-protein-1 kh3kh4(dd) domains in complex with the kh32 rna target
33	d2z0sa2	Alignment	not modelled	94.4	27	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)
34	c3krmB	Alignment	not modelled	94.4	25	PDB header: rna binding protein Chain: B: PDB Molecule: insulin-like growth factor 2 mrna-binding protein 1; PDBTitle: imp1 kh34
35	d1dt4a	Alignment	not modelled	94.2	29	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)
36	d2ctla1	Alignment	not modelled	94.1	37	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)
37	d2ctma1	Alignment	not modelled	94.0	13	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)
38	d2ctea1	Alignment	not modelled	94.0	20	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)
39	c6qeyA	Alignment	not modelled	93.9	19	PDB header: rna binding protein Chain: A: PDB Molecule: insulin-like growth factor 2 mrna-binding protein 1; PDBTitle: imp1 kh1 and kh2 domains create a structural platform with unique rna2 recognition and re-modelling properties
40	d2ctka1	Alignment	not modelled	93.5	32	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)
41	c3n89B	Alignment	not modelled	93.5	6	PDB header: cell cycle Chain: B: PDB Molecule: defective in germ line development protein 3, isoform a; PDBTitle: kh domains
42	c5wwwA	Alignment	not modelled	93.3	29	PDB header: rna binding protein/rna Chain: A: PDB Molecule: rna-binding e3 ubiquitin-protein ligase mex3c; PDBTitle: crystal structure of the kh1 domain of human rna-binding e3 ubiquitin-2 protein ligase mex-3c complex with rna
43	d2ctja1	Alignment	not modelled	93.3	23	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)
44	c6emlp	Alignment	not modelled	92.8	23	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein s0-a; PDBTitle: cryo-em structure of a late pre-40s ribosomal subunit from2 saccharomyces cerevisiae
45	c3zeyX	Alignment	not modelled	92.8	14	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s3, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
46	d2ctfa1	Alignment	not modelled	92.7	13	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)
47	d1tuaa2	Alignment	not modelled	92.7	33	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)
48	c1tuaA	Alignment	not modelled	92.6	35	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ape0754; PDBTitle: 1.5 a crystal structure of a protein of unknown function2 ape0754 from aeropyrum pernix
49	c2asbA	Alignment	not modelled	92.3	22	PDB header: transcription/rna Chain: A: PDB Molecule: transcription elongation protein nusa; PDBTitle: structure of a mycobacterium tuberculosis nusa-rna complex
50	c6qh2A	Alignment	not modelled	92.1	33	PDB header: signaling protein Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: solution nmr ensemble for a chimeric kh-s1 domain construct of2 exosomal polynucleotide phosphrylase at 298k compiled using the3 comand method
51	c2xznC	Alignment	not modelled	91.4	11	PDB header: ribosome Chain: C: PDB Molecule: kh domain containing protein; 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 2
52	d2uubc1	Alignment	not modelled	91.3	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)
53	d2fmra	Alignment	not modelled	91.1	27	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)
54	c1hh2P	Alignment	not modelled	89.8	27	PDB header: transcription regulation Chain: P: PDB Molecule: n utilization substance protein a;

						PDBTitle: crystal structure of nusa from thermotoga maritima
55	c1k0rB_	Alignment	not modelled	89.7	22	PDB header: transcription Chain: B: PDB Molecule: nusa; PDBTitle: crystal structure of mycobacterium tuberculosis nusa
56	d1egaa2	Alignment	not modelled	89.6	13	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
57	c2zkqc_	Alignment	not modelled	89.3	10	PDB header: ribosomal protein/rna Chain: C: PDB Molecule: rna expansion segment es4; PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
58	c6g18x_	Alignment	not modelled	88.9	28	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s23; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state c
59	c2e3uA_	Alignment	not modelled	87.8	24	PDB header: rna binding protein Chain: A: PDB Molecule: hypothetical protein ph1566; PDBTitle: crystal structure analysis of dim2p from pyrococcus horikoshii ot3
60	c5xyiD_	Alignment	not modelled	87.6	5	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s3, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
61	c1l2fA_	Alignment	not modelled	87.5	27	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
62	c4nbqB_	Alignment	not modelled	86.9	27	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: structure of the polynucleotide phosphorylase (cbu_0852) from coxiella2 burnetii
63	c4am3A_	Alignment	not modelled	86.0	23	PDB header: transferase/rna Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rna
64	c1w3f3A_	Alignment	not modelled	84.9	24	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
65	d2cpqa1	Alignment	not modelled	84.5	31	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)
66	c4aimA_	Alignment	not modelled	84.0	23	PDB header: transferase/peptide Chain: A: PDB Molecule: polyribonucleotide nucleotidyltransferase; PDBTitle: crystal structure of c. crescentus pnpase bound to rnae2 recognition peptide
67	c3u1kB_	Alignment	not modelled	83.9	27	PDB header: transferase Chain: B: PDB Molecule: polyribonucleotide nucleotidyltransferase 1, mitochondrial; PDBTitle: crystal structure of human pnpase
68	c3j20C_	Alignment	not modelled	82.9	20	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
69	c6flqF_	Alignment	not modelled	82.3	21	PDB header: transcription Chain: F: PDB Molecule: transcription termination/antitermination protein nusa; PDBTitle: cryoem structure of e.coli rna polymerase paused elongation complex2 bound to nusa
70	c1s1hC_	Alignment	not modelled	81.9	14	PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein s3; 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, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
71	d1wf3a2	Alignment	not modelled	78.1	21	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
72	d2je6i3	Alignment	not modelled	77.3	23	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)
73	c3ievA_	Alignment	not modelled	75.1	19	PDB header: nucleotide binding protein/rna Chain: A: PDB Molecule: gtp-binding protein era; PDBTitle: crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna
74	c4mntA_	Alignment	not modelled	73.5	23	PDB header: transcription regulator Chain: A: PDB Molecule: transcription termination factor nusa; PDBTitle: crystal structure of transcription termination factor nusa from2 planctomyces limnophilus dsm 3776
75	c4qmfB_	Alignment	not modelled	70.9	33	PDB header: rna binding protein Chain: B: PDB Molecule: krr1 small subunit processome component; PDBTitle: structure of the krr1 and faf1 complex from saccharomyces cerevisiae
76	c1egaB_	Alignment	not modelled	64.8	13	PDB header: hydrolase Chain: B: PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era
77	c3izbB_	Alignment	not modelled	63.9	20	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein rps3 (s3p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
78	c2yqrA_	Alignment	not modelled	61.2	24	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0907 protein; PDBTitle: solution structure of the kh domain in kiaa0907 protein
						PDB header: transcription

79	c5lm7A_	Alignment	not modelled	60.9	17	Chain: A: PDB Molecule: transcription termination/antitermination protein nusA; PDBTitle: crystal structure of the lambda n-nus factor complex
80	c5o5jC_	Alignment	not modelled	55.4	21	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
81	c4jvyA_	Alignment	not modelled	46.4	31	PDB header: rna binding protein Chain: A: PDB Molecule: female germline-specific tumor suppressor gld-1; PDBTitle: structure of the star (signal transduction and activation of rna)2 domain of gld-1 bound to rna
82	c1pnxC_	Alignment	not modelled	45.5	28	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: crystal structure of the wild type ribosome from e. coli, 30s subunit2 of 70s ribosome. this file, 1pnx, contains only molecules of the 30s3 ribosomal subunit. the 50s subunit is in the pdb file 1pny.
83	d1k1ga_	Alignment	not modelled	40.7	25	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)
84	c3j00C_	Alignment	not modelled	40.2	20	PDB header: ribosome/ribosomal protein Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: structure of the ribosome-secye complex in the membrane environment
85	c5eltB_	Alignment	not modelled	32.2	21	PDB header: rna binding protein Chain: B: PDB Molecule: kh domain-containing, rna-binding, signal transduction- PDBTitle: structure of the qua1-kh domain of t-star in complex with uauu rna
86	c4pfsA_	Alignment	not modelled	31.3	32	PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
87	c5el3D_	Alignment	not modelled	31.1	21	PDB header: rna binding protein Chain: D: PDB Molecule: kh domain-containing, rna-binding, signal transduction- PDBTitle: structure of the kh domain of t-star
88	c4waaA_	Alignment	not modelled	28.1	29	PDB header: protein binding/rna Chain: A: PDB Molecule: branchpoint-bridging protein; PDBTitle: crystal structure of selenomethionine msl5 protein in complex with rna2 at 2.2 a
89	c2qbfC_	Alignment	not modelled	26.0	21	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: crystal structure of the bacterial ribosome from escherichia coli in2 complex with ribosome recycling factor (rrf). this file contains the3 30s subunit of the second 70s ribosome. the entire crystal structure4 contains two 70s ribosomes and is described in remark 400.
90	c4jvhA_	Alignment	not modelled	22.5	35	PDB header: rna binding protein Chain: A: PDB Molecule: protein quaking; PDBTitle: structure of the star domain of quaking protein in complex with rna
91	d1wzla1	Alignment	not modelled	18.4	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
92	c2gy9C_	Alignment	not modelled	16.2	29	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal subunit protein s3; PDBTitle: structure of the 30s subunit of a pre-translocational e. coli ribosome2 obtained by fitting atomic models for rna and protein components into3 cryo-em map emd-1056
93	d2bl5a1	Alignment	not modelled	14.9	35	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)
94	d1j0ha1	Alignment	not modelled	13.3	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
95	c2kxoA_	Alignment	not modelled	12.5	14	PDB header: cell cycle Chain: A: PDB Molecule: cell division topological specificity factor; PDBTitle: solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
96	c1hnwC_	Alignment	not modelled	12.5	34	PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3; PDBTitle: structure of the thermus thermophilus 30s ribosomal subunit2 in complex with tetracycline
97	c2lvA_	Alignment	not modelled	12.1	30	PDB header: lantibiotic-binding-protein Chain: A: PDB Molecule: spai; PDBTitle: nmr structure the lantibiotic immunity protein spai
98	c3tekA_	Alignment	not modelled	11.6	13	PDB header: dna binding protein Chain: A: PDB Molecule: thermodbp-single stranded dna binding protein; PDBTitle: thermodbp: a non-canonical single-stranded dna binding protein with a2 novel structure and mechanism
99	d2z0sa1	Alignment	not modelled	11.0	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like