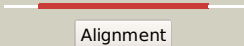

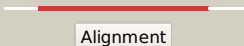

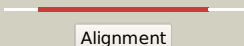







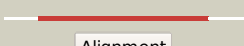




















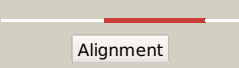
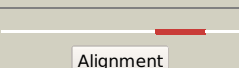
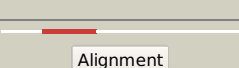
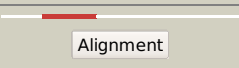
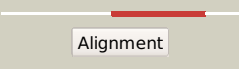
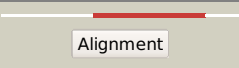
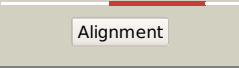
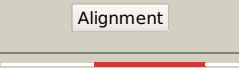
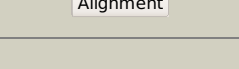
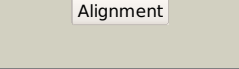
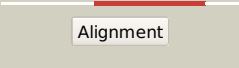
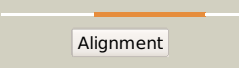
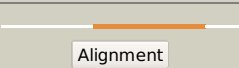
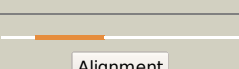
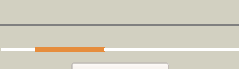
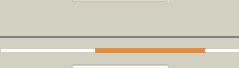
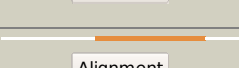
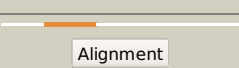
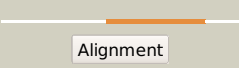
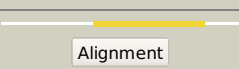
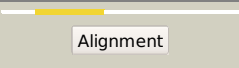
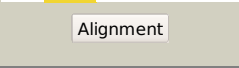
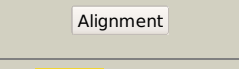
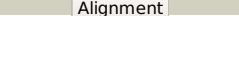
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0881 (-) _979365_980231
Date	Fri Jul 26 01:50:47 BST 2019
Unique Job ID	22441c82cd8bd0bd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ipaA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: rna 2'-o-ribose methyltransferase; PDBTitle: crystal structure of rna 2'-o ribose methyltransferase
2	c5kzkA_	 Alignment		100.0	22	PDB header: rna binding protein Chain: A: PDB Molecule: probable rna methyltransferase, trmh family; PDBTitle: crystal structure of rna methyltransferase from sinorhizobium2 meliloti
3	c4x3mB_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: rna 2'-o ribose methyltransferase; PDBTitle: crystal structure of ttha0275 from thermus thermophilus (hb8) in2 complex with adenosine in space group p212121
4	c2i6dA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: rna methyltransferase, trmh family; PDBTitle: the structure of a putative rna methyltransferase of the trmh family2 from porphyromonas gingivalis.
5	c3gyqB_	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: rrna (adenosine-2'-o-)-methyltransferase; PDBTitle: structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
6	c1x7pB_	 Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: rrna methyltransferase; PDBTitle: crystal structure of the spo methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
7	c1gz0H_	 Alignment		100.0	23	PDB header: transferase Chain: H: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase rlmb
8	d1gz0a1	 Alignment		100.0	25	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
9	c1gz0G_	 Alignment		100.0	25	PDB header: transferase Chain: G: PDB Molecule: hypothetical trna/rrna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase rlmb
10	c1zjrA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: trna (guanosine-2'-o-)-methyltransferase; PDBTitle: crystal structure of a. aeolicus trmh/spou trna modifying enzyme
11	d1v2xa_	 Alignment		100.0	27	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase

12	c5co4A	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: putative trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: structural insights into the 2-oh methylation of c/u34 on trna
13	d1ipaa1	Alignment		100.0	34	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
14	c4pzka	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine(34)-2'-o)-methyltransferase; PDBTitle: crystal structure of putative rna methyltransferase from bacillus2 anthracis.
15	c2ha8A	Alignment		100.0	23	PDB header: rna binding protein Chain: A: PDB Molecule: tar (hiv-1) rna loop binding protein; PDBTitle: methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
16	c3onpA	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: trna/rrna methyltransferase (spou); PDBTitle: crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
17	d1mxia	Alignment		100.0	20	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
18	c5gm8A	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: methylation at position 32 of trna catalyzed by trmj alters oxidative2 stress response in pseudomonas aeruginosa
19	c3ic6A	Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative methylase family protein; PDBTitle: crystal structure of putative methylase family protein from neisseria2 gonorrhoeae
20	c4cngB	Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: spou rrna methylase; PDBTitle: crystal structure of sulfolobus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
21	c5graA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of trmj from z. mobilis zm4
22	c3e5yB	Alignment	not modelled	100.0	25	PDB header: transferase Chain: B: PDB Molecule: trmh family rna methyltransferase; PDBTitle: crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
23	c3l8uA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: putative rrna methylase; PDBTitle: crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
24	c3ktyA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase; PDBTitle: crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
25	c4cndB	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of e.coli trmj
26	c4xboA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: trna (cytidine/uridine-2'-o)-methyltransferase trmj; PDBTitle: crystal structure of full length e.coli trmj in complex with sah
27	c3ilkB	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized trna/rrna methyltransferase hi0380; PDBTitle: the structure of a probable methylase family protein from haemophilus2 influenzae rd kw20
28	d1ipaa2	Alignment	not modelled	99.9	13	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain

29	c3dcmX	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: X: PDB Molecule: uncharacterized protein tm_1570; PDBTitle: crystal structure of the thermotoga maritima spout family rna-2 methyltransferase protein tm1570 in complex with s-adenosyl-l-3 methionine
30	c6ahwB	 Alignment	not modelled	99.8	25	PDB header: transferase Chain: B: PDB Molecule: circular-permuted trna (cytidine(34)-2'-o)- PDBTitle: crystal structure of circular-permuted yibk methyltransferase from2 haemophilus influenzae
31	d1gz0a2	 Alignment	not modelled	98.7	21	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
32	d1gz0f2	 Alignment	not modelled	98.6	21	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
33	c2yy8B	 Alignment	not modelled	96.7	17	PDB header: transferase Chain: B: PDB Molecule: upf0106 protein ph0461; PDBTitle: crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
34	c3kw2A	 Alignment	not modelled	96.6	15	PDB header: transferase Chain: A: PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
35	d2o3aa1	 Alignment	not modelled	96.3	14	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF0751-like
36	d1vhka2	 Alignment	not modelled	95.8	14	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
37	c1vhkA	 Alignment	not modelled	95.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yqeu; PDBTitle: crystal structure of an hypothetical protein
38	c5vm8A	 Alignment	not modelled	94.5	14	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of a ribosomal rna small subunit methyltransferase e2 from neisseria gonorrhoeae bound to s-adenosyl methionine
39	c5o96F	 Alignment	not modelled	90.9	16	PDB header: transferase Chain: F: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: structure of the putative methyltransferase lpg2936 from legionella2 pneumophila in complex with the bound cofactor sam
40	c4j3cB	 Alignment	not modelled	87.0	18	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s ribosomal rna methyltransferase rsme
41	c4e8bA	 Alignment	not modelled	85.5	16	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: crystal structure of 16s rrna methyltransferase rsme from e.coli
42	c4a1dG	 Alignment	not modelled	84.4	11	PDB header: ribosome Chain: G: PDB Molecule: rpl30; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
43	c3j21Z	 Alignment	not modelled	83.5	13	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l30e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
44	c2egwB	 Alignment	not modelled	83.3	15	PDB header: rna methyltransferase Chain: B: PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rrna methyltransferase with sah ligand
45	d1nxza2	 Alignment	not modelled	81.8	14	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
46	d2qi2a3	 Alignment	not modelled	81.6	14	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
47	c4l69A	 Alignment	not modelled	80.3	17	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase e; PDBTitle: rv2372c of mycobacterium tuberculosis is rsme like methyltransferase
48	c1vhyB	 Alignment	not modelled	79.9	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein hi0303; PDBTitle: crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
49	d1t0kb	 Alignment	not modelled	79.7	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
50	c3e20C	 Alignment	not modelled	78.5	17	PDB header: translation Chain: C: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
51	c3zf7g	 Alignment	not modelled	78.1	15	PDB header: ribosome Chain: G: PDB Molecule: PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
52	d1w41a1	 Alignment	not modelled	76.6	14	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like

						Family: L30e/L7ae ribosomal proteins
53	c2zkr6_	Alignment	not modelled	76.4	12	PDB header: ribosomal protein/rna Chain: 6: PDB Molecule: 60s ribosomal protein l30e; 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
54	d1vqof1	Alignment	not modelled	76.0	10	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
55	c3ai9X_	Alignment	not modelled	75.5	12	PDB header: transferase Chain: X: PDB Molecule: upf0217 protein mj1640; PDBTitle: crystal structure of duf358 protein reveals a putative spout-class2 rna methyltransferase
56	c3cpqB_	Alignment	not modelled	71.8	12	PDB header: ribosomal protein Chain: B: PDB Molecule: 50s ribosomal protein l30e; PDBTitle: crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
57	d2bo1a1	Alignment	not modelled	71.6	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
58	d1jj2f_	Alignment	not modelled	68.4	11	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
59	d1x52a1	Alignment	not modelled	65.6	12	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
60	d1k3ra2	Alignment	not modelled	63.0	21	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
61	c3v7qB_	Alignment	not modelled	62.7	25	PDB header: rna binding protein Chain: B: PDB Molecule: probable ribosomal protein ylqx; PDBTitle: crystal structure of b. subtilis ylqx at 1.55 a resolution
62	d2fc3a1	Alignment	not modelled	62.1	16	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
63	d1v6za2	Alignment	not modelled	60.8	20	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
64	d1rlga_	Alignment	not modelled	57.6	19	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
65	c2vgmA_	Alignment	not modelled	56.8	18	PDB header: cell cycle Chain: A: PDB Molecule: dom34; PDBTitle: structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
66	d2qmma1	Alignment	not modelled	56.1	16	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
67	d2vгна3	Alignment	not modelled	55.0	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
68	d1jvna2	Alignment	not modelled	55.0	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
69	c3on1A_	Alignment	not modelled	54.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2414 protein; PDBTitle: the structure of a protein with unknown function from bacillus2 halodurans c
70	c3agiB_	Alignment	not modelled	54.6	17	PDB header: translation/hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
71	c3agiD_	Alignment	not modelled	54.6	17	PDB header: translation/hydrolase Chain: D: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
72	c3obwA_	Alignment	not modelled	52.0	13	PDB header: hydrolase Chain: A: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
73	c3j15A_	Alignment	not modelled	51.7	19	PDB header: translation/transport protein Chain: A: PDB Molecule: protein pelota; PDBTitle: model of ribosome-bound archaeal pelota and abce1
74	c5ewrA_	Alignment	not modelled	50.5	13	PDB header: rna binding protein Chain: A: PDB Molecule: box c/d snorpp and u4 snrnp component snu13p; PDBTitle: c merolae u4 snrnp protein snu13
75	d2czwa1	Alignment	not modelled	49.6	19	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
76	d1xbia1	Alignment	not modelled	48.3	18	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
77	c5xyiM_	Alignment	not modelled	47.4	14	PDB header: ribosome Chain: M: PDB Molecule: ribosomal protein l7ae, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
78	c3ir9A_	Alignment	not modelled	46.4	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: c-terminal domain of peptide chain release factor from methanosarcina2 mazei.
						PDB header: ribosomal protein

79	c3o85A	Alignment	not modelled	46.1	16	Chain: A: PDB Molecule: ribosomal protein l7ae; PDBTitle: giardia lamblia 15.5kd rna binding protein
80	c2cx8A	Alignment	not modelled	45.9	17	PDB header: transferase Chain: A: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
81	c1dt9A	Alignment	not modelled	45.2	13	PDB header: translation Chain: A: PDB Molecule: protein (eukaryotic peptide chain release factor PDBTitle: the crystal structure of human eukaryotic release factor2 erf1-mechanism of stop codon recognition and peptidyl-trna3 hydrolysis
82	c4af1A	Alignment	not modelled	44.9	14	PDB header: hydrolase Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: archeal release factor arf1
83	d1saza1	Alignment	not modelled	44.3	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
84	c3mcaB	Alignment	not modelled	43.7	16	PDB header: translation regulation/hydrolase Chain: B: PDB Molecule: protein dom34; PDBTitle: structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
85	d2qwva1	Alignment	not modelled	43.6	12	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF1056-like
86	c2cx8B	Alignment	not modelled	42.7	20	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
87	d1dt9a2	Alignment	not modelled	42.4	13	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
88	c3obyB	Alignment	not modelled	40.5	15	PDB header: hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
89	c3agkA	Alignment	not modelled	39.9	18	PDB header: translation Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: crystal structure of archaeal translation termination factor, arf1
90	d1iuKa	Alignment	not modelled	38.4	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
91	c2ktvA	Alignment	not modelled	38.2	11	PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: human erf1 c-domain, "open" conformer
92	c2lbaA	Alignment	not modelled	37.9	11	PDB header: rna binding protein Chain: A: PDB Molecule: h/aca ribonucleoprotein complex subunit 2; PDBTitle: solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
93	c2v3jA	Alignment	not modelled	36.6	18	PDB header: ribosomal protein Chain: A: PDB Molecule: essential for mitotic growth 1; PDBTitle: the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase
94	d2ozba1	Alignment	not modelled	34.6	12	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
95	c3e20H	Alignment	not modelled	34.2	13	PDB header: translation Chain: H: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
96	d2aifa1	Alignment	not modelled	34.0	14	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
97	c4d9gA	Alignment	not modelled	33.2	12	PDB header: lyase Chain: A: PDB Molecule: putative diaminopropionate ammonia-lyase; PDBTitle: crystal structure of selenomethionine incorporated holo2 diaminopropionate ammonia lyase from escherichia coli
98	c1k3rA	Alignment	not modelled	32.8	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
99	c3r0zA	Alignment	not modelled	27.8	14	PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of apo d-serine deaminase from salmonella2 typhimurium
100	c4rg1A	Alignment	not modelled	26.7	28	PDB header: transferase Chain: A: PDB Molecule: c9orf114; PDBTitle: methyltransferase domain of c9orf114
101	d1o6da	Alignment	not modelled	24.7	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
102	d1to0a	Alignment	not modelled	22.4	13	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
103	c1t9hA	Alignment	not modelled	22.2	9	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase.
104	c2vhhA	Alignment	not modelled	22.0	9	PDB header: hydrolase Chain: A: PDB Molecule: cg3027-pa; PDBTitle: crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster