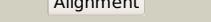
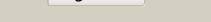
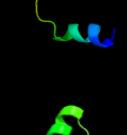
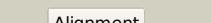
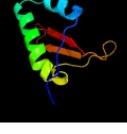


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD1955 (-) _2201750_2202103
Date	Mon Aug 5 13:25:05 BST 2019
Unique Job ID	79a1c2d35a68fb0e

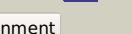
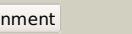
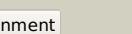
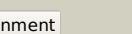
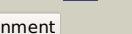
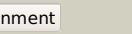
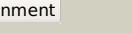
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ja9D_			86.4	19	PDB header: toxin Chain: D; PDB Molecule: toxin higb-2; PDBTitle: crystal structure of the higb2 toxin in complex with nb6
2	d1wmia1			50.5	10	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
3	d1ykha1			44.1	44	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: MED7 hinge region
4	c4dfcC_			34.3	28	PDB header: hydrolase/dna binding protein Chain: C; PDB Molecule: transcription-repair-coupling factor; PDBTitle: core uvra/trcf complex
5	c5u0pG_			32.0	44	PDB header: transcription Chain: G; PDB Molecule: mediator complex subunit 7; PDBTitle: cryo-em structure of the transcriptional mediator
6	c5svaU_			30.8	44	PDB header: transcription, transferase/dna Chain: U; PDB Molecule: mediator of rna polymerase ii transcription subunit 7; PDBTitle: mediator-rna polymerase ii pre-initiation complex
7	d1iccc_			30.6	23	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
8	c3bpqD_			23.3	19	PDB header: toxin Chain: D; PDB Molecule: toxin rele3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
9	d1ueua_			21.5	29	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
10	c5v6fA_			20.3	38	PDB header: sugar binding protein Chain: A; PDB Molecule: hemolysin-related protein; PDBTitle: crystal structure of the second beta-prism domain of rbmc from v.2 cholerae bound to mannotriose
11	c3g5oC_			17.9	15	PDB header: toxin/antitoxin Chain: C; PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2(rv2865-2 2866) from mycobacterium tuberculosis

12	d1lj0a	Alignment		17.4	29	Fold: Cytochrome b5-like heme/steroid binding domain Superfamily: Cytochrome b5-like heme/steroid binding domain Family: Cytochrome b5
13	d2b2na1	Alignment		12.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
14	c3o44G	Alignment		11.9	50	PDB header: toxin Chain: G: PDB Molecule: hemolysin; PDBTitle: crystal structure of the vibrio cholerae cytolsin (hlyA) heptameric2 pore
15	c3ue9A	Alignment		11.8	32	PDB header: ligase Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of adenylosuccinate synthetase (ampsase) (pura) from2 burkholderia thailandensis
16	d2o3la1	Alignment		11.1	14	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
17	c6bs7A	Alignment		10.4	27	PDB header: ligase Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of adenylosuccinate synthetase from legionella2 pneumophila philadelphia 1
18	c4m0gB	Alignment		10.1	24	PDB header: ligase Chain: B: PDB Molecule: adenylosuccinate synthetase; PDBTitle: the crystal structure of an adenylosuccinate synthetase from bacillus2 anthracis str. ames ancestor.
19	c2ybfB	Alignment		9.9	56	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase rad18; PDBTitle: complex of rad18 (rad6 binding domain) with rad6b
20	c2kheA	Alignment		9.6	20	PDB header: hydrolase Chain: A: PDB Molecule: toxin-like protein; PDBTitle: solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
21	c3f8tA	Alignment	not modelled	8.8	26	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase involved in replication control, cdc46/mcm PDBTitle: crystal structure analysis of a full-length mcm homolog from2 methanopyrus kandleri
22	d1qf5a	Alignment	not modelled	8.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
23	c4rt0B	Alignment	not modelled	8.6	43	PDB header: protein binding Chain: B: PDB Molecule: alginate biosynthesis protein alg44; PDBTitle: structure of the alg44 pilz domain from pseudomonas aeruginosa pao1 in2 complex with c-di-gmp
24	c3hjhA	Alignment	not modelled	8.6	28	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair-coupling factor; PDBTitle: a rigid n-terminal clamp restrains the motor domains of the bacterial2 transcription-repair coupling factor
25	d1pbva5	Alignment	not modelled	8.5	23	Fold: Streptavidin-like Superfamily: Quinohemoprotein amine dehydrogenase A chain, domain 3 Family: Quinohemoprotein amine dehydrogenase A chain, domain 3
26	c2mdtA	Alignment	not modelled	8.5	53	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: a pilT n-terminus domain protein sso1118 from hyperthermophilic2 archaeon sulfolobus sulfataricus p2
27	c3fpnB	Alignment	not modelled	8.4	23	PDB header: dna binding protein Chain: B: PDB Molecule: geobacillus stearothermophilus uvrB interaction domain; PDBTitle: crystal structure of uvrA-uvrB interaction domains
28	d2eyqa4	Alignment	not modelled	8.4	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain

29	d1dj2a	Alignment	not modelled	8.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
30	c5nwvA	Alignment	not modelled	8.3	55	PDB header: viral protein Chain: A: PDB Molecule: scrfp-tag, gp41; PDBTitle: nmr assignment and structure of a peptide derived from the fusion2 peptide of hiv-1 gp41 in the presence of dodecylphosphocholine3 micelles
31	c2d7uA	Alignment	not modelled	8.2	22	PDB header: ligase Chain: A: PDB Molecule: adenylosuccinate synthetase; PDBTitle: crystal structure of hypothetical adenylosuccinate synthetase, ph04382 from pyrococcus horikoshii ot3
32	c4z8vA	Alignment	not modelled	7.8	31	PDB header: protein binding Chain: A: PDB Molecule: avrxx01-orf1; PDBTitle: crystal structure of avrxx01-orf1:-orf2 complex, native.
33	c2wewA	Alignment	not modelled	7.7	26	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein m; PDBTitle: crystal structure of human apom in complex with myristic2 acid
34	c1iweB	Alignment	not modelled	7.3	15	PDB header: ligase Chain: B: PDB Molecule: adenylosuccinate synthetase; PDBTitle: imp complex of the recombinant mouse-muscle adenylosuccinate synthetase
35	d1iwea	Alignment	not modelled	7.2	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
36	d1axxa	Alignment	not modelled	7.0	26	Fold: Cytochrome b5-like heme/stEROid binding domain Superfamily: Cytochrome b5-like heme/stEROid binding domain Family: Cytochrome b5
37	c4qcoU	Alignment	not modelled	6.8	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in the pre-2 attack state of peptide bond formation containing acylated tRNA-3 substrates in the a and p sites. this entry contains the 30s subunit4 of the second 70s ribosome in the asu.
38	c4qcwU	Alignment	not modelled	6.8	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in the pre-2 attack state of peptide bond formation containing short substrate-3 mimic cytidine-puromycin in the a site and acylated tRNA in the p4 site. this entry contains the 30s subunit of the second 70s ribosome5 in the asu.
39	c4nw0U	Alignment	not modelled	6.8	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of antibiotic ge82832 bound to 70s ribosome
40	c4qcqU	Alignment	not modelled	6.8	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in the post-catalysis state of peptide bond formation containing dipeptidyl-3 tRNA in the a site and deacylated tRNA in the p site. this entry4 contains the 50s subunit of the first 70s ribosome in the asu.
41	c3uxtU	Alignment	not modelled	6.8	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: the structure of thermorubin in complex with the 70s ribosome from thermus thermophilus. this file contains the 30s subunit of one 70s3 ribosome. the entire crystal structure contains two 70s ribosomes.'
42	c4rb7U	Alignment	not modelled	6.8	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in complex2 with amicoumacin, mrna and three deacylated trnas in the a, p and e3 sites
43	c4qcuU	Alignment	not modelled	6.8	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in the pre-2 attack state of peptide bond formation containing short substrate-3 mimic cytidine-puromycin in the a site and acylated tRNA in the p4 site. this entry contains the 30s subunit of the first 70s ribosome5 in the asu.
44	c4nvwU	Alignment	not modelled	6.8	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of antibiotic dityromycin bound to 70s ribosome
45	c4dhbU	Alignment	not modelled	6.8	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of yaej bound to the 70s ribosome
46	c4rb5U	Alignment	not modelled	6.8	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in complex2 with amicoumacin, mrna and three deacylated trnas in the a, p and e3 sites
47	c4nvuU	Alignment	not modelled	6.8	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of antibiotic dityromycin bound to 70s ribosome
48	c4qcmU	Alignment	not modelled	6.8	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in the pre-2 attack state of peptide bond formation containing acylated tRNA-3 substrates in the a and p sites. this entry contains the 30s subunit4 of the first 70s ribosome in the asu.
49	c4nvyU	Alignment	not modelled	6.8	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of antibiotic ge82832 bound to 70s ribosome

50	c4qcyU_	Alignment	not modelled	6.8	43	ribosome in the pre-2 attack state of peptide bond formation containing short substrate-3 mimic cytidine-cytidine-puromycin in the a site and acylated trna in4 the p site. this entry contains the 30s subunit of the first 70s5 ribosome in the asu. PDB header: ribosome/inhibitor Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of yfia bound to the 70s ribosome. this pdb entry2 contains coordinates for the 30s subunit with bound yfia of the 1st3 ribosome in the asu
51	c3v2cU_	Alignment	not modelled	6.8	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in the2 post-catalysis state of peptide bond formation containing dipeptidyl-3 trna in the a site and deacylated trna in the p site. this entry4 contains the 30s subunit of the second 70s ribosome in the asu.
52	c4qcsU_	Alignment	not modelled	6.8	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in the pre-2 attack state of peptide bond formation containing short substrate-3 mimic cytidine-cytidine-puromycin in the a site and acylated trna in4 the p site. this entry contains the 30s subunit of the second 70s5 ribosome in the asu.
53	c4qd0U_	Alignment	not modelled	6.8	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in the pre-2 attack state of peptide bond formation containing short substrate-3 mimic cytidine-cytidine-puromycin in the a site and acylated trna in4 the p site. this entry contains the 30s subunit of the second 70s5 ribosome in the asu.
54	c4rb9U_	Alignment	not modelled	6.7	43	 PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in complex2 with pactamycin (soaked), mrna and three deacylated trnas in the a, p3 and e sites
55	c4rbdU_	Alignment	not modelled	6.7	43	 PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in complex2 with pactamycin (co-crystallized), mrna and three deacylated trna in the p3 site
56	c4qjtu_	Alignment	not modelled	6.7	43	 PDB header: ribosome Chain: U: PDB Molecule: PDBTitle: crystal structure of elongation factor 4 (ef4/lepa) bound to the2 thermus thermophilus 70s ribosome, 30s subunit of the 70s ribosome
57	c4rbjU_	Alignment	not modelled	6.7	43	 PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in complex2 with negamycin, mrna and three deacylated trnas in the a, p and e3 sites
58	c4rbhU_	Alignment	not modelled	6.7	43	 PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in complex2 with negamycin, mrna and three deacylated trnas in the a, p and e3 sites
59	c4rbbu_	Alignment	not modelled	6.7	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 70s ribosome in complex2 with pactamycin (soaked), mrna and three deacylated trnas in the a, p3 and e sites
60	c4k0pU_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of thermus thermophilus 70s containing trnas and2 mrna stop codon with pseudouridine
61	c4lfcU_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein thx; PDBTitle: crystal structure of 30s ribosomal subunit from thermus thermophilus
62	c3d5cU_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
63	c4l6mU_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of blasticidin s bound to thermus thermophilus 70s2 ribosome. this file contains the 30s subunit, trna and mrna molecules3 from the second 70s ribosome.
64	c4l6ku_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of blasticidin s bound to thermus thermophilus 70s2 ribosome. this file contains the 30s subunit, trna and mrna molecules3 from the first 70s ribosome.
65	c1i96U_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the 30s ribosomal subunit from thermus2 thermophilus in complex with the translation initiation3 factor if3 (c-terminal domain)
66	c4k0IU_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of thermus thermophilus 70s in complex with trnas2 and mrna containing a pseudouridine in a stop codon
67	c1n33V_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of the thermus thermophilus 30s ribosomal subunit2 bound to codon and near-cognate transfer rna anticodon3 stem-loop mismatched at the second codon position at the a4 site with paromomycin
68	c2e5IV_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein thx; PDBTitle: a snapshot of the 30s ribosomal subunit capturing mrna via2 the shine-dalgarno interaction
69	c4kfhU_	Alignment	not modelled	6.6	43	 PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the 70s ribosome bound with the q253p mutant2 release factor rf2. 30s of the a subunit
						 PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein thx;

70	c6mknV		Alignment	not modelled	6.6	43	PDBTitle: structure of the thermus thermophilus 30s ribosomal subunit complexed2 with an inosine (i34) modified anticodon stem loop (asl) of3 escherichia coli transfer rna arginine 2 (trnaarg2) bound to an mrna4 with an cgu-codon in the a-site and paromomycin
71	c4k0ku		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus 30s ribosomal subunit2 complexed with a serine-asl and mrna containing a stop codon
72	c4kfku		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the 70s ribosome bound with the q253p mutant of2 release factor rf2. 30s of the b subunit
73	c3pyuU		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: domain 3 of crpv igr ires rna; PDBTitle: crystal structure of a complex containing domain 3 of crpv igr ires2 rna bound to the 70s ribosome. this file contains the 30s subunit of3 the second 70s ribosome.
74	c3pysU		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: domain 3 of crpv igr ires rna; PDBTitle: crystal structure of a complex containing domain 3 of crpv igr ires2 rna bound to the 70s ribosome. this file contains the 30s subunit of3 the first 70s ribosome.
75	c5lmrV		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of bacterial 30s-if1-if3-mrna-trna translation pre-2 initiation complex(state-2b)
76	c4ji0U		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein thx; PDBTitle: crystal structure of 30s ribosomal subunit from thermus thermophilus
77	c5lmuV		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of bacterial 30s-if3-mrna-trna translation pre-initiation2 complex, closed form (state-4)
78	c5iwaV		Alignment	not modelled	6.6	43	PDB header: translation Chain: V: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the 30s ribosomal subunit from thermus2 thermophilus in complex with the ge81112 peptide antibiotic
79	c4x64U		Alignment	not modelled	6.6	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of 30s ribosomal subunit from thermus thermophilus
80	c5br8U		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: ambient-temperature crystal structure of 30s ribosomal subunit from2 thermus thermophilus in complex with paromomycin
81	c3pynU		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of a complex containing domain 3 from the psiv igr2 rna bound to the 70s ribosome. this file contains the 30s3 subunit of the first 70s ribosome.
82	c5lmsV		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of bacterial 30s-if1-if3-mrna-trna translation pre-2 initiation complex(state-2c)
83	c2y16U		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: the crystal structure of ef-tu and g24a-trna-trp bound to a2 cognate codon on the 70s ribosome.
84	c5lmpV		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of bacterial 30s-if1-if3-mrna translation pre-initiation2 complex (state-1c)
85	c4dr7U		Alignment	not modelled	6.6	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus (hb8) 30s ribosomal2 subunit with codon, crystallographically disordered near-cognate3 transfer rna anticodon stem-loop mismatched at the second codon4 position, and streptomycin bound
86	c5wnrU		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of 30s ribosomal subunit from thermus thermophilus
87	c5wnsU		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of 30s ribosomal subunit from thermus thermophilus
88	c3kisu		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: PDBTitle: structure of rele nuclease bound to the 70s ribosome (precleavage2 state; part 3 of 4)
89	c4dr4U		Alignment	not modelled	6.6	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of the thermus thermophilus (hb8) 30s ribosomal2 subunit with codon, cognate transfer rna anticodon stem-loop and3 multiple copies of paromomycin molecules bound
90	c2wrnU		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: the crystal structure of the 70s ribosome bound to ef-tu2 and trna (part 1 of 4).
91	c2wrqU		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: the crystal structure of the 70s ribosome bound to ef-tu2 and trna (part 3 of 4).
92	c3kiqu		Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: PDBTitle: structure of rele nuclease bound to the 70s ribosome (precleavage2 state; part 1 of 4)
93	c2knnU		Alignment	not modelled	6.6	43	PDB header: ribosome/antibiotic Chain: U: PDB Molecule: 30s ribosomal protein thx;

93	c5nhiU_	Alignment	not modelled	6.6	43	PDBTitle: the structures of capreomycin bound to the 70s ribosome. this file2 contains the 30s subunit for molecule i PDB header: ribosome Chain: V: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structure of bacterial 30s-if1-if2-if3-mrna-trna translation pre-2 initiation complex(state-iii)
94	c5lmvV_	Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of 30s ribosomal subunit from thermus thermophilus
95	c5wnqU_	Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of 30s ribosomal subunit from thermus thermophilus
96	c3d5aU_	Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of one 70s ribosome. the entire crystal structure4 contains two 70s ribosomes as described in remark 400.
97	c3pyqU_	Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: crystal structure of a complex containing domain 3 from the psiv igr2 ires rna bound to the 70s ribosome. this file contains the 30s3 subunit of the second 70s ribosome.
98	c4kvbU_	Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: thermus thermophilus hb27 30s ribosomal subunit lacking ribosomal2 protein s17
99	c6casU_	Alignment	not modelled	6.6	43	PDB header: ribosome Chain: U: PDB Molecule: 30s ribosomal protein thx; PDBTitle: serial femtosecond x-ray crystal structure of 30s ribosomal subunit2 from thermus thermophilus in complex with n1ms