Phyre^2

Email	l.a.kelley@imperial.ac.uk
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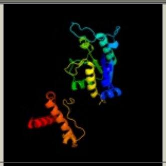
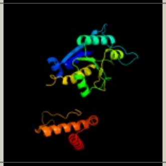
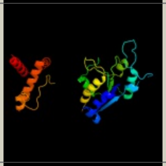
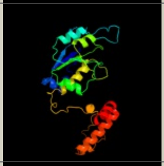
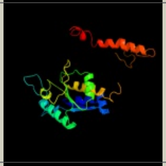
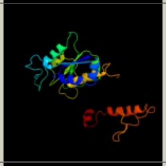
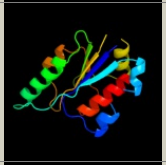
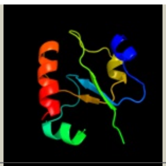
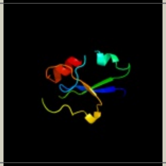
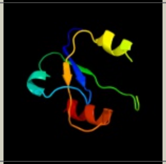
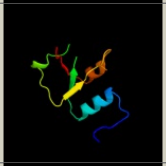
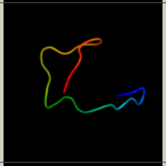
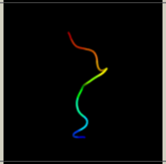
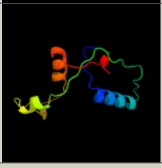
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uala_	Alignment		100.0	83	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
2	d1p9pa_	Alignment		100.0	100	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
3	c3ky7A_	Alignment		100.0	43	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
4	c3iefA_	Alignment		100.0	44	**PDB header:**transferase, rna binding protein **Chain:** A: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna guanine-n1-methyltransferase from2 bartonella henselae using mpcs.
5	c3quvB_	Alignment		100.0	45	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
6	c1oy5B_	Alignment		100.0	41	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
7	d1oy5a_	Alignment		100.0	41	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
8	c3knuD_	Alignment		100.0	45	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna (guanine-n(1)-)-methyltransferase; **PDBTitle:** crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
9	d1o6da_	Alignment		97.2	8	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
10	d1to0a_	Alignment		96.4	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
11	c2v3jA_	Alignment		96.3	14	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**essential for mitotic growth 1; **PDBTitle:** the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase

12	d1vh0a_	Alignment		96.2	22	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
13	d2v3ka1	Alignment		96.1	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**EMG1/NEP1-like
14	d1ns5a_	Alignment		95.0	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
15	c3o7bA_	Alignment		78.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosome biogenesis nep1 rna methyltransferase; **PDBTitle:** crystal structure of archaeoglobus fulgidus nep1 bound to s-2 adenosylhomocysteine
16	c3ai9X_	Alignment		46.1	24	**PDB header:**transferase **Chain:** X: **PDB Molecule:**upf0217 protein mj1640; **PDBTitle:** crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
17	d3d3ra1	Alignment		44.2	38	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
18	c3d3rA_	Alignment		43.1	38	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
19	d2ot2a1	Alignment		29.4	27	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
20	d1dj3a_	Alignment		28.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
21	d1dj2a_	Alignment	not modelled	27.4	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
22	d2qmma1	Alignment	not modelled	25.8	24	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
23	c1zmrA_	Alignment	not modelled	24.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase
24	c1zosE_	Alignment	not modelled	23.9	21	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**5'-methylthioadenosine / s-adenosylhomocysteine **PDBTitle:** structure of 5'-methylthionadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state3 inhibitor mt-imma
25	d2z1ca1	Alignment	not modelled	21.6	22	**Fold:**OB-fold **Superfamily:**HupF/HypC-like **Family:**HupF/HypC-like
26	d1sqsa_	Alignment	not modelled	21.1	9	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
27	d2z1aa2	Alignment	not modelled	20.3	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
28	c1xi4O_	Alignment	not modelled	19.2	22	**PDB header:**endocytosis/exocytosis **Chain:** O: **PDB Molecule:**clathrin light chain a; **PDBTitle:** clathrin d6 coat

29	c1rcuB_	Alignment	not modelled	18.9	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein vt76; **PDBTitle:** x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
30	d1rcua_	Alignment	not modelled	18.9	22	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
31	d1vjda_	Alignment	not modelled	18.0	27	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
32	d3bbda1	Alignment	not modelled	17.2	15	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**EMG1/NEP1-like
33	c1zggA_	Alignment	not modelled	16.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative low molecular weight protein-tyrosine- **PDBTitle:** solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
34	c3dcmX_	Alignment	not modelled	16.3	22	**PDB header:**transferase **Chain:** X: **PDB Molecule:**uncharacterized protein tm_1570; **PDBTitle:** crystal structure of the thermotoga maritima spout family2 rna-methyltransferase protein tm1570 in complex with s-3 adenosyl-l-methionine
35	d1qf5a_	Alignment	not modelled	15.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
36	d1jysa_	Alignment	not modelled	15.1	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
37	c2ky8A_	Alignment	not modelled	14.9	55	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**methyl-cpg-binding domain protein 2; **PDBTitle:** solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
38	c2cunA_	Alignment	not modelled	14.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
39	d1fdja_	Alignment	not modelled	14.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
40	c1w4zA_	Alignment	not modelled	13.6	13	**PDB header:**antibiotic biosynthesis **Chain:** A: **PDB Molecule:**ketoacyl reductase; **PDBTitle:** structure of actinorhodin polyketide (actiii) reductase
41	d16pka_	Alignment	not modelled	13.4	26	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
42	d1prtf_	Alignment	not modelled	13.0	33	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
43	d1vpea_	Alignment	not modelled	12.6	23	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
44	c3r7tA_	Alignment	not modelled	12.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of adenylosuccinate synthetase from campylobacter2 jejuni
45	d3dl3a1	Alignment	not modelled	12.6	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
46	d1m2ka_	Alignment	not modelled	12.2	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
47	d1gsaa1	Alignment	not modelled	12.2	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
48	d1v6sa_	Alignment	not modelled	11.8	20	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
49	d3bb6a1	Alignment	not modelled	11.6	8	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
50	d1hdia_	Alignment	not modelled	11.5	26	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
51	d1pj3a1	Alignment	not modelled	11.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
52	d1ig4a_	Alignment	not modelled	11.1	29	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
53	d1ltka_	Alignment	not modelled	10.8	26	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
54	d1phpa_	Alignment	not modelled	10.7	31	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
55	d2qwva1	Alignment	not modelled	10.6	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot

						Family:AF1056-like
56	d2fvka1	Alignment	not modelled	10.3	25	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
57	c2yvaB_	Alignment	not modelled	10.1	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
58	d2o3aa1	Alignment	not modelled	9.8	25	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
59	d1ddza2	Alignment	not modelled	9.3	56	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
60	d1qk9a_	Alignment	not modelled	9.2	36	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
61	c2k1lB_	Alignment	not modelled	9.2	45	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
62	c2k1kA_	Alignment	not modelled	9.2	45	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
63	c2k1kB_	Alignment	not modelled	9.2	45	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
64	c2k1lA_	Alignment	not modelled	9.2	45	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 1; **PDBTitle:** nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
65	c3lf2B_	Alignment	not modelled	9.1	18	**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
66	c3ff4A_	Alignment	not modelled	9.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
67	c1gshA_	Alignment	not modelled	8.9	15	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
68	d1ddza1	Alignment	not modelled	8.9	78	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
69	d1ub1a_	Alignment	not modelled	8.8	36	**Fold:**DNA-binding domain **Superfamily:**DNA-binding domain **Family:**Methyl-CpG-binding domain, MBD
70	c3ue9A_	Alignment	not modelled	8.8	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of adenylosuccinate synthetase (ampsase) (pura) from2 burkholderia thailandensis
71	c2yh5A_	Alignment	not modelled	8.7	21	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
72	c3majA_	Alignment	not modelled	8.7	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna processing chain a; **PDBTitle:** crystal structure of putative dna processing protein dpra from2 rhodopseudomonas palustris cga009
73	c3q3vA_	Alignment	not modelled	8.6	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
74	c1ddzA_	Alignment	not modelled	8.3	78	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
75	c3eh0C_	Alignment	not modelled	8.1	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
76	c3lasA_	Alignment	not modelled	8.1	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
77	d2cqaa1	Alignment	not modelled	8.0	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
78	d2qmwa1	Alignment	not modelled	8.0	10	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
79	d2rhca1	Alignment	not modelled	8.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
80	d1a5ca_	Alignment	not modelled	8.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
81	d3c2wa2	Alignment	not modelled	7.8	13	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**Phytochrome-specific domain

82	d2dsma1	Alignment	not modelled	7.7	43	**Fold:**YqaI-like **Superfamily:**YqaI-like **Family:**YqaI-like
83	c3eyxB_	Alignment	not modelled	7.6	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
84	d2a9va1	Alignment	not modelled	7.6	8	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
85	d2do3a1	Alignment	not modelled	7.5	26	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
86	c2q2qG_	Alignment	not modelled	7.5	14	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**beta-d-hydroxybutyrate dehydrogenase; **PDBTitle:** structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
87	d1xfba1	Alignment	not modelled	7.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
88	d2fr1a1	Alignment	not modelled	7.5	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
89	c3nkdB_	Alignment	not modelled	7.4	29	**PDB header:**immune system **Chain:** B: **PDB Molecule:**crispr-associated protein cas1; **PDBTitle:** structure of crisp-associated protein cas1 from escherichia coli str.2 k-12
90	c2iz6A_	Alignment	not modelled	7.3	18	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
91	c2pc4B_	Alignment	not modelled	7.3	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
92	d2pw6a1	Alignment	not modelled	7.1	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
93	d1gxha_	Alignment	not modelled	7.1	40	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
94	c2d7uA_	Alignment	not modelled	7.1	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of hypothetical adenylosuccinate synthetase, ph04382 from pyrococcus horikoshii ot3
95	c3ggsA_	Alignment	not modelled	7.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
96	c2ph3B_	Alignment	not modelled	6.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl carrier protein] reductase; **PDBTitle:** crystal structure of 3-oxoacyl-[acyl carrier protein] reductase2 ttha0415 from thermus thermophilus
97	d2vlqa1	Alignment	not modelled	6.8	20	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
98	d1zaia1	Alignment	not modelled	6.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
99	d1v2xa_	Alignment	not modelled	6.8	15	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase