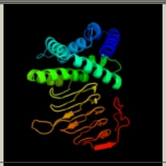
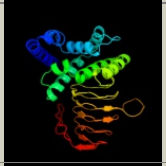
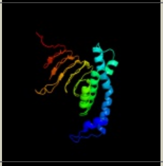
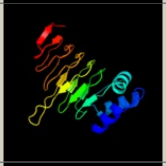
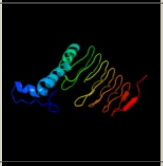
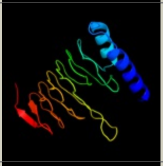
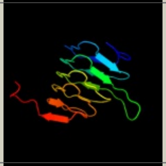
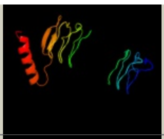
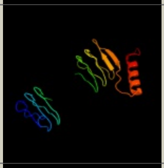
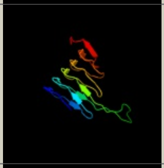
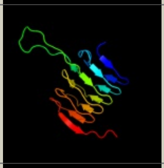
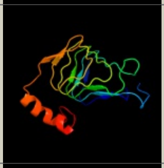
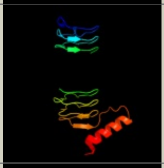
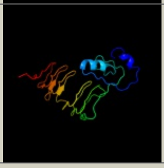
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A9D4
Date	Thu Jan 5 11:09:56 GMT 2012
Unique Job ID	59608beedb72eedf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t3da_	Alignment		100.0	97	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
2	c1t3dB_	Alignment		100.0	97	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
3	c3mc4A_	Alignment		100.0	54	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ww/rsp5/wwp domain:bacterial transferase **PDBTitle:** crystal structure of ww/rsp5/wwp domain: bacterial2 transferase hexapeptide repeat: serine o-acetyltransferase3 from brucella melitensis
4	d1ssqa_	Alignment		100.0	75	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
5	c3f1xA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
6	c3q1xA_	Alignment		100.0	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
7	d1ocxa_	Alignment		99.9	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
8	c3ectA_	Alignment		99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide-repeat containing-acetyltransferase; **PDBTitle:** crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae
9	c2ic7A_	Alignment		99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltose transacetylase; **PDBTitle:** crystal structure of maltose transacetylase from2 geobacillus kaustophilus
10	d1krra_	Alignment		99.9	30	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
11	d3tdta_	Alignment		99.9	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Tetrahydrodipicolinate-N-succinlytransferase, THDP-succinlytransferase, DapD

12	c3r0sA_	Alignment		99.9	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
13	c3i3aC_	Alignment		99.9	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n- **PDBTitle:** structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
14	c3srtB_	Alignment		99.9	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**maltose o-acetyltransferase; **PDBTitle:** the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
15	c3fttA_	Alignment		99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase sacol2570; **PDBTitle:** crystal structure of the galactoside o-acetyltransferase2 from staphylococcus aureus
16	d1mr7a_	Alignment		99.9	24	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
17	d1j2za_	Alignment		99.9	33	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
18	d1xata_	Alignment		99.9	26	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
19	d2jf2a1	Alignment		99.9	27	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
20	d3bswa1	Alignment		99.9	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**PglD-like
21	c3jqyB_	Alignment	not modelled	99.9	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystal strucutre of the polysia specific acetyltransferase neuo
22	c3cj8B_	Alignment	not modelled	99.9	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2-carboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
23	c2iu9C_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
24	c3fsbB_	Alignment	not modelled	99.9	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**qdtc; **PDBTitle:** crystal structure of qdtc, the dtdp-3-amino-3,6-dideoxy-d-2 glucose n-acetyl transferase from thermoanaerobacterium3 thermosaccharolyticum in complex with coa and dtdp-3-amino-4 quinovose
25	c3eevC_	Alignment	not modelled	99.8	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
26	c3pmoA_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; **PDBTitle:** the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
27	c3mqhD_	Alignment	not modelled	99.8	34	**PDB header:**transferase **Chain:** D: **PDB Molecule:**lipopolysaccharides biosynthesis acetyltransferase; **PDBTitle:** crystal structure of the 3-n-acetyl transferase wlbb from

						bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
28	c3eg4A_	Alignment	not modelled	99.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase from brucella melitensis3 biovar abortus 2308
29	d1g97a1	Alignment	not modelled	99.8	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
30	c3eh0C_	Alignment	not modelled	99.8	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
31	c2wlgA_	Alignment	not modelled	99.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
32	c1hm8A_	Alignment	not modelled	99.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine-1-phosphate uridyltransferase; **PDBTitle:** crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a
33	d2oi6a1	Alignment	not modelled	99.7	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
34	d1v3wa_	Alignment	not modelled	99.7	26	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
35	c2oi6A_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
36	c2v0hA_	Alignment	not modelled	99.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridyltransferase (glmu)
37	c3ixcA_	Alignment	not modelled	99.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide transferase family protein; **PDBTitle:** crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
38	c3r3rA_	Alignment	not modelled	99.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ferripyochelin binding protein; **PDBTitle:** structure of the yrda ferripyochelin binding protein from salmonella2 enterica
39	d1xhda_	Alignment	not modelled	99.7	26	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
40	c3fsyC_	Alignment	not modelled	99.6	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**tetrahydrodipicolinate n-succinyltransferase; **PDBTitle:** structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis
41	c3r1wA_	Alignment	not modelled	99.6	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
42	c2ggqA_	Alignment	not modelled	99.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate **PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii
43	c3c8vA_	Alignment	not modelled	99.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
44	c2rijA_	Alignment	not modelled	99.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 2,3,4,5-tetrahydropyridine-2-carboxylate n- **PDBTitle:** crystal structure of a putative 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase (cj1605c, dapd) from campylobacter3 jejuni at 1.90 a resolution
45	c1qreA_	Alignment	not modelled	99.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** a closer look at the active site of gamma-carbonic anhydrases: high2 resolution crystallographic studies of the carbonic anhydrase from3 methanosarcina thermophila
46	d1qrea_	Alignment	not modelled	99.2	12	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
47	d2f9ca1	Alignment	not modelled	99.0	17	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**YdcK-like
48	c2qkxA_	Alignment	not modelled	98.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
49	d1fxja1	Alignment	not modelled	98.8	14	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
50	c3kwdA_	Alignment	not modelled	98.8	22	**PDB header:**lyase, protein binding, photosynthesis **Chain:** A: **PDB Molecule:**carbon dioxide concentrating mechanism protein;

						PDBTitle: inactive truncation of the beta-carboxysomal gamma-carbonic anhydrase,2 ccmm, form 1
51	d1yp2a1	Alignment	not modelled	98.8	14	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
52	c1yp3C_	Alignment	not modelled	98.7	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucose-1-phosphate adenylyltransferase small **PDBTitle:** crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
53	c3d98A_	Alignment	not modelled	98.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
54	c3brkX_	Alignment	not modelled	98.6	21	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from2 agrobacterium tumefaciens
55	c1fwyA_	Alignment	not modelled	98.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
56	d2icya1	Alignment	not modelled	19.4	26	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
57	d1o57a2	Alignment	not modelled	18.4	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
58	c1b0nB_	Alignment	not modelled	17.0	31	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**protein (sini protein); **PDBTitle:** sinr protein/sini protein complex
59	d1b0nb_	Alignment	not modelled	17.0	31	**Fold:**Dimerisation interlock **Superfamily:**SinR repressor dimerisation domain-like **Family:**SinR repressor dimerisation domain-like
60	c2ioaA_	Alignment	not modelled	15.7	13	**PDB header:**ligase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional glutathionylspermidine **PDBTitle:** e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
61	c3qxyA_	Alignment	not modelled	15.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-lysine methyltransferase setd6; **PDBTitle:** human setd6 in complex with rela lys310
62	c3oqvA_	Alignment	not modelled	13.5	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**albc; **PDBTitle:** albc, a cyclodipeptide synthase from streptomyces noursei
63	d2ivxa2	Alignment	not modelled	9.0	19	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
64	c3smtA_	Alignment	not modelled	9.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd3; **PDBTitle:** crystal structure of human set domain-containing protein3
65	c3bitA_	Alignment	not modelled	8.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fact complex subunit spt16; **PDBTitle:** crystal structure of yeast spt16 n-terminal domain
66	c2vjjA_	Alignment	not modelled	8.5	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**tailspike protein; **PDBTitle:** tailspike protein of e.coli bacteriophage hk620 in complex2 with hexasaccharide
67	c2d7cD_	Alignment	not modelled	8.5	11	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**rab11 family-interacting protein 3; **PDBTitle:** crystal structure of human rab11 in complex with fip3 rab-2 binding domain
68	c3gt2A_	Alignment	not modelled	8.1	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
69	d3blhb1	Alignment	not modelled	7.8	18	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
70	c2hv8D_	Alignment	not modelled	7.7	19	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**rab11 family-interacting protein 3; **PDBTitle:** crystal structure of gtp-bound rab11 in complex with fip3
71	c2z9fC_	Alignment	not modelled	7.5	21	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**cellulose synthase operon protein d; **PDBTitle:** crystal structure of axcesd protein from acetobacter xylinum
72	c2zkrq_	Alignment	not modelled	6.9	19	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
73	c3oo2A_	Alignment	not modelled	6.6	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
74	c2zuuA_	Alignment	not modelled	6.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lacto-n-biose phosphorylase; **PDBTitle:** crystal structure of galacto-n-biose/lacto-n-biose i phosphorylase in2 complex with glcnac
75	d1ex4a1	Alignment	not modelled	6.4	27	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase

76	c4a1aP_	Alignment	not modelled	6.2	16	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l21; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
77	d1ihwa_	Alignment	not modelled	5.9	27	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
78	c3iz5U_	Alignment	not modelled	5.8	19	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
79	c3izcU_	Alignment	not modelled	5.8	16	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein rpl21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
80	d1hska2	Alignment	not modelled	5.8	22	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
81	c2x9qA_	Alignment	not modelled	5.6	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cyclodipeptide synthetase; **PDBTitle:** structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.
82	d1uxya2	Alignment	not modelled	5.3	26	**Fold:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Superfamily:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
83	c2cu2A_	Alignment	not modelled	5.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative mannose-1-phosphate guanylyl transferase; **PDBTitle:** crystal structure of mannose-1-phosphate geranyltransferase from2 thermus thermophilus hb8
84	d1ugpa_	Alignment	not modelled	5.3	16	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
85	c3qwvA_	Alignment	not modelled	5.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**set and mynd domain-containing protein 2; **PDBTitle:** crystal structure of histone lysine methyltransferase smyd2 in complex2 with the cofactor product adohcy
86	d2g46a1	Alignment	not modelled	5.2	8	**Fold:**beta-clip **Superfamily:**SET domain **Family:**Viral histone H3 Lysine 27 Methyltransferase
87	d2z1ca1	Alignment	not modelled	5.2	13	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
88	c1ds5F_	Alignment	not modelled	5.2	33	**PDB header:**transferase **Chain:** F: **PDB Molecule:**casein kinase, beta chain; **PDBTitle:** dimeric crystal structure of the alpha subunit in complex2 with two beta peptides mimicking the architecture of the3 tetrameric protein kinase ck2 holoenzyme.
89	d2ar0a1	Alignment	not modelled	5.1	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like