






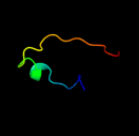







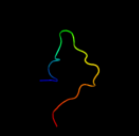

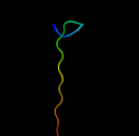



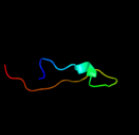

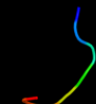
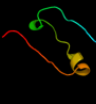



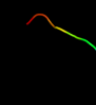




Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P76509
Date	Thu Jan 5 12:23:48 GMT 2012
Unique Job ID	8324eda0d41b0d24

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1aajB_	 Alignment		48.6	24	PDB header: methyltransferase Chain: B: PDB Molecule: adenine-n6-dna-methyltransferase taqi; PDBTitle: structure of adenine-n6-dna-methyltransferase taqi
2	c1g38A_	 Alignment		40.8	24	PDB header: transferase/dna Chain: A: PDB Molecule: modification methylase taqi; PDBTitle: adenine-specific methyltransferase m. taq i/dna complex
3	c3dczA_	 Alignment		21.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative rnfg subunit of electron transport complex; PDBTitle: crystal structure of a putative rnfg subunit of electron transport2 complex (tm0246) from thermotoga maritima at 1.65 a resolution
4	c3uzuA_	 Alignment		20.4	29	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
5	c2nn6H_	 Alignment		20.3	17	PDB header: hydrolase/transferase Chain: H: PDB Molecule: exosome complex exonuclease rrp4; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
6	c2hl7A_	 Alignment		17.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
7	d1nv8a_	 Alignment		15.4	50	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N5-glutamine methyltransferase, HemK
8	c3lkdB_	 Alignment		14.3	29	PDB header: transferase Chain: B: PDB Molecule: type i restriction-modification system PDBTitle: crystal structure of the type i restriction-modification2 system methyltransferase subunit from streptococcus3 thermophilus, northeast structural genomics consortium4 target sur80
9	c2advB_	 Alignment		12.9	21	PDB header: hydrolase Chain: B: PDB Molecule: glutaryl 7- aminocephalosporanic acid acylase; PDBTitle: crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 mutational study of activation mechanism
10	d1g2qa_	 Alignment		12.6	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
11	c3tqsB_	 Alignment		12.2	33	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii

12	d2nn6h3	Alignment		12.0	18	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
13	d1wy7a1	Alignment		11.1	38	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Ta1320-like
14	d1zq9a1	Alignment		11.0	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
15	c3q87B_	Alignment		11.0	57	PDB header: transferase activator/transferase Chain: B: PDB Molecule: n6 adenine specific dna methylase; PDBTitle: structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
16	d2h00a1	Alignment		10.6	38	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Methyltransferase 10 domain
17	c2kw0A_	Alignment		10.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: ccmh protein; PDBTitle: solution structure of n-terminal domain of ccmh from escherichia.coli
18	c3k0bA_	Alignment		10.0	56	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	d1fexa_	Alignment		9.9	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
20	d1o9ga_	Alignment		9.4	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase AviRa
21	d1m15a1	Alignment	not modelled	8.9	10	Fold: Guanido kinase N-terminal domain Superfamily: Guanido kinase N-terminal domain Family: Guanido kinase N-terminal domain
22	c3egiA_	Alignment	not modelled	8.9	43	PDB header: transferase Chain: A: PDB Molecule: trimethylguanosine synthase homolog; PDBTitle: methyltransferase domain of human trimethylguanosine2 synthase tgs1 bound to m7gpppa (inactive form)
23	d1ws6a1	Alignment	not modelled	8.6	71	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhhF-like
24	c2zixB_	Alignment	not modelled	8.5	8	PDB header: hydrolase Chain: B: PDB Molecule: crossover junction endonuclease eme1; PDBTitle: crystal structure of the mus81-eme1 complex
25	d2gtaa1	Alignment	not modelled	8.1	6	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
26	d1pn0a3	Alignment	not modelled	7.9	26	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: PHBH-like
27	d2okca1	Alignment	not modelled	7.4	24	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like
28	c3fbcC_	Alignment	not modelled	7.3	17	PDB header: transcription Chain: C: PDB Molecule: mediator of rna polymerase ii transcription subunit 7; PDBTitle: structure of the mediator submodule med7n/31
						Fold: S-adenosyl-L-methionine-dependent methyltransferases

29	d1qyra_	Alignment	not modelled	7.2	29	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
30	c1oftC_	Alignment	not modelled	6.9	22	PDB header: bacterial cell division inhibitor Chain: C: PDB Molecule: hypothetical protein pa3008; PDBTitle: crystal structure of sula from pseudomonas aeruginosa
31	dlyf3a1	Alignment	not modelled	6.8	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N6 adenine-specific DNA methylase, DAM
32	d2nn6g3	Alignment	not modelled	6.6	10	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
33	c3ldgA_	Alignment	not modelled	6.5	56	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein smu.472; PDBTitle: crystal structure of smu.472, a putative methyltransferase complexed2 with sah
34	d2gtad1	Alignment	not modelled	6.5	6	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
35	d2ar0a1	Alignment	not modelled	6.4	36	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like
36	c3lduA_	Alignment	not modelled	6.4	56	PDB header: transferase Chain: A: PDB Molecule: putative methylase; PDBTitle: the crystal structure of a possible methylase from2 clostridium difficile 630.
37	dlyuba_	Alignment	not modelled	6.2	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA adenine dimethylase-like
38	c3evzA_	Alignment	not modelled	6.0	57	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: crystal strucure of methyltransferase from pyrococcus furiosus
39	dltz7a1	Alignment	not modelled	5.8	55	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
40	d1r5qa_	Alignment	not modelled	5.8	15	Fold: KaiA/RbsU domain Superfamily: KaiA/RbsU domain Family: Circadian clock protein KaiA, C-terminal domain
41	c2zxkB_	Alignment	not modelled	5.6	11	PDB header: oxidoreductase Chain: B: PDB Molecule: red chlorophyll catabolite reductase, PDBTitle: crystal structure of semet-red chlorophyll catabolite2 reductase
42	c3grrA_	Alignment	not modelled	5.3	26	PDB header: transferase Chain: A: PDB Molecule: dimethyladenosine transferase; PDBTitle: crystal structure of the complex between s-adenosyl homocysteine and2 methanocaldococcus jannaschi dim1.
43	c3fydA_	Alignment	not modelled	5.3	26	PDB header: transferase Chain: A: PDB Molecule: probable dimethyladenosine transferase; PDBTitle: crystal structure of dim1 from the thermophilic archeon,2 methanocaldococcus jannaschi
44	dleswa_	Alignment	not modelled	5.3	55	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
45	d1sdda2	Alignment	not modelled	5.2	30	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multi domain cupredoxins