Phyre^2

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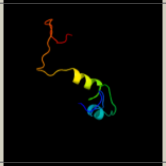
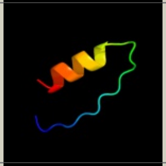
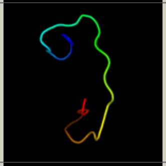
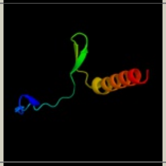
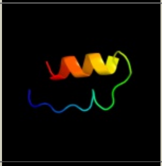
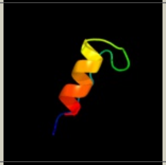
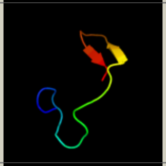
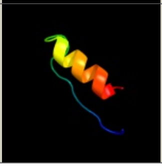
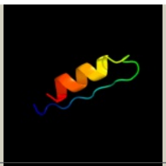
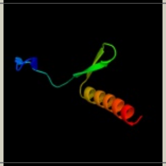
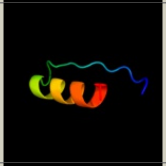
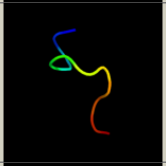
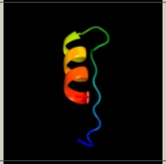
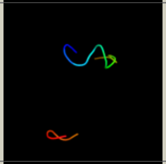
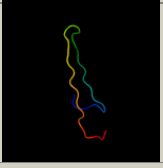
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uc2a_	Alignment		100.0	29	**Fold:**Hypothetical protein PH1602 **Superfamily:**Hypothetical protein PH1602 **Family:**Hypothetical protein PH1602
2	c2epgB_	Alignment		100.0	31	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha1785; **PDBTitle:** crystal structure of ttha1785
3	d1el6a_	Alignment		56.3	26	**Fold:**Baseplate structural protein gp11 **Superfamily:**Baseplate structural protein gp11 **Family:**Baseplate structural protein gp11
4	d1xmta_	Alignment		52.7	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
5	d2pd4a1	Alignment		47.7	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
6	c2btwA_	Alignment		43.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alr0975 protein; **PDBTitle:** crystal structure of alr0975
7	d1fxkc_	Alignment		35.0	16	**Fold:**Long alpha-hairpin **Superfamily:**Prefoldin **Family:**Prefoldin
8	c3emkA_	Alignment		34.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
9	d1hxha_	Alignment		31.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
10	d2bu3a1	Alignment		29.4	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Phytochelatin synthase
11	c3grkE_	Alignment		27.4	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis

12	c2jjyD_	Alignment		26.7	8	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of francisella tularensis enoyl reductase2 (ftfabi) with bound nad
13	c2zdiC_	Alignment		25.6	27	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**prefoldin subunit alpha; **PDBTitle:** crystal structure of prefoldin from pyrococcus horikoshii2 ot3
14	c3ek2D_	Alignment		25.4	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of eonyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
15	c2c4rL_	Alignment		24.9	33	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
16	d2h7ma1	Alignment		24.5	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
17	c2bpbB_	Alignment		20.5	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
18	c2o2sA_	Alignment		20.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan
19	d1jmxa1	Alignment		20.1	11	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
20	c2quoA_	Alignment		19.6	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**heat-labile enterotoxin b chain; **PDBTitle:** crystal structure of c terminal fragment of clostridium2 perfringens enterotoxin
21	d1pbya1	Alignment	not modelled	19.5	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
22	d1w96a2	Alignment	not modelled	19.5	43	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
23	d2j9ga2	Alignment	not modelled	18.9	27	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
24	c1jmuE_	Alignment	not modelled	18.6	67	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**protein mu-1; **PDBTitle:** crystal structure of the reovirus mu1/sigma3 complex
25	d1ulza2	Alignment	not modelled	18.4	43	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
26	d1kx7a_	Alignment	not modelled	17.9	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
27	c2ptgA_	Alignment	not modelled	17.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** crystal structure of eimeria tenella enoyl reductase
28	d1uoua3	Alignment	not modelled	17.7	7	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
29	c2iq6B	Alignment	not modelled	17.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nimc/nima family protein;

29	[illegible]	Alignment	not modelled	17.1	15	**PDBTitle:** crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
30	c1w4zA_	Alignment	not modelled	17.0	20	**PDB header:**antibiotic biosynthesis **Chain:** A: **PDB Molecule:**ketoacyl reductase; **PDBTitle:** structure of actinorhodin polyketide (actiii) reductase
31	c3gdfA_	Alignment	not modelled	16.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
32	c2nq8B_	Alignment	not modelled	16.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** malarial enoyl acyl acp reductase bound with inh-nad adduct
33	c2foiB_	Alignment	not modelled	16.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** synthesis, biological activity, and x-ray crystal structural analysis2 of diaryl ether inhibitors of malarial enoyl acp reductase.
34	c3svtA_	Alignment	not modelled	16.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
35	d1xq1a_	Alignment	not modelled	15.8	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
36	d1wkqa_	Alignment	not modelled	15.8	41	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
37	c3cu4A_	Alignment	not modelled	15.7	27	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c family protein; **PDBTitle:** omcf, outer membrance cytochrome f from geobacter2 sulfurreducens
38	d2rhca1	Alignment	not modelled	15.7	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
39	d1r0ua_	Alignment	not modelled	15.3	24	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Hypothetical protein YwiB
40	d1ulua_	Alignment	not modelled	15.1	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
41	d1h5qa_	Alignment	not modelled	14.2	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
42	d1uh5a_	Alignment	not modelled	13.1	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
43	d2ag5a1	Alignment	not modelled	13.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
44	c3giwA_	Alignment	not modelled	12.9	18	**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
45	c3db0B_	Alignment	not modelled	12.8	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lin2891 protein; **PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution
46	c2d0sA_	Alignment	not modelled	12.6	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the cytochrome c552 from moderate2 thermophilic bacterium, hydrogenophilus thermoluteolus
47	c2v07A_	Alignment	not modelled	12.3	27	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**cytochrome c6; **PDBTitle:** structure of the arabidopsis thaliana cytochrome c6a v52q2 variant
48	c3gr6A_	Alignment	not modelled	12.3	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of the staphylococcus aureus enoyl-acyl2 carrier protein reductase (fabi) in complex with nadp and3 triclosan
49	c3ku1E_	Alignment	not modelled	12.0	40	**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
50	d2tpta3	Alignment	not modelled	11.6	3	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
51	c2p91A_	Alignment	not modelled	11.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadh]; **PDBTitle:** crystal structure of enoyl-[acyl-carrier-protein] reductase (nadh)2 from aquifex aeolicus vf5
52	d1cc5a_	Alignment	not modelled	11.4	36	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
53	d1qsga_	Alignment	not modelled	11.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						PDB header:transferase

54	c3ckkA_	Alignment	not modelled	10.8	100	**Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of human methyltransferase-like protein 1
55	d1mz4a_	Alignment	not modelled	10.7	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
56	c3qivA_	Alignment	not modelled	10.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase or 3-oxoacyl-[acyl-carrier- **PDBTitle:** crystal structure of a putative short-chain dehydrogenase or 3-2 oxoacyl-[acyl-carrier-protein] reductase from mycobacterium3 paratuberculosis atcc baa-968 / k-10
57	d1fcdc1	Alignment	not modelled	10.5	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
58	d1tt2a_	Alignment	not modelled	10.4	10	**Fold:**OB-fold **Superfamily:**Staphylococcal nuclease **Family:**Staphylococcal nuclease
59	d1cyja_	Alignment	not modelled	10.4	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
60	d1brwa3	Alignment	not modelled	10.4	13	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
61	c3g5tA_	Alignment	not modelled	10.4	80	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 3-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate 3-methyltransferase2 from yeast
62	d1wvec1	Alignment	not modelled	10.4	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
63	d2fd5a2	Alignment	not modelled	10.3	20	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
64	c2bh1Y_	Alignment	not modelled	10.1	23	**PDB header:**transport protein **Chain:** Y: **PDB Molecule:**general secretion pathway protein e,; **PDBTitle:** x-ray structure of the general secretion pathway complex of2 the n-terminal domain of epse and the cytosolic domain of3 epsl of vibrio cholerae
65	d2bh1x1	Alignment	not modelled	10.1	23	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**EspE N-terminal domain-like **Family:**GSPII protein E N-terminal domain-like
66	c3dliB_	Alignment	not modelled	10.0	100	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of a sam dependent methyltransferase from2 archaeoglobus fulgidus
67	c3bkwB_	Alignment	not modelled	9.8	80	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine dependent methyltransferase; **PDBTitle:** crystal structure of s-adenosylmethionine dependent methyltransferase2 (np_104914.1) from mesorhizobium loti at 1.60 a resolution
68	c1j6qA_	Alignment	not modelled	9.7	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c maturation protein e; **PDBTitle:** solution structure and characterization of the heme2 chaperone ccme
69	d1j6qa_	Alignment	not modelled	9.7	26	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
70	c3lf2B_	Alignment	not modelled	9.6	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain oxidoreductase q9hya2; **PDBTitle:** nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an atypical catalytic center
71	d1ja9a_	Alignment	not modelled	9.5	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
72	c3fzgA_	Alignment	not modelled	9.4	80	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of the 16s rrna methylase arma
73	c3dlcA_	Alignment	not modelled	9.4	80	**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
74	d1vz6a_	Alignment	not modelled	9.4	12	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**ArgJ-like
75	d2h00a1	Alignment	not modelled	9.2	45	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Methyltransferase 10 domain
76	d1xxla_	Alignment	not modelled	9.2	80	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
77	c2p35A_	Alignment	not modelled	9.1	80	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-aconitate 2-methyltransferase; **PDBTitle:** crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
78	c2qioA_	Alignment	not modelled	9.0	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** x-ray structure of enoyl-acyl carrier protein reductase

						from bacillus2 anthracis with triclosan
79	c2p8jA_	Alignment	not modelled	9.0	60	**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
80	c3dxyA_	Alignment	not modelled	9.0	60	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(7)-)-methyltransferase; **PDBTitle:** crystal structure of ectrmb in complex with sam
81	d2avna1	Alignment	not modelled	9.0	60	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**UbiE/COQ5-like
82	c3i9fB_	Alignment	not modelled	9.0	80	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative type 11 methyltransferase; **PDBTitle:** crystal structure of a putative type 11 methyltransferase2 from sulfolobus solfataricus
83	c3l8dA_	Alignment	not modelled	9.0	80	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** crystal structure of methyltransferase from bacillus2 thuringiensis
84	c3k31B_	Alignment	not modelled	8.9	4	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of eonyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
85	c3d2lC_	Alignment	not modelled	8.8	100	**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
86	d1wfwa_	Alignment	not modelled	8.7	20	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
87	c2hxgB_	Alignment	not modelled	8.7	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-arabinose isomerase; **PDBTitle:** crystal structure of mn2+ bound ecai
88	c3merA_	Alignment	not modelled	8.7	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**slr1183 protein; **PDBTitle:** crystal structure of the methyltransferase slr1183 from2 synechocystis sp. pcc 6803, northeast structural genomics3 consortium target sgr145
89	c3opnA_	Alignment	not modelled	8.7	60	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hemolysin; **PDBTitle:** the crystal structure of a putative hemolysin from lactococcus lactis
90	d2fk8a1	Alignment	not modelled	8.6	100	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
91	d1kpga_	Alignment	not modelled	8.6	80	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Mycolic acid cyclopropane synthase
92	c2fk8A_	Alignment	not modelled	8.6	100	**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
93	d1ctja_	Alignment	not modelled	8.6	27	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
94	c2x5sB_	Alignment	not modelled	8.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
95	c3egeA_	Alignment	not modelled	8.5	80	**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
96	c3h2bB_	Alignment	not modelled	8.4	60	**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
97	c3g07C_	Alignment	not modelled	8.3	60	**PDB header:**transferase **Chain:** C: **PDB Molecule:**7sk snrna methylphosphate capping enzyme; **PDBTitle:** methyltransferase domain of human bicoid-interacting protein2 3 homolog (drosophila)
98	c3tl3A_	Alignment	not modelled	8.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
99	d2fcta1	Alignment	not modelled	8.3	32	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like