

Phyre²

Email elg6752@vandals.uidaho.edu
Description [upf31_pBP136Km](#)
Date Thu Apr 29 18:42:12 BST 2021
Unique Job ID 404c522ea6d0d006
Sequence [MRYPGGKGGA ...](#) [Download FASTA](#)
Job Type **normal**
Job Expiry



Summary

Top model

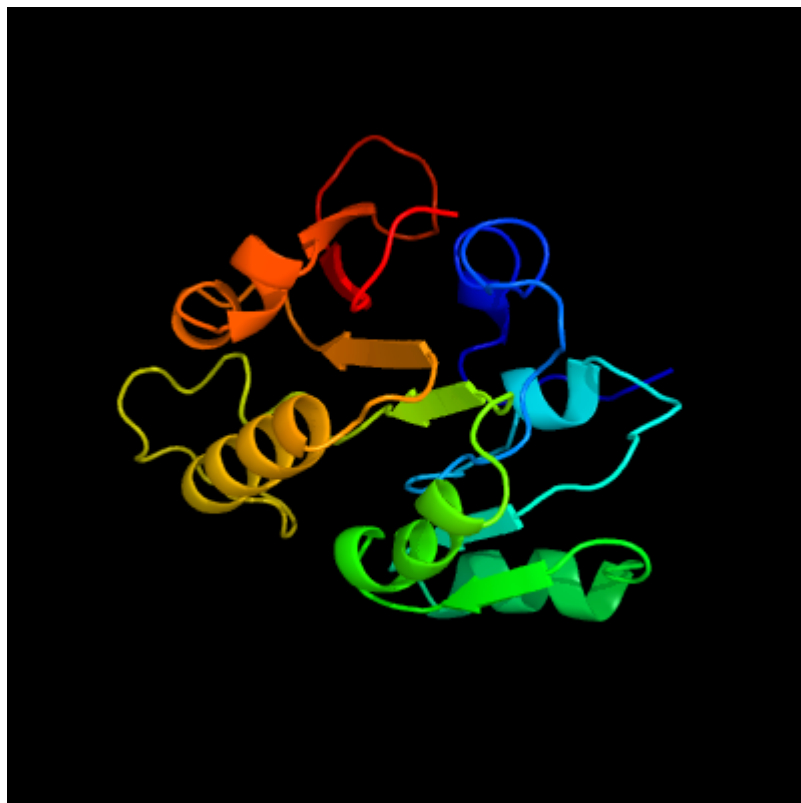


Image coloured by rainbow N → C terminus

Model dimensions (Å): X:45.259 Y:38.600 Z:41.472

Model (left) based on template [d2dpma_](#)

Top template information

Fold: S-adenosyl-L-methionine-dependent methyltransferases

Superfamily: S-adenosyl-L-methionine-dependent methyltransferases

Family: N6 adenine-specific DNA methylase, DAM

Confidence and coverage

Confidence: **100.0%** Coverage: **70%**

157 residues (70% of your sequence) have been modelled with 100.0% confidence by the single highest scoring template.

3D viewing

[Interactive 3D view in JSmol](#)

For other options to view your downloaded structure offline see the [FAQ](#).

Sequence analysis

[View PSI-Blast Pseudo-Multiple Sequence Alignment](#)

[Download FASTA](#)

Secondary structure and disorder
prediction [\[Show\]](#)

Domain analysis [\[Show\]](#)

Detailed template information
[\[Show\]](#)

Binding site prediction

Automated 3DLigandsite submission is temporarily suspended due to server load. However you may submit models directly to 3DLigandSite [HERE](#)

Phyre is **now FREE for commercial users!**

All images and data generated by Phyre2 are free to use in any publication with acknowledgement

Please cite: The Phyre2 web portal for protein modeling,
prediction and analysis.

Kelley LA *et al.*. *Nature Protocols* 10, 845-858 (2015) [\[pdf\]](#)
[\[Citation link\]](#)

If you use the binding site predictions from 3DLigandSite,
please also cite:

3DLigandSite: predicting ligand-binding sites using similar
structures.

Wass MN, Kelley LA and Sternberg MJ *Nucleic Acids
Research* 38, W469-73 (2010) [\[PubMed\]](#)

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Component software
Template detection:
[HHpred 1.51](#)
Secondary structure
prediction: [Psi-pred 2.5](#)
Disorder prediction:
[Disopred 2.4](#)
Transmembrane
prediction:
[Memsat SVM](#)
Multi-template modelling
and *ab initio*: [Poing 1.0](#)



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
Figure 1 displays the protein structure and disorder analysis of the human protein. The protein is shown as a series of alpha-helices and loops. The disorder analysis indicates regions of high confidence (red) and low confidence (green/yellow).

The protein structure is shown in four segments, with the following amino acid sequences and secondary structure predictions (SS):


- Segment 1 (1-60): MRYPGGKGGAGVYQTII NNIPPHDTYI ETHLGGGNI LERKRPAARSIGIDIDPEVI EVWR. SS: [Helix 1-10].
- Segment 2 (70-120): QLDVPGL ELYHGDAVDWLESHQFTGSEFVYADPPYVMDSRRGKLYRYEYDDADHVRLLD. SS: [Helix 11-15].
- Segment 3 (130-180): VLARLP CAVMVSGYSSTIYDSSPLASWRTIDFNAMTRGGIAIERLWMNYPEPAKLHDLRY. SS: [Helix 16-20].
- Segment 4 (190-220): LGSNFRERERIKRKKARWQAKIAKLDPLERAAMECLRELEAAE. SS: [Helix 21-25].


The disorder analysis shows regions of high confidence (red) and low confidence (green/yellow). The protein is shown as a series of alpha-helices and loops. The disorder analysis indicates regions of high confidence (red) and low confidence (green/yellow).

Confidence Key

High(9)  Low (0)

? Disordered (21%)

 Alpha helix (44%)

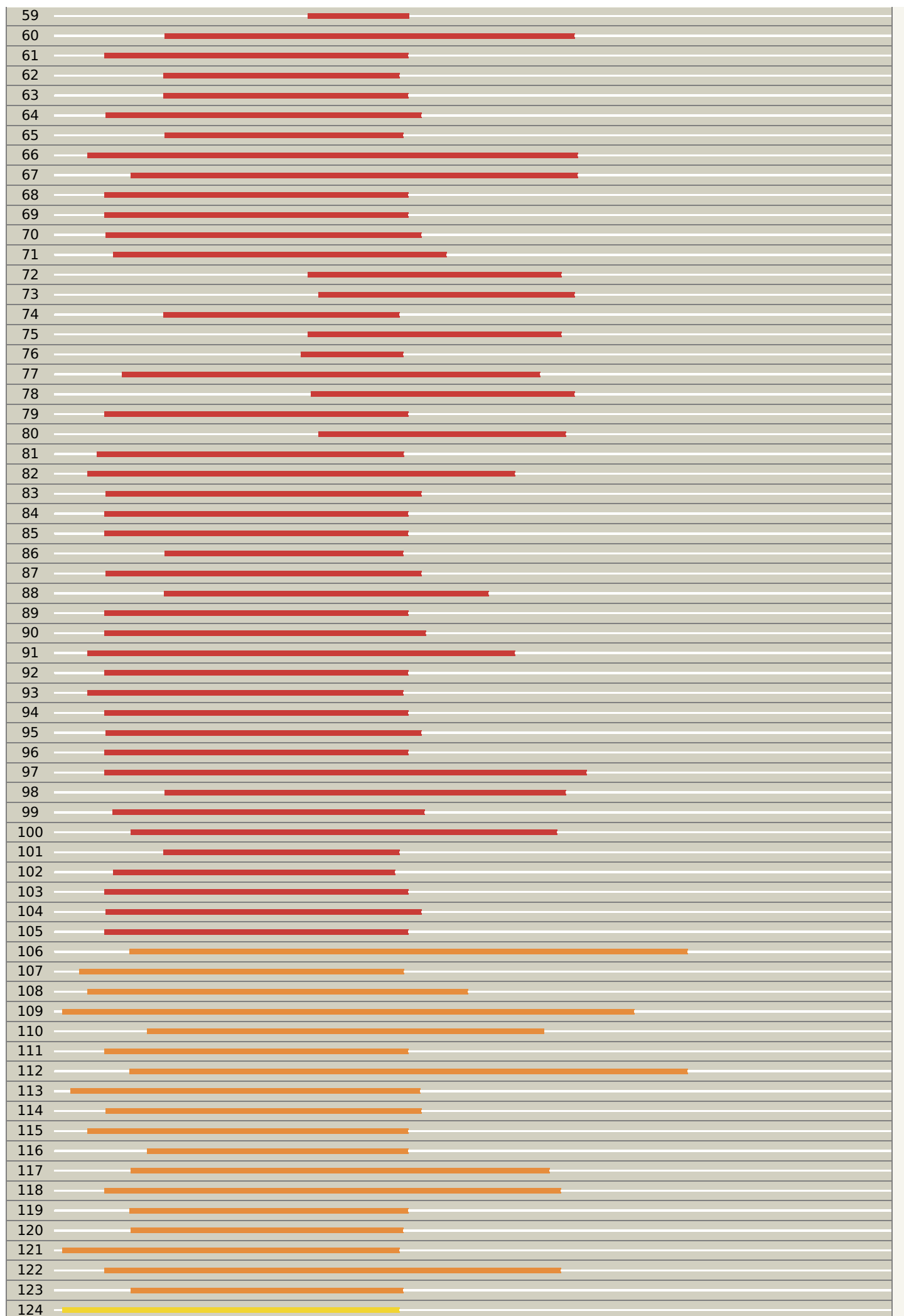
 Beta strand (14%)

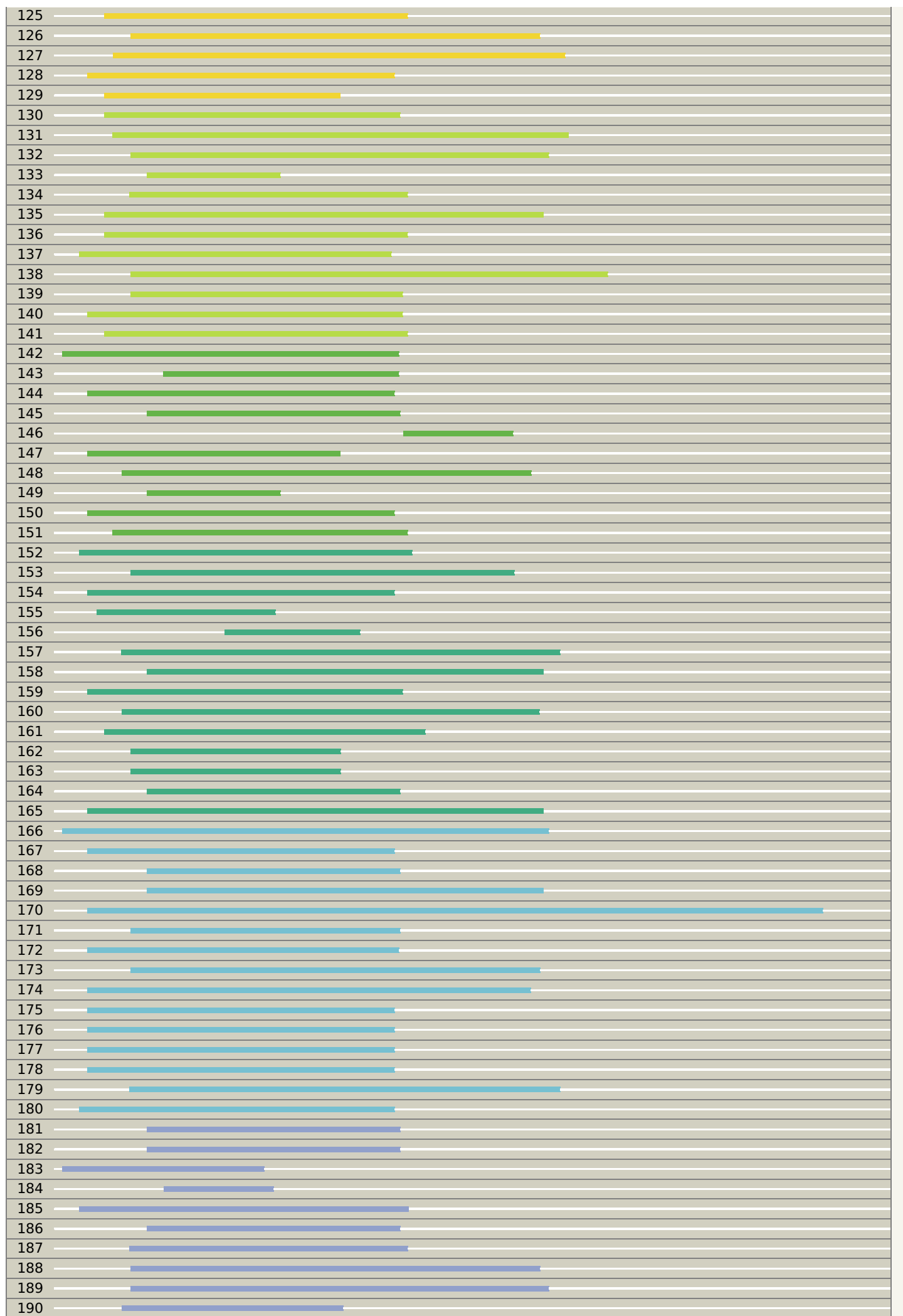
Phyre2

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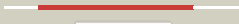



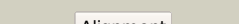

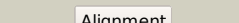

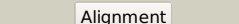

Domain analysis










Rank	Aligned region
1	d2dpma_
2	d1yf3a1
3	c2g1pB_
4	c7m6bB_
5	d2fpoa1
6	c3lduA_
7	c3ldgA_
8	c3egiA_
9	c3v8vB_
10	c3vseA_
11	d2esra1
12	c5e72A_
13	c3p9nA_
14	d2as0a2
15	d2b78a2
16	c1wxwA_
17	d1wxxa2
18	c3k0bA_
19	c3tm4A_
20	c2as0A_
21	
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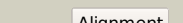

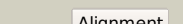







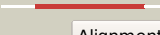






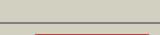

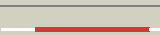

191	
192	

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2dpma_	 Alignment		100.0	29	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N6 adenine-specific DNA methylase, DAM
2	dlyf3a1	 Alignment		100.0	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N6 adenine-specific DNA methylase, DAM
3	c2g1pB_	 Alignment		100.0	22	PDB header: transferase/dna Chain: B: PDB Molecule: dna adenine methylase; PDBTitle: structure of e. coli dna adenine methyltransferase (dam)
4	c7m6bB_	 Alignment		100.0	34	PDB header: transferase Chain: B: PDB Molecule: site-specific dna-methyltransferase (adenine-specific); PDBTitle: the crystal structure of mcbe1
5	d2fpoa1	 Alignment		98.1	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
6	c3lduA_	 Alignment		98.1	20	PDB header: transferase Chain: A: PDB Molecule: putative methylase; PDBTitle: the crystal structure of a possible methylase from2 clostridium difficile 630.
7	c3ldgA_	 Alignment		98.0	18	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein smu.472; PDBTitle: crystal structure of smu.472, a putative methyltransferase complexed2 with sah
8	c3egiA_	 Alignment		98.0	14	PDB header: transferase Chain: A: PDB Molecule: trimethylguanosine synthase homolog; PDBTitle: methyltransferase domain of human trimethylguanosine synthase tgs12 bound to m7gpppa (inactive form)
9	c3v8vB_	 Alignment		97.9	20	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase I; PDBTitle: crystal structure of bifunctional methyltransferase ycbY (rlmk) from2 escherichia coli, sam binding
10	c3vseA_	 Alignment		97.9	13	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of methyltransferase
11	d2esra1	 Alignment		97.9	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like

12	c5e72A	Alignment		97.8	26	PDB header: transferase Chain: A: PDB Molecule: n2, n2-dimethylguanosine trna methyltransferase; PDBTitle: crystal structure of the archaeal trna m2g/m22g10 methyltransferase2 (atrm11) in complex with s-adenosyl-l-methionine (sam) from3 thermococcus kodakarensis
13	c3p9nA	Alignment		97.7	22	PDB header: transferase Chain: A: PDB Molecule: possible methyltransferase (methylase); PDBTitle: rv2966c of m. tuberculosis is a rsmd-like methyltransferase
14	d2as0a2	Alignment		97.7	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: hypothetical RNA methyltransferase
15	d2b78a2	Alignment		97.7	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: hypothetical RNA methyltransferase
16	c1wxwA	Alignment		97.6	11	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ttha1280; PDBTitle: crystal structure of tt1595, a putative sam-dependent2 methyltransferase from thermus thermophilus hb8
17	d1wxxa2	Alignment		97.6	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: hypothetical RNA methyltransferase
18	c3k0bA	Alignment		97.6	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted n6-adenine-specific dna methylase; PDBTitle: crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365
19	c3tm4A	Alignment		97.5	18	PDB header: transferase Chain: A: PDB Molecule: trna (guanine n2-)-methyltransferase trm14; PDBTitle: crystal structure of trm14 from pyrococcus furiosus in complex with s-2 adenosylmethionine
20	c2as0A	Alignment		97.4	20	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ph1915; PDBTitle: crystal structure of ph1915 (apc 5817): a hypothetical rna2 methyltransferase
21	d2fhpa1	Alignment	not modelled	97.4	23	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
22	c3c0kB	Alignment	not modelled	97.4	15	PDB header: transferase Chain: B: PDB Molecule: upf0064 protein yccw; PDBTitle: crystal structure of a ribosomal rna methyltransferase
23	d1ws6a1	Alignment	not modelled	97.4	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
24	c4dmgA	Alignment	not modelled	97.4	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein ttha1493; PDBTitle: thermus thermophilus m5c1942 methyltransferase rlmo
25	c2b78A	Alignment	not modelled	97.4	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein smu.776; PDBTitle: a putative sam-dependent methyltransferase from streptococcus mutans
26	c2esrB	Alignment	not modelled	97.3	15	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: conserved hypothetical protein- streptococcus pyogenes
27	c3axtA	Alignment	not modelled	97.3	16	PDB header: transferase Chain: A: PDB Molecule: probable n(2),n(2)-dimethylguanosine trna methyltransferase PDBTitle: complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
28	d2ifta1	Alignment	not modelled	97.1	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like

29	c3gdhC	 Alignment	not modelled	97.1	16	PDB header: transferase Chain: C: PDB Molecule: trimethylguanosine synthase homolog; PDBTitle: methyltransferase domain of human trimethylguanosine synthase 1 (tgs1)2 bound to m7gtp and adenosyl-homocysteine (active form)
30	d1nv8a	 Alignment	not modelled	97.1	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N5-glutamine methyltransferase, HemK
31	d2igta1	 Alignment	not modelled	97.0	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: hypothetical RNA methyltransferase
32	c5hjmA	 Alignment	not modelled	97.0	14	PDB header: transferase Chain: A: PDB Molecule: trna (guanine(37)-n1)-methyltransferase trm5a; PDBTitle: crystal structure of pyrococcus abyssi trm5a complexed with mta
33	d1wy7a1	 Alignment	not modelled	96.9	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ta1320-like
34	d1uwva2	 Alignment	not modelled	96.8	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: (Uracil-5-)-methyltransferase
35	d1uira	 Alignment	not modelled	96.7	28	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
36	d1xj5a	 Alignment	not modelled	96.6	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
37	c3ll7A	 Alignment	not modelled	96.6	18	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase pg_1098 from2 porphyromonas gingivalis w83
38	c6bq6B	 Alignment	not modelled	96.6	25	PDB header: transferase Chain: B: PDB Molecule: thermospermine synthase; PDBTitle: crystal structure of medicago truncatula thermospermine synthase2 (mttsp2) in complex with thermospermine
39	c2q41D	 Alignment	not modelled	96.5	22	PDB header: transferase Chain: D: PDB Molecule: spermidine synthase 1; PDBTitle: ensemble refinement of the protein crystal structure of spermidine2 synthase from arabidopsis thaliana gene at1g23820
40	c3q87B	 Alignment	not modelled	96.5	15	PDB header: transferase activator/transferase Chain: B: PDB Molecule: n6 adenine specific dna methylase; PDBTitle: structure of e. cuniculi mtq2-trm112 complex responsible for the2 methylation of erf1 translation termination factor
41	c6zxyB	 Alignment	not modelled	96.4	15	PDB header: rna binding protein Chain: B: PDB Molecule: trna (guanine(10)-n2)-dimethyltransferase; PDBTitle: structure of archaeoglobus fulgidus trm11 m2g10 trna methyltransferase2 enzyme
42	c5xj2C	 Alignment	not modelled	96.3	15	PDB header: transferase/rna Chain: C: PDB Molecule: uncharacterized rna methyltransferase sp_1029; PDBTitle: structure of sprlmcid with u747 rna
43	c6pbda	 Alignment	not modelled	96.3	27	PDB header: transferase/dna Chain: A: PDB Molecule: modification methylase ccrmi; PDBTitle: dna n6-adenine methyltransferase ccrmi in complex with double-stranded2 dna oligonucleotide containing its recognition sequence gaatc
44	c1uwva	 Alignment	not modelled	96.3	21	PDB header: transferase Chain: A: PDB Molecule: 23s rrna (uracil-5-)-methyltransferase ruma; PDBTitle: crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
45	d2dula1	 Alignment	not modelled	96.3	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TRM1-like
46	c6h2uA	 Alignment	not modelled	96.2	17	PDB header: transferase Chain: A: PDB Molecule: methyltransferase-like protein 5; PDBTitle: crystal structure of human mettl5-trmt112 complex, the 18s rrna2 m6a1832 methyltransferase at 1.6a resolution
47	c3bwbA	 Alignment	not modelled	96.1	27	PDB header: transferase Chain: A: PDB Molecule: spermidine synthase; PDBTitle: crystal structure of the apo form of spermidine synthase from2 trypanosoma cruzi at 2.5 a resolution
48	d2pkwa1	 Alignment	not modelled	96.0	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhiQ-like
49	d2oyra1	 Alignment	not modelled	96.0	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhiQ-like
50	c3c6kC	 Alignment	not modelled	95.9	16	PDB header: transferase Chain: C: PDB Molecule: spermine synthase; PDBTitle: crystal structure of human spermine synthase in complex2 with spermidine and 5-methylthioadenosine
51	c3tmaA	 Alignment	not modelled	95.9	16	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of trmn from thermus thermophilus
52	d1iy9a	 Alignment	not modelled	95.8	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
		 Alignment				Fold: S-adenosyl-L-methionine-dependent methyltransferases

53	d1boa_	Alignment	not modelled	95.8	24	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Type II DNA methylase
54	d1g60a_	Alignment	not modelled	95.8	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Type II DNA methylase
55	c2qm3A_	Alignment	not modelled	95.7	17	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of a predicted methyltransferase from pyrococcus2 furiosus
56	c3bt7A_	Alignment	not modelled	95.7	13	PDB header: transferase/rna Chain: A: PDB Molecule: trna (uracil-5-)-methyltransferase; PDBTitle: structure of e. coli 5-methyluridine methyltransferase trma in complex2 with 19 nucleotide t-arm analogue
57	c3lbyA_	Alignment	not modelled	95.6	11	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein smu.1697c; PDBTitle: crystal structure of smu.1697c, a putative methyltransferase from2 streptococcus mutans in complex with sah
58	c1wg8B_	Alignment	not modelled	95.4	27	PDB header: transferase Chain: B: PDB Molecule: predicted s-adenosylmethionine-dependent PDBTitle: crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
59	c2zifB_	Alignment	not modelled	95.4	36	PDB header: transferase Chain: B: PDB Molecule: putative modification methylase; PDBTitle: crystal structure of ttha0409, putative dna modification methylase2 from thermus thermophilus hb8- complexed with s-adenosyl-l-methionine
60	d1inla_	Alignment	not modelled	95.3	21	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
61	c3grrA_	Alignment	not modelled	95.2	24	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
62	c6qmmA_	Alignment	not modelled	95.2	19	PDB header: transferase Chain: A: PDB Molecule: polyamine aminopropyltransferase; PDBTitle: crystal structure of synecochoccus spermidine synthase in complex with2 putrescine, spermidine and mta
63	d2b2ca1	Alignment	not modelled	95.2	28	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
64	d1zq9a1	Alignment	not modelled	95.1	23	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
65	c2hteB_	Alignment	not modelled	95.1	25	PDB header: transferase Chain: B: PDB Molecule: spermidine synthase; PDBTitle: the crystal structure of spermidine synthase from p. falciparum in2 complex with 5'-methylthioadenosine
66	c3lpmA_	Alignment	not modelled	95.1	16	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
67	c2ozvA_	Alignment	not modelled	95.0	15	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein atu0636; PDBTitle: crystal structure of a predicted o-methyltransferase, protein atu6362 from agrobacterium tumefaciens.
68	c3fydA_	Alignment	not modelled	95.0	24	PDB header: transferase Chain: A: PDB Molecule: probable dimethyladenosine transferase; PDBTitle: crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
69	c2yx1A_	Alignment	not modelled	94.9	18	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein mj0883; PDBTitle: crystal structure of m.jannaschii trna m1g37 methyltransferase
70	c4jxiA_	Alignment	not modelled	94.8	17	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: crystal structure of ribosomal rna small subunit methyltransferase a2 from rickettsia bellii determined by iodide sad phasing
71	c6h1dA_	Alignment	not modelled	94.7	18	PDB header: gene regulation Chain: A: PDB Molecule: hemk methyltransferase family member 2; PDBTitle: crystal structure of c2lorf127-trmt112 in complex with sah
72	c1nw6A_	Alignment	not modelled	94.6	18	PDB header: transferase Chain: A: PDB Molecule: modification methylase rsri; PDBTitle: structure of the beta class n6-adenine dna methyltransferase rsri2 bound to sinefungin
73	c4zcfA_	Alignment	not modelled	94.3	21	PDB header: hydrolase-dna complex Chain: A: PDB Molecule: restriction endonuclease ecop15i, modification subunit; PDBTitle: structural basis of asymmetric dna methylation and atp-triggered long-2 range diffusion by ecop15i
74	c2pssC_	Alignment	not modelled	94.1	25	PDB header: transferase Chain: C: PDB Molecule: spermidine synthase; PDBTitle: the structure of plasmodium falciparum spermidine synthase in its apo-2 form
75	d1eg2a_	Alignment	not modelled	94.0	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Type II DNA methylase
76	c5hfjF_	Alignment	not modelled	93.9	24	PDB header: dna binding protein Chain: F: PDB Molecule: adenine specific dna methyltransferase (dpna); PDBTitle: crystal structure of m1.hpyavi-sam complex

77	c2r6zA_	 Alignment	not modelled	93.9	17	PDB header: transferase Chain: A: PDB Molecule: upf0341 protein in rsp 3' region; PDBTitle: crystal structure of the sam-dependent methyltransferase ngo1261 from2 neisseria gonorrhoeae, northeast structural genomics consortium3 target ngr48
78	c6k0wD_	 Alignment	not modelled	93.8	20	PDB header: dna binding protein Chain: D: PDB Molecule: adenine specific dna methyltransferase (mod); PDBTitle: dna methyltransferase in complex with sinefungin
79	c3uzuA_	 Alignment	not modelled	93.8	23	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
80	c6k0wB_	 Alignment	not modelled	93.7	21	PDB header: dna binding protein Chain: B: PDB Molecule: adenine specific dna methyltransferase (mod); PDBTitle: dna methyltransferase in complex with sinefungin
81	d1ne2a_	 Alignment	not modelled	93.5	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ta1320-like
82	c4bluB_	 Alignment	not modelled	93.5	15	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase j; PDBTitle: crystal structure of escherichia coli 23s rrna (a2030-n6)-2 methyltransferase rlmj
83	c6nvmA_	 Alignment	not modelled	93.4	19	PDB header: transferase Chain: A: PDB Molecule: rrna adenine n-6-methyltransferase; PDBTitle: crystal structure of 23s rna methyltransferase erme
84	c3tqsB_	 Alignment	not modelled	93.3	22	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
85	c6ifsB_	 Alignment	not modelled	93.3	22	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: ksga from bacillus subtilis 168
86	c6j27D_	 Alignment	not modelled	93.3	15	PDB header: transferase Chain: D: PDB Molecule: n(4)-bis(aminopropyl)spermidine synthase; PDBTitle: crystal structure of the branched-chain polyamine synthase from2 thermus thermophilus (tth-bpsa) in complex with n4-3 aminopropylspermidine and 5'-methylthioadenosine
87	c3fuxB_	 Alignment	not modelled	93.2	19	PDB header: transferase Chain: B: PDB Molecule: dimethyladenosine transferase; PDBTitle: t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121
88	c3gqvA_	 Alignment	not modelled	93.0	17	PDB header: transferase Chain: A: PDB Molecule: spermidine synthase; PDBTitle: crystal structure of a probable spermidine synthase from2 corynebacterium glutamicum atcc 13032
89	d2frna1	 Alignment	not modelled	92.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Met-10+ protein-like
90	c3fteA_	 Alignment	not modelled	92.5	22	PDB header: transferase/rna Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of a. aeolicus ksga in complex with rna
91	d2oo3a1	 Alignment	not modelled	92.4	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: LPG1296-like
92	c3a26A_	 Alignment	not modelled	92.2	15	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein ph0793; PDBTitle: crystal structure of p. horikoshii tyw2 in complex with2 mesado
93	d2f8la1	 Alignment	not modelled	92.2	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like
94	c3a27A_	 Alignment	not modelled	92.1	11	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein mj1557; PDBTitle: crystal structure of m. jannaschii tyw2 in complex with2 adomet
95	d1qyra_	 Alignment	not modelled	91.9	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
96	c3tkaA_	 Alignment	not modelled	91.8	26	PDB header: transferase Chain: A: PDB Molecule: ribosomal rna small subunit methyltransferase h; PDBTitle: crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
97	d1dusa_	 Alignment	not modelled	91.7	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein MJ0882
98	c5wcjA_	 Alignment	not modelled	91.6	15	PDB header: transferase Chain: A: PDB Molecule: methyltransferase-like protein 13; PDBTitle: crystal structure of human methyltransferase-like protein 13 in2 complex with sah
99	c3evzA_	 Alignment	not modelled	91.6	13	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal structure of methyltransferase from pyrococcus furiosus
100	c3dmgA_	 Alignment	not modelled	91.3	13	PDB header: transferase Chain: A: PDB Molecule: probable ribosomal rna small subunit methyltransferase; PDBTitle: t. thermophilus 16s rrna n2 g1207 methyltransferase (rsmc) in complex2 with adohcy

101	d1mjfa_	Alignment	not modelled	91.1	29	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
102	d2o07a1	Alignment	not modelled	91.0	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
103	c5yacA_	Alignment	not modelled	90.9	14	PDB header: rna binding protein Chain: A: PDB Molecule: trna (guanine(37)-n1)-methyltransferase trm5b; PDBTitle: crystal structure of wt trm5b from pyrococcus abyssi
104	d2b3ta1	Alignment	not modelled	90.2	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N5-glutamine methyltransferase, HemK
105	c1m6yA_	Alignment	not modelled	90.2	21	PDB header: transferase Chain: A: PDB Molecule: s-adenosyl-methyltransferase mraw; PDBTitle: crystal structure analysis of tm0872, a putative sam-dependent2 methyltransferase, complexed with sah
106	c6b92A_	Alignment	not modelled	89.7	13	PDB header: transferase Chain: A: PDB Molecule: u6 small nuclear rna (adenine-(43)-n(6))-methyltransferase; PDBTitle: crystal structure of the n-terminal domain of human mettl16 in complex2 with sah
107	c6qe6A_	Alignment	not modelled	88.2	5	PDB header: transferase Chain: A: PDB Molecule: trna (adenine(22)-n(1))-methyltransferase; PDBTitle: structure of m. capricolum trmk in complex with the natural cofactor2 product s-adenosyl-homocysteine (sah)
108	c1aqjB_	Alignment	not modelled	88.1	19	PDB header: methyltransferase Chain: B: PDB Molecule: adenine-n6-dna-methyltransferase taqi; PDBTitle: structure of adenine-n6-dna-methyltransferase taqi
109	c2vs1A_	Alignment	not modelled	87.8	18	PDB header: transferase Chain: A: PDB Molecule: uncharacterized rna methyltransferase pyrab10780; PDBTitle: the crystal structure of pyrococcus abyssi trna (uracil-54, c5)-2 methyltransferase in complex with s-adenosyl-l-homocysteine
110	d1dcta_	Alignment	not modelled	87.5	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: C5 cytosine-specific DNA methylase, DCM
111	d1qama_	Alignment	not modelled	87.5	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
112	d2h00a1	Alignment	not modelled	87.0	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Methyltransferase 10 domain
113	c4dztA_	Alignment	not modelled	86.6	18	PDB header: transferase Chain: A: PDB Molecule: protein-(glutamine-n5) methyltransferase, release factor- PDBTitle: the crystal structure of protein-(glutamine-n5) methyltransferase2 (release factor-specific) from alicyclobacillus acidocaldarius subsp.3 acidocaldarius dsm 446
114	d1yuba_	Alignment	not modelled	85.4	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
115	c6q56C_	Alignment	not modelled	85.1	12	PDB header: rna binding protein Chain: C: PDB Molecule: trna (adenine(22)-n(1))-methyltransferase; PDBTitle: crystal structure of the b. subtilis m1a22 trna methyltransferase trmk
116	d1o9ga_	Alignment	not modelled	84.4	24	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase AviRa
117	c2yxlA_	Alignment	not modelled	82.7	13	PDB header: transferase Chain: A: PDB Molecule: 450aa long hypothetical fmu protein; PDBTitle: crystal structure of ph0851
118	d1m6ya2	Alignment	not modelled	82.3	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: MraW-like putative methyltransferases
119	c1q38A_	Alignment	not modelled	81.4	25	PDB header: transferase/dna Chain: A: PDB Molecule: modification methylase taqi; PDBTitle: adenine-specific methyltransferase m. taq i/dna complex
120	d1sqga2	Alignment	not modelled	81.2	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: NOL1/NOP2/sun