Phyre^2

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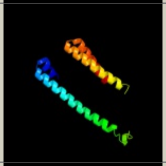
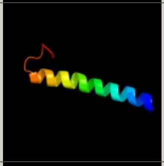
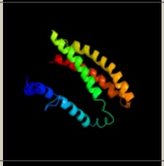
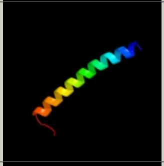
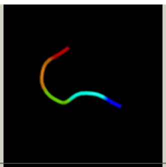
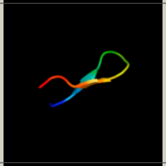
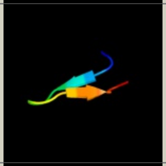
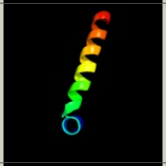
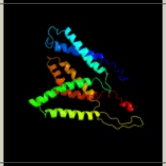
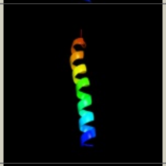
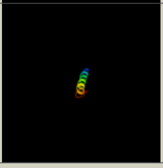
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mkuA_	Alignment		100.0	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multi antimicrobial extrusion protein (na(+)/drug **PDBTitle:** structure of a cation-bound multidrug and toxin compound extrusion2 (mate) transporter
2	d2r6gf2	Alignment		14.4	11	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
3	d1v54c_	Alignment		13.9	9	**Fold:**Cytochrome c oxidase subunit III-like **Superfamily:**Cytochrome c oxidase subunit III-like **Family:**Cytochrome c oxidase subunit III-like
4	d1u94a2	Alignment		11.9	29	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
5	c1wrgA_	Alignment		11.7	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain; **PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
6	c2yvxD_	Alignment		10.8	13	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
7	d1xp8a2	Alignment		10.5	14	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
8	d1ubea2	Alignment		10.4	43	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
9	d2yvxa3	Alignment		10.4	13	**Fold:**MgtE membrane domain-like **Superfamily:**MgtE membrane domain-like **Family:**MgtE membrane domain-like
10	d1lghb_	Alignment		10.3	8	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
11	d1mo6a2	Alignment		10.3	43	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain

12	d2a5yb1	Alignment		10.1	100	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CED-4 C-terminal domain-like
13	d1sg7a1	Alignment		10.0	8	**Fold:**ChaB-like **Superfamily:**ChaB-like **Family:**ChaB-like
14	c1sg7A_	Alignment		10.0	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cation transport regulator chab; **PDBTitle:** nmr solution structure of the putative cation transport2 regulator chab
15	c3ipdB_	Alignment		9.5	10	**PDB header:**exocytosis **Chain:** B: **PDB Molecule:**syntaxin-1a; **PDBTitle:** helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
16	d1jo5a_	Alignment		9.0	16	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
17	c2zqpY_	Alignment		8.8	10	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** crystal structure of secye translocon from thermus2 thermophilus
18	d2d5ba1	Alignment		8.7	15	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
19	d2r6gg1	Alignment		7.7	24	**Fold:**MetI-like **Superfamily:**MetI-like **Family:**MetI-like
20	c1m57H_	Alignment		7.4	24	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
21	c1b9uA_	Alignment	not modelled	7.3	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
22	c2k1aA_	Alignment	not modelled	7.2	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
23	c2l35A_	Alignment	not modelled	7.1	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dap12-nkg2c_tm; **PDBTitle:** structure of the dap12-nkg2c transmembrane heterotrimer
24	c1cdlG_	Alignment	not modelled	7.0	17	**PDB header:**calcium-binding protein **Chain:** G: **PDB Molecule:**calcium/calmodulin-dependent protein kinase type **PDBTitle:** target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
25	c2o5gB_	Alignment	not modelled	7.0	17	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**smooth muscle myosin light chain kinase peptide; **PDBTitle:** calmodulin-smooth muscle light chain kinase peptide complex
26	c2ntxB_	Alignment	not modelled	6.9	20	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**emb cab41934.1;
27	c1ygyA_	Alignment	not modelled	6.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
28	c1z65A_	Alignment	not modelled	6.9	63	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**prion-like protein doppel;

						PDBTitle: mouse doppel 1-30 peptide
29	d2hqxa1	Alignment	not modelled	6.8	30	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
30	c2hqxB_	Alignment	not modelled	6.8	30	**PDB header:**transcription **Chain:** B: **PDB Molecule:**p100 co-activator tudor domain; **PDBTitle:** crystal structure of human p100 tudor domain conserved2 region
31	d3dtub2	Alignment	not modelled	6.8	25	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
32	c3pnwX_	Alignment	not modelled	6.8	13	**PDB header:**protein binding/immune system **Chain:** X: **PDB Molecule:**tudor domain-containing protein 3; **PDBTitle:** crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab
33	c2eeyA_	Alignment	not modelled	6.7	22	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis; **PDBTitle:** structure of gk0241 protein from geobacillus kaustophilus
34	c2eqkA_	Alignment	not modelled	6.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tudor domain-containing protein 4; **PDBTitle:** solution structure of the tudor domain of tudor domain-2 containing protein 4
35	d1nkzb_	Alignment	not modelled	6.5	12	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
36	c2k9pA_	Alignment	not modelled	6.4	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pheromone alpha factor receptor; **PDBTitle:** structure of tm1_tm2 in lppg micelles
37	c2be6F_	Alignment	not modelled	6.4	11	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel alpha-1c subunit; **PDBTitle:** 2.0 a crystal structure of the cav1.2 iq domain-ca/cam complex
38	c1ql1A_	Alignment	not modelled	6.4	24	**PDB header:**virus **Chain:** A: **PDB Molecule:**pf1 bacteriophage coat protein b; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
39	d1u78a2	Alignment	not modelled	6.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
40	d1mhna_	Alignment	not modelled	6.2	18	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
41	d2hw4a1	Alignment	not modelled	6.2	17	**Fold:**PHP14-like **Superfamily:**PHP14-like **Family:**Janus/Ocnus
42	c3gg9C_	Alignment	not modelled	6.2	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase oxidoreductase protein; **PDBTitle:** crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
43	c2hw4A_	Alignment	not modelled	6.2	17	**PDB header:**structural genomics, hydrolase **Chain:** A: **PDB Molecule:**14 kda phosphohistidine phosphatase; **PDBTitle:** crystal structure of human phosphohistidine phosphatase
44	c2d9tA_	Alignment	not modelled	6.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tudor domain-containing protein 3; **PDBTitle:** solution structure of the tudor domain of tudor domain2 containing protein 3 from mouse
45	c3egjA_	Alignment	not modelled	6.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase; **PDBTitle:** n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae.
46	d1rqga1	Alignment	not modelled	6.0	13	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
47	d1uptb_	Alignment	not modelled	6.0	19	**Fold:**GRIP domain **Superfamily:**GRIP domain **Family:**GRIP domain
48	d1u61a_	Alignment	not modelled	5.9	19	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**RNase III catalytic domain-like
49	c1i97U_	Alignment	not modelled	5.9	33	**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 tetracycline
50	c2kvvA_	Alignment	not modelled	5.9	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative excisionase; **PDBTitle:** solution nmr of putative excisionase from klebsiella pneumoniae,2 northeast structural genomics consortium target target kpr49
51	c3ci9B_	Alignment	not modelled	5.8	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
52	c2b2aA_	Alignment	not modelled	5.8	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**telomerase reverse transcriptase; **PDBTitle:** crystal structure of the ten domain of the telomerase2 reverse transcriptase
						PDB header:transcription/rna

53	c1qfqB_	Alignment	not modelled	5.8	42	**Chain:** B: **PDB Molecule:**36-mer n-terminal peptide of the n protein; **PDBTitle:** bacteriophage lambda n-protein-nutboxb-rna complex
54	c2fynH_	Alignment	not modelled	5.8	19	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
55	c4a4fA_	Alignment	not modelled	5.7	33	**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 with2 symmetrically dimethylated arginine
56	c1g5vA_	Alignment	not modelled	5.7	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**survival motor neuron protein 1; **PDBTitle:** solution structure of the tudor domain of the human smn2 protein
57	d1eysh2	Alignment	not modelled	5.7	15	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
58	d1m56d_	Alignment	not modelled	5.6	11	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
59	c3mp7B_	Alignment	not modelled	5.6	18	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
60	d1ik0a_	Alignment	not modelled	5.6	21	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
61	c3s6n2_	Alignment	not modelled	5.6	8	**PDB header:**splicing **Chain:** 2: **PDB Molecule:**survival of motor neuron protein-interacting protein 1; **PDB Fragment:**gemin2-binding domain; **PDBTitle:** crystal structure of the gemin2-binding domain of smn, gemin2 in2 complex with smd1/d2/f/e/g from human
62	c3txsC_	Alignment	not modelled	5.6	21	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**terminase dna packaging enzyme small subunit; **PDBTitle:** crystal structure of phage 44rr small terminase gp16
63	d3b60a2	Alignment	not modelled	5.6	9	**Fold:**ABC transporter transmembrane region **Superfamily:**ABC transporter transmembrane region **Family:**ABC transporter transmembrane region
64	c2ow8v_	Alignment	not modelled	5.5	33	**PDB header:**ribosome **Chain:** V: **PDB Molecule:** **PDBTitle:** crystal structure of a 70s ribosome-trna complex reveals functional2 interactions and rearrangements. this file, 2ow8, contains the 30s3 ribosome subunit, two trna, and mrna molecules. 50s ribosome subunit4 is in the file 1vsa.
65	c2dbqA_	Alignment	not modelled	5.5	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
66	d2d9ta1	Alignment	not modelled	5.5	13	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
67	c3kf9B_	Alignment	not modelled	5.4	33	**PDB header:**cell cycle/calcium-binding protein **Chain:** B: **PDB Molecule:**myosin light chain kinase 2, skeletal/cardiac muscle; **PDBTitle:** crystal structure of the sdcen/skmlck complex
68	c2hydB_	Alignment	not modelled	5.4	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
69	c3bbo2_	Alignment	not modelled	5.4	15	**PDB header:**ribosome **Chain:** 2: **PDB Molecule:**ribosomal protein l32; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
70	d1d8ja_	Alignment	not modelled	5.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**The central core domain of TFIIE beta
71	c2yggA_	Alignment	not modelled	5.4	17	**PDB header:**metal binding protein/transport protein **Chain:** A: **PDB Molecule:**sodium/hydrogen exchanger 1; **PDBTitle:** complex of cambr and cam
72	c2uxbU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**ribosomal protein thx; **PDBTitle:** crystal structure of an extended trna anticodon stem loop2 in complex with its cognate mrna gggu in the context of3 the thermus thermophilus 30s subunit.
73	c2uuaU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 30s ribosomal subunit2 complexed with a valine-asl with cmo5u in position 343 bound to an mrna with a guc-codon in the a-site and4 paromomycin.
74	d2gu3a1	Alignment	not modelled	5.3	11	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**PepSY-like
75	c2j02U_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 3 of 4)3 this file contains the 30s subunit, mrna, a-, p- and4 e-site trnas and paromomycin for molecule ii.
76	c1hnwV_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 30s ribosomal subunit2 in complex with tetracycline
						PDB header:ribosome

77	c1j5eV_	Alignment	not modelled	5.3	33	**Chain:** V: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 30s ribosomal subunit
78	c2uxcU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**ribosomal protein thx; **PDBTitle:** crystal structure of an extended trna anticodon stem loop2 in complex with its cognate mrna ucgu in the context of3 the thermus thermophilus 30s subunit.
79	c3ficU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** t. thermophilus 70s ribosome in complex with mrna, trnas and ef-2 tu.gdp.kirromycin ternary complex, fitted to a 6.4 a cryo-em map.3 this file contains the 30s subunit and the ligands
80	c1xmqV_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** crystal structure of t6a37-asllysuuu aaa-mrna bound to the decoding2 center
81	c2uucU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 30s ribosomal subunit2 complexed with a valine-asl with cmo5u in position 343 bound to an mrna with a gua-codon in the a-site and4 paromomycin.
82	c2vqfU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** modified uridines with c5-methylene substituents at the2 first position of the trna anticodon stabilize u-g wobble3 pairing during decoding
83	c1ibkV_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 30s ribosomal subunit2 in complex with the antibiotic paromomycin
84	c1hr0V_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** crystal structure of initiation factor if1 bound to the 30s2 ribosomal subunit
85	c1hnzV_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 30s ribosomal subunit2 in complex with hygromycin b
86	c1n32V_	Alignment	not modelled	5.3	33	**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 first codon position at the a4 site with paromomycin
87	c2uubU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 30s ribosomal subunit2 complexed with a valine-asl with cmo5u in position 343 bound to an mrna with a guu-codon in the a-site and4 paromomycin.
88	c3zvoU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** crystal structure of the hybrid state of ribosome in complex with2 the guanosine triphosphatase release factor 3
89	c3oi4U_	Alignment	not modelled	5.3	33	**PDB header:**ribosome/antibiotic **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 70s ribosome complexed with2 telithromycin. this file contains the 30s subunit of one 70s3 ribosome. the entire crystal structure contains two 70s ribosomes.
90	c3oi2U_	Alignment	not modelled	5.3	33	**PDB header:**ribosome/antibiotic **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 70s ribosome complexed with2 telithromycin. this file contains the 30s subunit of one 70s3 ribosome. the entire crystal structure contains two 70s ribosomes.
91	c3mr8U_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** recognition of the amber stop codon by release factor rf1. this entry2 3mr8 contains 30s ribosomal subunit. the 50s ribosomal subunit can be3 found in pdb entry 3ms1. molecule b in the same asymmetric unit is4 deposited as 3mrz (50s) and 3ms0 (30s).
92	c2j00U_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 1 of 4).3 this file contains the 30s subunit, mrna, a-, p- and4 e-site trnas and paromomycin for molecule i.
93	c2y12U_	Alignment	not modelled	5.3	33	**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 near-cognate codon on the 70s ribosome
94	c2vqeU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** modified uridines with c5-methylene substituents at the2 first position of the trna anticodon stabilize u-g wobble3 pairing during decoding
95	c3ms0U_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** recognition of the amber stop codon by release factor rf1. this entry2 3ms0 contains 30s ribosomal subunit. the 50s ribosomal subunit can be3 found in pdb entry 3mrz. molecule a in the same asymmetric unit is4 deposited as 3mr8 (30s) and 3ms1 (50s).
96	c1ar1B_	Alignment	not modelled	5.3	25	**PDB header:**complex (oxidoreductase/antibody) **Chain:** B: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
97	c1qleB_	Alignment	not modelled	5.3	25	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**cytochrome c oxidase polypeptide ii; **PDBTitle:** cryo-structure of the paracoccus denitrificans four-

						subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
98	c3ogeU_	Alignment	not modelled	5.3	33	**PDB header:**ribosome/antibiotic **Chain:** U: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** structure of the thermus thermophilus ribosome complexed with2 chloramphenicol. this file contains the 30s subunit of one 70s3 ribosome. the entire crystal structure contains two 70s ribosomes.
99	c1gixX_	Alignment	not modelled	5.3	33	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**30s ribosomal protein thx; **PDBTitle:** crystal structure of the ribosome at 5.5 a resolution. this file,2 1gix, contains the 30s ribosome subunit, three trna, and mrna3 molecules. 50s ribosome subunit is in the file 1giy