Phyre^2

Email	l.a.kelley@imperial.ac.uk
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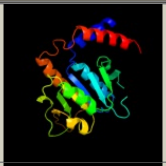
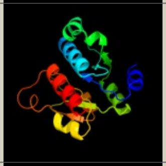
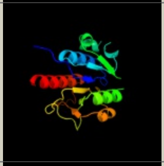
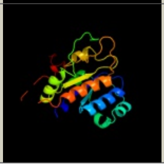
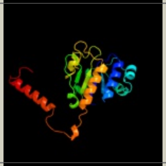
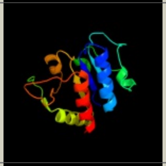
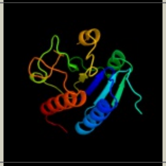
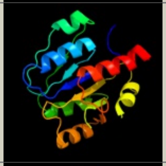
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zjrA_	Alignment		100.0	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanosine-2'-o-)-methyltransferase; **PDBTitle:** crystal structure of a. aeolicus trmh/spou trna modifying enzyme
2	d1v2xa_	Alignment		100.0	53	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
3	d1gz0a1	Alignment		100.0	28	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
4	c1gz0G_	Alignment		100.0	28	**PDB header:**transferase **Chain:** G: **PDB Molecule:**hypothetical trna/rrna methyltransferase yjfh; **PDBTitle:** 23s ribosomal rna g2251 2'o-methyltransferase rlmb
5	c2ha8A_	Alignment		100.0	22	**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
6	c1x7pB_	Alignment		100.0	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna methyltransferase; **PDBTitle:** crystal structure of the spou methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
7	c1ipaA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna 2'-o-ribose methyltransferase; **PDBTitle:** crystal structure of rna 2'-o ribose methyltransferase
8	c2i6dA_	Alignment		100.0	28	**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.
9	c3gyqB_	Alignment		100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna (adenosine-2'-o-)-methyltransferase; **PDBTitle:** structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
10	d1ipaa1	Alignment		100.0	27	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
11	c3ic6A_	Alignment		100.0	16	**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

12	d1mxia_	Alignment		100.0	23	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
13	c3ilkB_	Alignment		100.0	18	**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
14	c3onpA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna/rrna methyltransferase (spou); **PDBTitle:** crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
15	c3e5yB_	Alignment		100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trmh family rna methyltransferase; **PDBTitle:** crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
16	c3l8uA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
17	c3ktyA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable methyltransferase; **PDBTitle:** crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
18	c3dcmX_	Alignment		99.9	18	**PDB header:**transferase **Chain:** X: **PDB Molecule:**uncharacterized protein tm_1570; **PDBTitle:** crystal structure of the thermotoga maritima spout family2 rna-methyltransferase protein tm1570 in complex with s-3 adenosyl-l-methionine
19	d1vhka2	Alignment		97.4	15	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
20	c1vhkA_	Alignment		97.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
21	c2yy8B_	Alignment	not modelled	96.6	18	**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
22	c3kw2A_	Alignment	not modelled	96.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
23	c2egwB_	Alignment	not modelled	96.3	10	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
24	c3ai9X_	Alignment	not modelled	96.2	16	**PDB header:**transferase **Chain:** X: **PDB Molecule:**upf0217 protein mj1640; **PDBTitle:** crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
25	d1nxza2	Alignment	not modelled	96.2	10	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
26	d2o3aa1	Alignment	not modelled	95.4	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
27	c1vhyB_	Alignment	not modelled	94.7	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein hi0303; **PDBTitle:** crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
28	d2qwva1	Alignment	not modelled	94.3	15	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like

29	d1v6za2	Alignment	not modelled	92.3	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
30	d2qmma1	Alignment	not modelled	88.1	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
31	c2cx8B_	Alignment	not modelled	86.9	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyl transferase; **PDBTitle:** crystal structure of methyltransferase with ligand(sah)
32	c1z85B_	Alignment	not modelled	60.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein tm1380; **PDBTitle:** crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
33	c1k3rA_	Alignment	not modelled	49.6	25	**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
34	d1ml4a2	Alignment	not modelled	47.2	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
35	d1a9xa3	Alignment	not modelled	40.3	12	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
36	c2v3jA_	Alignment	not modelled	39.2	16	**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
37	d2b7oa1	Alignment	not modelled	38.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
38	d1o6da_	Alignment	not modelled	38.6	26	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
39	d1j6ua2	Alignment	not modelled	31.8	11	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
40	d1to0a_	Alignment	not modelled	31.0	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
41	d1k3ra2	Alignment	not modelled	30.7	26	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
42	c1j6uA_	Alignment	not modelled	30.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-alanine ligase murc; **PDBTitle:** crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
43	d1vh0a_	Alignment	not modelled	29.8	11	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
44	d1ns5a_	Alignment	not modelled	29.6	26	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
45	d1mx3a1	Alignment	not modelled	29.3	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
46	d1ekxa2	Alignment	not modelled	28.9	15	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
47	c2omeA_	Alignment	not modelled	27.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**c-terminal-binding protein 2; **PDBTitle:** crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
48	d1qpoa1	Alignment	not modelled	25.7	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
49	c2wl8D_	Alignment	not modelled	25.7	14	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** x-ray crystal structure of pex19p
50	d1o4ua1	Alignment	not modelled	25.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
51	c3gg9C_	Alignment	not modelled	24.8	6	**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
52	c3o7bA_	Alignment	not modelled	23.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosome biogenesis nep1 rna methyltransferase; **PDBTitle:** crystal structure of archaeoglobus fulgidus nep1 bound to s-2 adenosylhomocysteine
53	c3czpA_	Alignment	not modelled	21.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
54	c1qpoA_	Alignment	not modelled	20.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis

55	c2y0fD_	Alignment	not modelled	19.9	29	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
56	c2o8vA_	Alignment	not modelled	19.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
57	c2oq2B_	Alignment	not modelled	19.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
58	d1sura_	Alignment	not modelled	18.1	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
59	c2x3yA_	Alignment	not modelled	18.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** crystal structure of gmha from burkholderia pseudomallei
60	c2yqeA_	Alignment	not modelled	17.7	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**jumonji/arid domain-containing protein 1d; **PDBTitle:** solution structure of the arid domain of jarid1d protein
61	d1nkua_	Alignment	not modelled	17.3	29	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase I (Tag)
62	c2jg6A_	Alignment	not modelled	16.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
63	c3ajfA_	Alignment	not modelled	16.6	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structural insigths into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus
64	c2zy3A_	Alignment	not modelled	16.4	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
65	c2w2kB_	Alignment	not modelled	16.3	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-mandelate dehydrogenase; **PDBTitle:** crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
66	c3q4gA_	Alignment	not modelled	16.2	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
67	c1dvpA_	Alignment	not modelled	15.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
68	c2fe3B_	Alignment	not modelled	15.1	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**peroxide operon regulator; **PDBTitle:** the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
69	c2b7pA_	Alignment	not modelled	14.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
70	d2f06a1	Alignment	not modelled	14.8	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
71	d2v3ka1	Alignment	not modelled	14.5	17	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**EMG1/NEP1-like
72	c2jbmA_	Alignment	not modelled	14.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
73	c3mwmA_	Alignment	not modelled	14.4	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
74	d1e8ca2	Alignment	not modelled	14.4	8	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
75	d1x7da_	Alignment	not modelled	13.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Ornithine cyclodeaminase-like
76	c2qipA_	Alignment	not modelled	13.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function vpa0982; **PDBTitle:** crystal structure of a protein of unknown function vpa0982 from vibrio2 parahaemolyticus rimd 2210633
77	d1o17a2	Alignment	not modelled	12.8	45	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
78	c2o03A_	Alignment	not modelled	12.6	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
						PDB header:sugar binding protein

79	c3fxaA_	Alignment	not modelled	12.5	12	**Chain:** A: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
80	c2goyC_	Alignment	not modelled	12.4	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase; **PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
81	d2gy9b1	Alignment	not modelled	12.3	23	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
82	d1dvpa1	Alignment	not modelled	12.1	19	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
83	c2nacA_	Alignment	not modelled	11.8	12	**PDB header:**oxidoreductase(aldehyde(d),nad+(a)) **Chain:** A: **PDB Molecule:**nad-dependent formate dehydrogenase; **PDBTitle:** high resolution structures of holo and apo formate dehydrogenase
84	d1pg5a2	Alignment	not modelled	11.3	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
85	c2zkqb_	Alignment	not modelled	11.2	18	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
86	c3navB_	Alignment	not modelled	10.8	7	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
87	d1q9ua_	Alignment	not modelled	10.4	21	**Fold:**TBP-like **Superfamily:**TT1751-like **Family:**TT1751-like
88	c1x3lA_	Alignment	not modelled	10.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph0495; **PDBTitle:** crystal structure of the ph0495 protein from pyrococccus horikoshii2 ot3
89	d1oaoc_	Alignment	not modelled	10.0	15	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
90	c1o4uA_	Alignment	not modelled	9.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
91	d1kkxa_	Alignment	not modelled	9.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**ARID-like **Family:**ARID domain
92	c3hpbA_	Alignment	not modelled	9.2	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**snx5 protein; **PDBTitle:** crystal structure of snx5-px domain in p212121 space group
93	c3bchA_	Alignment	not modelled	9.1	21	**PDB header:**cell adhesion, ribosomal protein **Chain:** A: **PDB Molecule:**40s ribosomal protein sa; **PDBTitle:** crystal structure of the human laminin receptor precursor
94	d1duvg2	Alignment	not modelled	9.1	10	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
95	d1hjra_	Alignment	not modelled	8.9	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**RuvC resolvase
96	d1dxya1	Alignment	not modelled	8.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
97	c2kwuA_	Alignment	not modelled	8.7	40	**PDB header:**protein binding/signaling protein **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
98	c3l0gD_	Alignment	not modelled	8.7	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
99	c3bbnB_	Alignment	not modelled	8.7	13	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.