


















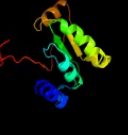


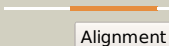

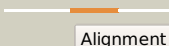
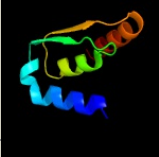
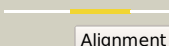

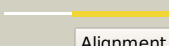
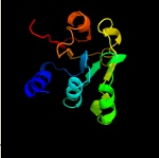
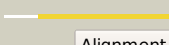

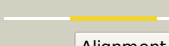

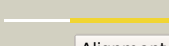

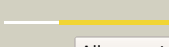

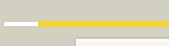

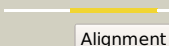


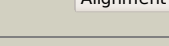
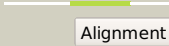

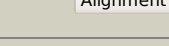
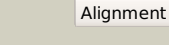


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0725c_(-)_817542_818447
Date	Fri Jul 26 01:50:30 BST 2019
Unique Job ID	5917d2f87ba408d9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2uyoa1	 Alignment		100.0	51	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: ML2640-like
2	c3ieiD	 Alignment		100.0	22	PDB header: transferase Chain: D: PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
3	d1rjda	 Alignment		100.0	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Leucine carboxy methyltransferase Ppm1
4	c3mntA	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: leucine carboxyl methyltransferase 1; PDBTitle: crystal structure of human leucine carboxyl methyltransferase 1
5	c2zwaA	 Alignment		99.9	21	PDB header: transferase Chain: A: PDB Molecule: leucine carboxyl methyltransferase 2; PDBTitle: crystal structure of trna wybutosine synthesizing enzyme2 tyw4
6	c2qe6B	 Alignment		99.4	28	PDB header: transferase Chain: B: PDB Molecule: uncharacterized protein tfu_2867; PDBTitle: crystal structure of a putative methyltransferase (tfu_2867) from2 thermobifida fusca yx at 1.95 a resolution
7	c3giwA	 Alignment		98.6	19	PDB header: unknown function Chain: A: PDB Molecule: protein of unknown function duf574; PDBTitle: crystal structure of a duf574 family protein (sav_2177) from2 streptomyces avermitilis ma-4680 at 1.45 a resolution
8	c3lcvB	 Alignment		90.2	23	PDB header: transferase Chain: B: PDB Molecule: sisomicin-gentamicin resistance methylase sgm; PDBTitle: crystal structure of antibiotic related methyltransferase
9	d1oria	 Alignment		89.3	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
10	c1orhA	 Alignment		87.7	13	PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 1; PDBTitle: structure of the predominant protein arginine methyltransferase prmt1
11	d1f3la	 Alignment		87.7	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase

12	c5lkjA	 Alignment		82.2	12	PDB header: transferase Chain: A: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: crystal structure of mouse carm1 in complex with ligand sa684
13	c3b3jA	 Alignment		80.0	10	PDB header: transferase Chain: A: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: the 2.55 a crystal structure of the apo catalytic domain of2 coactivator-associated arginine methyl transferase i(carm1:28-507,3 residues 28-146 and 479-507 not ordered)
14	c4y30B	 Alignment		79.7	12	PDB header: transferase Chain: B: PDB Molecule: protein arginine n-methyltransferase 6; PDBTitle: crystal structure of human protein arginine methyltransferase prmt62 bound to sah and epz020411
15	d1r74a	 Alignment		77.4	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
16	c4uy5A	 Alignment		76.0	18	PDB header: transferase Chain: A: PDB Molecule: histidine-specific methyltransferase egtD; PDBTitle: crystal structure of histidine-specific methyltransferase egtD from2 mycobacterium smegmatis
17	c5fubA	 Alignment		75.5	14	PDB header: transferase Chain: A: PDB Molecule: protein arginine methyltransferase 2; PDBTitle: crystal structure of zebrafish protein arginine methyltransferase 22 catalytic domain with sah
18	c2v7eB	 Alignment		74.5	11	PDB header: transferase Chain: B: PDB Molecule: histone-arginine methyltransferase carm1; PDBTitle: crystal structure of coactivator-associated arginine2 methyltransferase 1 (carm1), unliganded
19	c3gwzB	 Alignment		73.9	17	PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr
20	c4qvgC	 Alignment		73.3	16	PDB header: transferase Chain: C: PDB Molecule: sibi; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 sibi in its apo form
21	c5fwaA	 Alignment	not modelled	72.6	10	PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 2; PDBTitle: crystal structure of mus musculus protein arginine methyltransferase 22 with cp1
22	c6dnzA	 Alignment	not modelled	69.9	12	PDB header: gene regulation Chain: A: PDB Molecule: arginine n-methyltransferase, putative; PDBTitle: trypanosoma brucei prmt1 enzyme-prozyme heterotetrameric complex with2 adohcy
23	d1g6q1	 Alignment	not modelled	69.2	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
24	c3r0qA	 Alignment	not modelled	68.7	12	PDB header: transferase Chain: A: PDB Molecule: probable protein arginine n-methyltransferase 4.2; PDBTitle: a uniquely open conformation revealed in the crystal structure of2 arabidopsis thaliana protein arginine methyltransferase 10
25	d2fyta1	 Alignment	not modelled	68.1	13	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Arginine methyltransferase
26	d1fp1d2	 Alignment	not modelled	67.8	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
27	c3lccA	 Alignment	not modelled	67.6	10	PDB header: transferase Chain: A: PDB Molecule: putative methyl chloride transferase; PDBTitle: structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana
28	c5dnlB	 Alignment	not modelled	66.6	9	PDB header: transferase Chain: B: PDB Molecule: protein lysine methyltransferase 2;

28	c9upb_	Alignment	not modelled	68.0	9	PDBTitle: the structure of pkmt2 from rickettsia typhi in complex with adohcy Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
29	d1tw3a2	Alignment	not modelled	66.0	15	PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 6; PDBTitle: human hmt1 hnrrp methyltransferase-like protein 6 (s. cerevisiae)
30	c4hc4A_	Alignment	not modelled	63.3	14	PDB header: transferase Chain: A: PDB Molecule: polyamine aminopropyltransferase; PDBTitle: crystal structure of synecochoccus spermidine synthase in complex with2 putrescine, spermidine and mta
31	c1x1aA_	Alignment	not modelled	61.6	12	PDB header: transferase Chain: A: PDB Molecule: crtf-related protein; PDBTitle: crystal structure of bchu complexed with s-adenosyl-l-methionine
32	c6qmmA_	Alignment	not modelled	60.3	22	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of tnmh
33	c6clwA_	Alignment	not modelled	59.2	16	PDB header: transferase Chain: B: PDB Molecule: phosphoethanolamine n-methyltransferase 2; PDBTitle: semet haemonchus contortus phosphoethanolamine n-methyltransferase 22 in complex with s-adenosyl-l-methionine
34	c4krhB_	Alignment	not modelled	57.6	9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
35	d1uira_	Alignment	not modelled	57.4	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: the crystal structure of a possilbe exported protein from bordetella2 parapertussis
36	c3ocjA_	Alignment	not modelled	57.0	20	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
37	c3bwbA_	Alignment	not modelled	55.2	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase
38	d1jg1a_	Alignment	not modelled	53.7	13	PDB header: transferase Chain: A: PDB Molecule: methyl transferase from methanosarcina acetivorans; PDBTitle: crystal structure of methyl transferase from methanosarcina2 acetivorans at 1.6 angstroms resolution, northeast structural3 genomics consortium (nesg) target mvr53.
39	c6mroA_	Alignment	not modelled	53.2	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
40	d1xj5a_	Alignment	not modelled	53.0	17	PDB header: transferase Chain: A: PDB Molecule: protein rdmb; PDBTitle: crystal structure of aclacinomycin-10-hydroxylase (rdmb) in complex2 with sinefungin (sfg)
41	d1iy9a_	Alignment	not modelled	52.0	21	PDB header: transferase Chain: A: PDB Molecule: 16s rna methylase; PDBTitle: crystal structure of rrna methylase from escherichia coli
42	c1xduA_	Alignment	not modelled	50.1	13	PDB header: transferase Chain: A: PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mfa2 complexed with sinefungin
43	c3b89A_	Alignment	not modelled	49.2	16	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
44	c3g2qA_	Alignment	not modelled	49.1	22	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
45	d2o07a1	Alignment	not modelled	48.9	27	PDB header: transferase Chain: D: PDB Molecule: caffeic acid o-methyltransferase; PDBTitle: crystal structure of perennial ryegrass lpomt1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
46	d1tpya_	Alignment	not modelled	48.8	14	PDB header: transferase Chain: B: PDB Molecule: precorrin-6y methylase; PDBTitle: crystal structure of c-terminal domain of precorrin-6y c5,15-2 methyltransferase from rhodobacter capsulatus
47	c3p9kD_	Alignment	not modelled	48.7	14	PDB header: transferase Chain: A: PDB Molecule: protein lysine methyltransferase 1; PDBTitle: the structure of pkmt1 from rickettsia prowazekii
48	c3njrB_	Alignment	not modelled	45.9	16	PDB header: transferase Chain: A: PDB Molecule: small rna 2'-o-methyltransferase; PDBTitle: methyltransferase domain of small rna 2'-o-methyltransferase
49	c5do0A_	Alignment	not modelled	45.9	10	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
50	c4xcxA_	Alignment	not modelled	44.0	15	PDB header: transferase Chain: B: PDB Molecule: thermospermine synthase; PDBTitle: crystal structure of medicago truncatula thermospermine synthase2 (mttsp2) in complex with thermospermine
51	d1qzza2	Alignment	not modelled	43.4	9	PDB header: transferase Chain: A: PDB Molecule: carminomycin 4-o-methyltransferase; PDBTitle: crystal structure of carminomycin-4-o-methyltransferase
52	c6bq6B_	Alignment	not modelled	43.0	21	
53	c1tw3A_	Alignment	not modelled	41.9	17	

						(dnrk) in2 complex with s-adenosyl-l-homocystein (sah) and 4-methoxy-e-3 rhodomycin t (m-et)
54	c3mczB	Alignment	not modelled	41.7	15	PDB header: transferase Chain: B; PDB Molecule: o-methyltransferase; PDBTitle: the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
55	c2pa4B	Alignment	not modelled	40.8	25	PDB header: transferase Chain: B; PDB Molecule: utp-glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of udp-glucose pyrophosphorylase from corynebacteria2 glutamicum in complex with magnesium and udp-glucose
56	d1fp2a2	Alignment	not modelled	40.7	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
57	d1l1ea	Alignment	not modelled	40.7	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
58	c6ifsB	Alignment	not modelled	40.5	18	PDB header: transferase Chain: B; PDB Molecule: ribosomal rna small subunit methyltransferase a; PDBTitle: ksga from bacillus subtilis 168
59	c4lwoG	Alignment	not modelled	37.9	11	PDB header: transferase Chain: G; PDB Molecule: arginine n-methyltransferase, putative; PDBTitle: crystal structure of prmt6
60	c2veoA	Alignment	not modelled	37.9	18	PDB header: hydrolase Chain: A; PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
61	c3jwhA	Alignment	not modelled	37.8	13	PDB header: transferase Chain: A; PDB Molecule: hen1; PDBTitle: crystal structure analysis of the methyltransferase domain of2 bacterial-avhen1-c
62	c3fzgA	Alignment	not modelled	35.5	12	PDB header: transferase Chain: A; PDB Molecule: 16s rrna methylase; PDBTitle: structure of the 16s rrna methylase arma
63	c2q41D	Alignment	not modelled	35.4	13	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
64	c3g2qB	Alignment	not modelled	34.9	24	PDB header: transferase Chain: B; PDB Molecule: pcza361.24; PDBTitle: crystal structure of the glycopeptide n-methyltransferase mtf2 complexed with sinefungin
65	c6i5zA	Alignment	not modelled	34.6	15	PDB header: transferase Chain: A; PDB Molecule: o-methyltransferase 1; PDBTitle: papaver somniferum o-methyltransferase
66	c6dnzB	Alignment	not modelled	33.6	15	PDB header: gene regulation Chain: B; PDB Molecule: arginine n-methyltransferase, putative; PDBTitle: trypanosoma brucei prmt1 enzyme-prozyme heterotetrameric complex with2 adohcy
67	c5xlxD	Alignment	not modelled	33.5	14	PDB header: transferase Chain: D; PDB Molecule: chemotaxis protein methyltransferase 1; PDBTitle: crystal structure of the c-terminal domain of cher1 containing sah
68	c3dp7B	Alignment	not modelled	33.4	12	PDB header: transferase Chain: B; PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
69	c3vc2J	Alignment	not modelled	33.3	11	PDB header: transferase Chain: J; PDB Molecule: geranyl diphosphate 2-c-methyltransferase; PDBTitle: crystal structure of geranyl diphosphate c-methyltransferase from2 streptomyces coelicolor a3(2) in complex with mg2+, geranyl3 diphosphate, and s-adenosyl-l-homocysteine
70	d1kpga	Alignment	not modelled	32.8	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Mycolic acid cyclopropane synthase
71	d1m2ka	Alignment	not modelled	32.3	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
72	c3lbfC	Alignment	not modelled	32.0	12	PDB header: transferase Chain: C; PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli
73	d1i1na	Alignment	not modelled	31.5	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase
74	d1mn4a	Alignment	not modelled	29.8	37	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: DNA-binding domain from NDT80
75	c3bgvC	Alignment	not modelled	28.1	7	PDB header: transferase Chain: C; PDB Molecule: mrna cap guanine-n7 methyltransferase; PDBTitle: crystal structure of mrna cap guanine-n7 methyltransferase2 in complex with sah
76	d2o5ha1	Alignment	not modelled	27.2	40	Fold: NMB0513-like Superfamily: NMB0513-like Family: NMB0513-like
77	c4pneA	Alignment	not modelled	26.4	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: methyltransferase-like protein; PDBTitle: crystal structure of the [4+2]-cyclase spnf
						PDB header: transferase Chain: A; PDB Molecule: cyclopropane-fatty-acyl-phospholipid

78	c5z9oA	Alignment	not modelled	26.4	10	synthase; PDBTitle: the crystal structure of cyclopropane-fatty-acyl-phospholipid synthase2 from lactobacillus acidophilus
79	c2ip2B	Alignment	not modelled	26.2	14	PDB header: transferase Chain: B: PDB Molecule: probable phenazine-specific methyltransferase; PDBTitle: structure of the pyocyanin biosynthetic protein phzm
80	c5i1fA	Alignment	not modelled	26.2	17	PDB header: transferase Chain: A: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of utp-glucose-1-phosphate uridylyltransferase from2 burkholderia vietnamiensis in complex with uridine-5'-diphosphate-3 glucose
81	d1mjfa	Alignment	not modelled	26.1	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
82	c6pi9A	Alignment	not modelled	25.9	21	PDB header: transferase Chain: A: PDB Molecule: 16s rrna (guanine(1405)-n(7))-methyltransferase; PDBTitle: crystal structure of 16s rrna methylase rmtf in complex with s-2 adenosyl-l-homocysteine
83	c4p7cB	Alignment	not modelled	25.3	10	PDB header: transferase Chain: B: PDB Molecule: trna (mo5u34)-methyltransferase; PDBTitle: crystal structure of putative methyltransferase from pseudomonas2 syringae pv. tomato
84	d1kyza2	Alignment	not modelled	24.7	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
85	c4a6dA	Alignment	not modelled	24.7	15	PDB header: transferase Chain: A: PDB Molecule: hydroxyindole o-methyltransferase; PDBTitle: crystal structure of human n-acetylserotonin2 methyltransferase (asmt) in complex with sam
86	c3wssA	Alignment	not modelled	24.7	11	PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 7; PDBTitle: crystal structure of c.elegans prmt7 in complex with sah (p43212)
87	c2ux8G	Alignment	not modelled	24.6	17	PDB header: transferase Chain: G: PDB Molecule: glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of sphingomonas elodea atcc 31461 glucose-2 1-phosphate uridylyltransferase in complex with glucose-3 1-phosphate.
88	c3pnnA	Alignment	not modelled	24.1	38	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
89	d2csua1	Alignment	not modelled	23.7	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
90	c2ggqA	Alignment	not modelled	23.7	22	PDB header: transferase Chain: A: PDB Molecule: 401aa long hypothetical glucose-1-phosphate PDBTitle: complex of hypothetical glucose-1-phosphate thymidyltransferase from2 sulfolobus tokodaii
91	c4d7kB	Alignment	not modelled	23.7	17	PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferases; PDBTitle: crystal structure of n,n-8-amino-8-demethyl-d-riboflavin2 dimethyltransferase (rosa) from streptomyces davawensis
92	c2cmgA	Alignment	not modelled	23.1	17	PDB header: transferase Chain: A: PDB Molecule: spermidine synthase; PDBTitle: crystal structure of spermidine synthase from helicobacter2 pylori
93	c2e3dB	Alignment	not modelled	22.8	19	PDB header: transferase Chain: B: PDB Molecule: utp--glucose-1-phosphate uridylyltransferase; PDBTitle: crystal structure of e. coli glucose-1-phosphate2 uridylyltransferase
94	c3bt7A	Alignment	not modelled	22.5	13	PDB header: transferase/rna Chain: A: PDB Molecule: trna (uracil-5-)-methyltransferase; PDBTitle: structure of e. coli 5-methyluridine methyltransferase trna in complex2 with 19 nucleotide t-arm analogue
95	c5i2hB	Alignment	not modelled	22.4	14	PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase family 2; PDBTitle: crystal structure of o-methyltransferase family 2 protein plim_11472 from planctomyces limnophilus dsm 3776 complex with apigenin
96	d1xvaa	Alignment	not modelled	22.2	12	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Glycine N-methyltransferase
97	c4yajA	Alignment	not modelled	21.9	20	PDB header: ligase Chain: A: PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
98	c3gjaA	Alignment	not modelled	21.5	14	PDB header: transferase Chain: A: PDB Molecule: spermidine synthase; PDBTitle: crystal structure of a probable spermidine synthase from2 corynebacterium glutamicum atcc 13032
99	d1nm2a1	Alignment	not modelled	21.3	16	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
100	c1dl5A	Alignment	not modelled	21.2	11	PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: protein-l-isoaspartate o-methyltransferase
101	c1af7A	Alignment	not modelled	21.0	22	PDB header: methyltransferase Chain: A: PDB Molecule: chemotaxis receptor methyltransferase cher; PDBTitle: cher from salmonella typhimurium Fold: S-adenosyl-L-methionine-dependent methyltransferases

102	d1vbfa_	Alignment	not modelled	21.0	10	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Protein-L-isoaspartyl O-methyltransferase
103	c6j27D_	Alignment	not modelled	20.7	26	PDB header: transferase Chain: D: PDB Molecule: n(4)-bis(aminopropyl)spermidine synthase; PDBTitle: crystal structure of the branched-chain polyamine synthase from <i>Thermus thermophilus</i> (Tth-BPSA) in complex with N4-3 aminopropylspermidine and 5'-methylthioadenosine
104	d1rssa_	Alignment	not modelled	20.5	13	Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7
105	c3brkX_	Alignment	not modelled	20.3	20	PDB header: transferase Chain: X: PDB Molecule: glucose-1-phosphate adenyllyltransferase; PDBTitle: crystal structure of adp-glucose pyrophosphorylase from <i>Agrobacterium tumefaciens</i>