Phyre2

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Description	P07364
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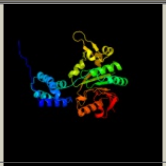
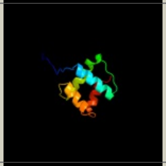
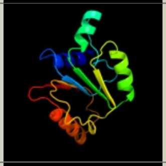
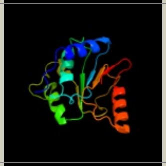
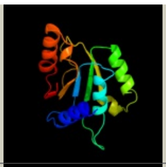
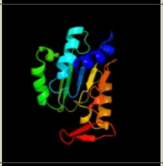
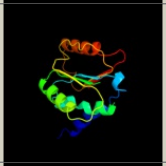
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1af7A_	Alignment		100.0	87	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**chemotaxis receptor methyltransferase cher; **PDBTitle:** cher from salmonella typhimurium
2	d1af7a2	Alignment		100.0	88	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Chemotaxis receptor methyltransferase CheR, C-terminal domain
3	d1af7a1	Alignment		99.7	85	**Fold:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Superfamily:**Chemotaxis receptor methyltransferase CheR, N-terminal domain **Family:**Chemotaxis receptor methyltransferase CheR, N-terminal domain
4	d2bzga1	Alignment		99.6	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
5	c3bgdB_	Alignment		99.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiopurine s-methyltransferase; **PDBTitle:** thiopurine s-methyltransferase
6	d1r74a_	Alignment		99.4	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
7	c3ofkA_	Alignment		99.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nodulation protein s; **PDBTitle:** crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wm9 in complex with s-adenosyl-l-homocysteine (sah)
8	d1jqea_	Alignment		99.3	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Histamine methyltransferase
9	d1xvaa_	Alignment		99.3	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
10	d2gh1a1	Alignment		99.2	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**BC2162-like
11	c3lccA_	Alignment		99.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyl chloride transferase; **PDBTitle:** structure of a sam-dependent halide methyltransferase from arabidopsis2 thaliana

12	c3jwgA_	Alignment		99.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase type 12; **PDBTitle:** crystal structure analysis of the methyltransferase domain2 of bacterial-cthen1-c
13	c3e23A_	Alignment		99.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein rpa2492; **PDBTitle:** crystal structure of the rpa2492 protein in complex with2 sam from rhodopseudomonas palustris, northeast structural3 genomics consortium target rpr299
14	c3m70A_	Alignment		99.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tellurite resistance protein tehb homolog; **PDBTitle:** crystal structure of tehb from haemophilus influenzae
15	d1ve3a1	Alignment		99.2	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
16	d2ex4a1	Alignment		99.1	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
17	d1pjza_	Alignment		99.1	11	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Thiopurine S-methyltransferase
18	c1z3cA_	Alignment		99.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** encephalitozooan cuniculi mrna cap (guanine-n7)2 methyltransferasein complexed with azoadomet
19	c3g2qA_	Alignment		99.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pcza361.24; **PDBTitle:** crystal structure of the glycopeptide n-methyltransferase mtfa2 complexed with sinefungin
20	d1ri5a_	Alignment		99.1	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**mRNA cap (Guanine N-7) methyltransferase
21	c3ou7A_	Alignment	not modelled	99.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** dhpi-sam-hep complex
22	c3g5tA_	Alignment	not modelled	99.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase2 from yeast
23	c3bkxB_	Alignment	not modelled	99.1	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of cyclopropane-fatty-acyl-phospholipid synthase-2 like protein (yp_807781.1) from lactobacillus casei atcc 334 at 1.853 a resolution
24	c2yr0A_	Alignment	not modelled	99.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ttha0223; **PDBTitle:** crystal structure of hypothetical methyltransferase ttha0223 from2 thermus thermophilus hb8
25	c3ujcA_	Alignment	not modelled	99.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoethanolamine n-methyltransferase; **PDBTitle:** phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
26	c3bgvC_	Alignment	not modelled	99.0	18	**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
27	c3ocjA_	Alignment	not modelled	99.0	24	**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
28	d1wzna1	Alignment	not modelled	99.0	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases

						Family:CAC2371-like
29	c3dtnA_	Alignment	not modelled	99.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative methyltransferase mm_2633; **PDBTitle:** crystal structure of putative methyltransferase-mm_26332 from methanosarcina mazei .
30	c3e7pA_	Alignment	not modelled	99.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of of putative methyltransferase from bacteroides2 vulgatus atcc 8482
31	d1xtpa_	Alignment	not modelled	99.0	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**AD-003 protein-like
32	c1vl5B_	Alignment	not modelled	99.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**unknown conserved protein bh2331; **PDBTitle:** crystal structure of a putative methyltransferase (bh2331) from2 bacillus halodurans c-125 at 1.95 a resolution
33	c3jwhA_	Alignment	not modelled	99.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hen1; **PDBTitle:** crystal structure analysis of the methyltransferase domain2 of bacterial-avhen1-c
34	d1vl5a_	Alignment	not modelled	98.9	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
35	c3h2bB_	Alignment	not modelled	98.9	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of the sam-dependent methyltransferase2 cg3271 from corynebacterium glutamicum in complex with s-3 adenosyl-l-homocysteine and pyrophosphate. northeast4 structural genomics consortium target cgr113a
36	d1im8a_	Alignment	not modelled	98.9	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein HI0319 (YecO)
37	d2fcaa1	Alignment	not modelled	98.9	10	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
38	c3f4kA_	Alignment	not modelled	98.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of a probable methyltransferase from2 bacteroides thetaiotaomicron. northeast structural3 genomics target btr309.
39	c3g07C_	Alignment	not modelled	98.9	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**7sk snrna methylphosphate capping enzyme; **PDBTitle:** methyltransferase domain of human bicoid-interacting protein2 3 homolog (drosophila)
40	c3dliB_	Alignment	not modelled	98.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
41	d1xxla_	Alignment	not modelled	98.9	23	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
42	d2avna1	Alignment	not modelled	98.9	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
43	d2a14a1	Alignment	not modelled	98.9	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arylamine N-methyltransferase
44	c2p8jA_	Alignment	not modelled	98.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine-dependent methyltransferase; **PDBTitle:** crystal structure of s-adenosylmethionine-dependent methyltransferase2 (np_349143.1) from clostridium acetobutylicum at 2.00 a resolution
45	d1yzha1	Alignment	not modelled	98.8	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TrmB-like
46	d1l1ea_	Alignment	not modelled	98.8	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
47	c2vdwA_	Alignment	not modelled	98.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vaccinia virus capping enzyme d1 subunit; **PDBTitle:** guanosine n7 methyl-transferase sub-complex (d1-d12) of the2 vaccinia virus mrna capping enzyme
48	c2fk8A_	Alignment	not modelled	98.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methoxy mycolic acid synthase 4; **PDBTitle:** crystal structure of hma (mmaa4) from mycobacterium tuberculosis2 complexed with s-adenosylmethionine
49	d2i6ga1	Alignment	not modelled	98.8	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TehB-like
50	c3bxoA_	Alignment	not modelled	98.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n,n-dimethyltransferase; **PDBTitle:** crystal structure of streptomyces venezuelae desvi
51	c3cggB_	Alignment	not modelled	98.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution
52	c3locA_	Alignment	not modelled	98.8	15	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**nadb-rossmann superfamily protein;

52	[illegible]	Alignment	not modelled	98.8	15	**PDBTitle:** the crystal structure of a protein in the nadb-rossmann2 superfamily from streptococcus agalactiae to 1.8a
53	d2o57a1	Alignment	not modelled	98.8	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
54	d1dusa_	Alignment	not modelled	98.8	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
55	c3mggB_	Alignment	not modelled	98.8	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of methyl transferase from methanosarcina2 mazei
56	c3b89A_	Alignment	not modelled	98.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** crystal structure of rrna methylase from escherichia coli
57	d1d2ha_	Alignment	not modelled	98.8	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glycine N-methyltransferase
58	c3hnrA_	Alignment	not modelled	98.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable methyltransferase bt9727_4108; **PDBTitle:** crystal structure of a probable methyltransferase2 bt9727_4108 from bacillus thuringiensis subsp. northeast3 structural genomics consortium target id bur219
59	c3dlcA_	Alignment	not modelled	98.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative s-adenosyl-l-methionine-dependent **PDBTitle:** crystal structure of a putative s-adenosyl-l-methionine-dependent2 methyltransferase (mmp1179) from methanococcus maripaludis at 1.15 a3 resolution
60	c3ggdA_	Alignment	not modelled	98.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of sam-dependent methyltransferase (yp_325210.1)2 from anabaena variabilis atcc 29413 at 2.11 a resolution
61	d2fk8a1	Alignment	not modelled	98.8	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
62	c3l8dA_	Alignment	not modelled	98.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of methyltransferase from bacillus2 thuringiensis
63	c3gwzB_	Alignment	not modelled	98.8	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mmcr; **PDBTitle:** structure of the mitomycin 7-o-methyltransferase mmcr
64	c3fzgA_	Alignment	not modelled	98.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of the 16s rrna methylase arma
65	d1tpya_	Alignment	not modelled	98.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
66	c3ku1E_	Alignment	not modelled	98.7	13	**PDB header:**transferase **Chain:** E: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of streptococcus pneumoniae sp1610, a2 putative trna (m1a22) methyltransferase, in complex with s-3 adenosyl-l-methionine
67	c2g8nB_	Alignment	not modelled	98.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phenylethanolamine n-methyltransferase; **PDBTitle:** structure of hpnmt with inhibitor 3-hydroxymethyl-7-(n-4-2 chlorophenylaminosulfonyl)-thiq and adohcy
68	d1nkva_	Alignment	not modelled	98.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical Protein YjhP
69	c3p2kA_	Alignment	not modelled	98.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of an antibiotic related methyltransferase
70	c3eeyJ_	Alignment	not modelled	98.7	20	**PDB header:**transferase **Chain:** J: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of putative rrna-methylase from clostridium2 thermocellum
71	d2g72a1	Alignment	not modelled	98.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Arylamine N-methyltransferase
72	c3lcvB_	Alignment	not modelled	98.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sisomicin-gentamicin resistance methylase sgm; **PDBTitle:** crystal structure of antibiotic related methyltransferase
73	d1nv8a_	Alignment	not modelled	98.7	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK
74	c3dmgA_	Alignment	not modelled	98.7	20	**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
75	d1kpga_	Alignment	not modelled	98.7	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
76	c3pfhD	Alignment	not modelled	98.7	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**n-methyltransferase;

76	c3pmD_	Alignment	not modelled	98.7	22	**PDBTitle:** x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n
77	c3grzA_	Alignment	not modelled	98.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal protein l11 methyltransferase; **PDBTitle:** crystal structure of ribosomal protein l11 methylase from2 lactobacillus delbrueckii subsp. bulgaricus
78	c3g5lA_	Alignment	not modelled	98.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative s-adenosylmethionine dependent **PDBTitle:** crystal structure of putative s-adenosylmethionine2 dependent methyltransferase from listeria monocytogenes
79	d1dl5a1	Alignment	not modelled	98.6	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
80	c3mtiA_	Alignment	not modelled	98.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
81	c2p7iB_	Alignment	not modelled	98.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a sam dependent methyl-transferase type 12 family2 protein (eca1738) from pectobacterium atrosepticum scri1043 at 1.74 a3 resolution
82	d1kpia_	Alignment	not modelled	98.6	15	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
83	c3cc8A_	Alignment	not modelled	98.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of a putative methyltransferase (bce_1332) from2 bacillus cereus atcc 10987 at 1.64 a resolution
84	c3mczB_	Alignment	not modelled	98.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**o-methyltransferase; **PDBTitle:** the structure of an o-methyltransferase family protein from2 burkholderia thailandensis.
85	d2p7ia1	Alignment	not modelled	98.6	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
86	c2gs9A_	Alignment	not modelled	98.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein tt1324; **PDBTitle:** crystal structure of tt1324 from thermus thermophilis hb8
87	d1p91a_	Alignment	not modelled	98.6	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
88	d2nxca1	Alignment	not modelled	98.6	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Ribosomal protein L11 methyltransferase PrmA
89	d1xcla_	Alignment	not modelled	98.6	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
90	c3dp7B_	Alignment	not modelled	98.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of sam-dependent methyltransferase from bacteroides2 vulgatus atcc 8482
91	c2pxxA_	Alignment	not modelled	98.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein mgc2408; **PDBTitle:** human putative methyltransferase mgc2408
92	c3dxyA_	Alignment	not modelled	98.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of ectrmb in complex with sam
93	d1zx0a1	Alignment	not modelled	98.5	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
94	c3ccfB_	Alignment	not modelled	98.5	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cyclopropane-fatty-acyl-phospholipid synthase; **PDBTitle:** crystal structure of putative methyltransferase (yp_321342.1) from2 anabaena variabilis atcc 29413 at 1.90 a resolution
95	c3e8sA_	Alignment	not modelled	98.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative sam dependent methyltransferase; **PDBTitle:** crystal structure of putative sam dependent methyltransferase in2 complex with sah (np_744700.1) from pseudomonas putida kt2440 at 2.103 a resolution
96	d1vbfa_	Alignment	not modelled	98.5	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
97	d1y8ca_	Alignment	not modelled	98.5	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**CAC2371-like
98	c3egeA_	Alignment	not modelled	98.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase from antibiotic biosynthesis **PDBTitle:** crystal structure of putative methyltransferase from antibiotic2 biosynthesis pathway (yp_324569.1) from anabaena variabilis atcc3 29413 at 2.40 a resolution
99	c3d2lC_	Alignment	not modelled	98.5	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of sam-dependent methyltransferase (zp_00538691.1)2 from exiguobacterium sp. 255-15 at 1.90 a resolution
						PDB header:structural genomics, unknown function

100	c3merA_	Alignment	not modelled	98.5	21	**Chain:** A: **PDB Molecule:**slr1183 protein; **PDBTitle:** crystal structure of the methyltransferase slr1183 from2 synechocystis sp. pcc 6803, northeast structural genomics3 consortium target sgr145
101	c3mq2A_	Alignment	not modelled	98.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methyltransferase; **PDBTitle:** crystal structure of 16s rrna methyltranferase kamb
102	d1l3ia_	Alignment	not modelled	98.5	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Precorrin-6Y methyltransferase (CbiT)
103	d1jsxa_	Alignment	not modelled	98.5	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
104	c2ip2B_	Alignment	not modelled	98.5	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable phenazine-specific methyltransferase; **PDBTitle:** structure of the pyocyanin biosynthetic protein phzm
105	c3gnlB_	Alignment	not modelled	98.5	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein, duf633, lmof2365_1472; **PDBTitle:** structure of uncharacterized protein (lmof2365_1472) from2 listeria monocytogenes serotype 4b
106	c3i53A_	Alignment	not modelled	98.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**o-methyltransferase; **PDBTitle:** crystal structure of an o-methyltransferase (ncsb1) from2 neocarzinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
107	c2iipD_	Alignment	not modelled	98.5	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinamide n-methyltransferase; **PDBTitle:** human nicotinamide n-methyltransferase
108	c3lbfC_	Alignment	not modelled	98.4	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**protein-l-isoaspartate o-methyltransferase; **PDBTitle:** crystal structure of protein l-isoaspartyl methyltransferase from2 escherichia coli
109	c2r3sA_	Alignment	not modelled	98.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative o-methyltransferase (npun_r0239) from2 nostoc punctiforme pcc 73102 at 2.15 a resolution
110	c3lpmA_	Alignment	not modelled	98.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase small domain protein2 from listeria monocytogenes
111	d1p1ca_	Alignment	not modelled	98.4	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Guanidinoacetate methyltransferase
112	c3busB_	Alignment	not modelled	98.4	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of rebm
113	c3opnA_	Alignment	not modelled	98.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hemolysin; **PDBTitle:** the crystal structure of a putative hemolysin from lactococcus lactis
114	c2esrB_	Alignment	not modelled	98.4	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** conserved hypothetical protein- streptococcus pyogenes
115	d1jg1a_	Alignment	not modelled	98.4	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
116	c3sm3A_	Alignment	not modelled	98.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sam-dependent methyltransferases; **PDBTitle:** crystal structure of sam-dependent methyltransferases q8puk2_metma2 from methanosarcina mazei. northeast structural genomics consortium3 target mar262.
117	d1r18a_	Alignment	not modelled	98.4	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Protein-L-isoaspartyl O-methyltransferase
118	c3m33B_	Alignment	not modelled	98.4	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein from2 deinococcus radiodurans r1
119	d2esra1	Alignment	not modelled	98.4	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhhF-like
120	d2b3ta1	Alignment	not modelled	98.4	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N5-glutamine methyltransferase, HemK