Phyre2

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Description	RVBD3366_(spoU)_3777908_3778372
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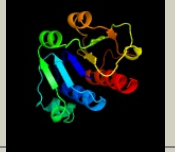
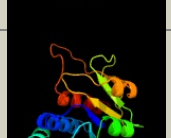
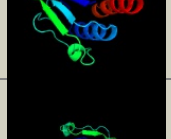
Unique Job ID	407eff1a76ed143f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mxia_	Alignment		100.0	47	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
2	c4pzkA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (cytidine(34)-2'-o)-methyltransferase; **PDBTitle:** crystal strucrure of putative rna methyltransferase from bacillus2 anthracis.
3	c1gz0H_	Alignment		100.0	19	**PDB header:**transferase **Chain:** H: **PDB Molecule:**hypothetical trna/rrna methyltransferase yjfh; **PDBTitle:** 23s ribosomal rna g2251 2'o-methyltransferase rlmb
4	c5co4A_	Alignment		100.0	49	**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
5	c1x7pB_	Alignment		100.0	26	**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
6	c4x3mB_	Alignment		100.0	31	**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
7	c1gz0G_	Alignment		100.0	19	**PDB header:**transferase **Chain:** G: **PDB Molecule:**hypothetical trna/rrna methyltransferase yjfh; **PDBTitle:** 23s ribosomal rna g2251 2'o-methyltransferase rlmb
8	d1gz0a1	Alignment		100.0	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
9	c1ipaA_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna 2'-o-ribose methyltransferase; **PDBTitle:** crystal structure of rna 2'-o ribose methyltransferase
10	c2i6dA_	Alignment		100.0	21	**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.
11	c3e5yB_	Alignment		100.0	49	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trmh family rna methyltransferase; **PDBTitle:** crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei

12	c5kzkA_	Alignment		100.0	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**probable rna methyltransferase, trmh family; **PDBTitle:** crystal structure of rrna methyltransferase from sinorhizobium2 meliloti
13	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
14	d1ipaa1	Alignment		100.0	33	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
15	d1v2xa_	Alignment		100.0	29	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
16	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
17	c3l8uA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
18	c2ha8A_	Alignment		100.0	18	**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
19	c3onpA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna/rrna methyltransferase (spou); **PDBTitle:** crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
20	c3ic6A_	Alignment		100.0	20	**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
21	c5gm8A_	Alignment	not modelled	100.0	25	**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
22	c4xboA_	Alignment	not modelled	100.0	20	**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
23	c5graA_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (cytidine/uridine-2'-o-)-methyltransferase trmj; **PDBTitle:** crystal structure of trmj from z. mobilis zm4
24	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
25	c4cngB_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**spou rrna methylase; **PDBTitle:** crystal structure of sulfolobus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
26	c3ktyA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable methyltransferase; **PDBTitle:** crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
27	c4cndB_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (cytidine/uridine-2'-o-)-methyltransferase trmj; **PDBTitle:** crystal structure of e.coli trmj
28	c3dcmX_	Alignment	not modelled	99.9	17	**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
29	c6ahwB_	Alignment	not modelled	99.9	47	**PDB header:**transferase **Chain:** B: **PDB Molecule:**circular-permutated trna (cytidine(34)-2'-o)- **PDBTitle:** crystal structure of circular-permutated yibk methyltransferase from2 haemophilus influenzae
30	d1vhka2	Alignment	not modelled	97.4	12	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
31	c2yy8B_	Alignment	not modelled	97.2	11	**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
32	c1vhkA_	Alignment	not modelled	97.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
33	c1vhyB_	Alignment	not modelled	96.7	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein hi0303; **PDBTitle:** crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
34	d1nxza2	Alignment	not modelled	96.2	17	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
35	d2o3aa1	Alignment	not modelled	95.9	12	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
36	c2egwB_	Alignment	not modelled	95.4	11	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
37	c5o96F_	Alignment	not modelled	95.3	15	**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
38	c4j3cB_	Alignment	not modelled	94.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribosomal rna small subunit methyltransferase e; **PDBTitle:** crystal structure of 16s ribosomal rna methyltransferase rsme
39	c4e8bA_	Alignment	not modelled	94.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase e; **PDBTitle:** crystal structure of 16s rrna methyltransferase rsme from e.coli
40	c5vm8A_	Alignment	not modelled	94.7	13	**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
41	c3kw2A_	Alignment	not modelled	92.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
42	d1v6za2	Alignment	not modelled	91.9	16	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
43	c1z85B_	Alignment	not modelled	91.2	17	**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
44	c4l69A_	Alignment	not modelled	90.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase e; **PDBTitle:** rv2372c of mycobacterium tuberculosis is rsme like methyltransferse
45	c2cx8A_	Alignment	not modelled	89.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyl transferase; **PDBTitle:** crystal structure of methyltransferase with ligand(sah)
46	c3ai9X_	Alignment	not modelled	82.4	9	**PDB header:**transferase **Chain:** X: **PDB Molecule:**upf0217 protein mj1640; **PDBTitle:** crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
47	d1k3ra2	Alignment	not modelled	81.6	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
48	c2cx8B_	Alignment	not modelled	77.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyl transferase; **PDBTitle:** crystal structure of methyltransferase with ligand(sah)
49	d1saza1	Alignment	not modelled	75.4	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
50	d2qmma1	Alignment	not modelled	74.3	15	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
51	d2qwva1	Alignment	not modelled	66.5	10	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
52	c1k3rA_	Alignment	not modelled	61.7	13	**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

53	d1otha2	Alignment	not modelled	52.5	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
54	c4rg1A_	Alignment	not modelled	47.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**c9orf114; **PDBTitle:** methyltransferase domain of c9orf114
55	c4fmwA_	Alignment	not modelled	45.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna (guanine-9-)-methyltransferase domain-containing **PDBTitle:** crystal structure of methyltransferase domain of human rna (guanine-9-2) methyltransferase domain containing protein 2
56	d1pvva2	Alignment	not modelled	36.0	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
57	c4jwhB_	Alignment	not modelled	34.3	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine(9)-n1)-methyltransferase; **PDBTitle:** crystal structure of sptrm10(full length)-sah complex
58	d1duvg2	Alignment	not modelled	33.5	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
59	c4jwjA_	Alignment	not modelled	32.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine(9)-n1)-methyltransferase; **PDBTitle:** crystal structure of sctrm10(84)-sah complex
60	d1vlva2	Alignment	not modelled	32.2	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
61	d1ml4a2	Alignment	not modelled	22.5	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
62	c2e2kC_	Alignment	not modelled	22.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formamidase; **PDBTitle:** helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
63	c2w37A_	Alignment	not modelled	20.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
64	c3j1rD_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** D: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
65	c3j1rO_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** O: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
66	c3j1rC_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** C: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
67	c3j1rR_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** R: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
68	c3j1rH_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** H: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
69	c3j1rL_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** L: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
70	c3j1rT_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** T: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
71	c3j1rM_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** M: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
72	c3j1rF_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** F: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
73	c3j1rN_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** N: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
74	c3j1rB_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** B: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
75	c3j1rP_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** P: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
76	c3j1rI_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** I: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
77	c3j1rS_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** S: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
78	c3j1rA_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** A: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
						PDB header:cell adhesion, structural protein

79	c3j1rK_	Alignment	not modelled	18.8	38	**Chain:** K: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
80	c3j1rG_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** G: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
81	c3j1rJ_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** J: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
82	c3j1rQ_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** Q: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
83	c3j1rE_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** E: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
84	c3j1rU_	Alignment	not modelled	18.8	38	**PDB header:**cell adhesion, structural protein **Chain:** U: **PDB Molecule:**archaeal adhesion filament core; **PDBTitle:** filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
85	c1a1sA_	Alignment	not modelled	17.9	13	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus
86	d1dxha2	Alignment	not modelled	14.5	10	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
87	c2n9rA_	Alignment	not modelled	12.3	36	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide padbs1r1; **PDBTitle:** novel antimicrobial peptide padbs1r1 designed from the ribosomal2 protein l39e from pyrobaculum aerophilum using bioinformatics
88	c5nfjA_	Alignment	not modelled	11.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mitochondrial ribonuclease p protein 1; **PDBTitle:** crystal structure of the methyltransferase subunit of human2 mitochondrial ribonuclease p (mrpp1) bound to s-adenosyl-methionine3 (sam)
89	c3d6nB_	Alignment	not modelled	10.5	12	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
90	c1fvoB_	Alignment	not modelled	10.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
91	c4ep1B_	Alignment	not modelled	10.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of anabolic ornithine carbamoyltransferase from2 bacillus anthracis
92	c1vlvA_	Alignment	not modelled	10.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
93	d2ivya1	Alignment	not modelled	9.0	13	**Fold:**Ferredoxin-like **Superfamily:**TTP0101/SSO1404-like **Family:**TTP0101/SSO1404-like
94	c2vhiG_	Alignment	not modelled	8.8	11	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cg3027-pa; **PDBTitle:** crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
95	d1pg5a2	Alignment	not modelled	8.7	6	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
96	d1ekxa2	Alignment	not modelled	8.6	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
97	c3updA_	Alignment	not modelled	8.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
98	c6emvA_	Alignment	not modelled	7.6	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine(9)-/adenine(9)-n1)-methyltransferase; **PDBTitle:** crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis.
99	c2ef0A_	Alignment	not modelled	7.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus