Phyre^2

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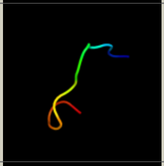
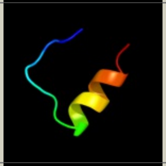
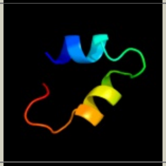
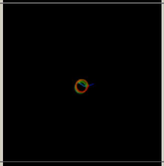
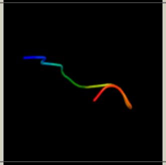
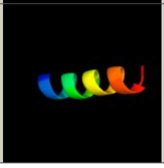
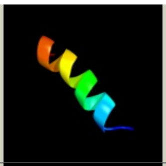
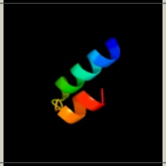
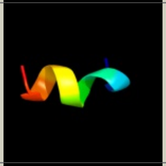
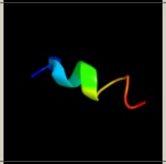
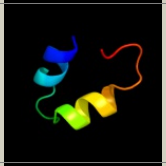
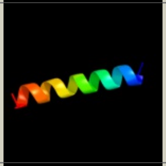
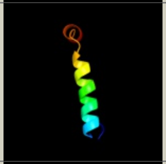
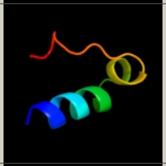
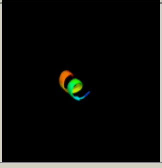
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pkxa2	Alignment		40.6	37	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
2	c1zczA_	Alignment		39.0	39	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
3	d1g8ma2	Alignment		33.2	26	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
4	d1zcza2	Alignment		29.4	42	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
5	c1thzA_	Alignment		29.0	26	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
6	c2kw0A_	Alignment		28.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
7	d1cy9a_	Alignment		27.4	36	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
8	c2hl7A_	Alignment		26.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
9	c4a1oB_	Alignment		24.1	50	**PDB header:**transferase-hydrolase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
10	c3c4mD_	Alignment		23.9	29	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**parathyroid hormone; **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)
11	c3c4mC_	Alignment		23.9	29	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**parathyroid hormone; **PDBTitle:** structure of human parathyroid hormone in complex with the2 extracellular domain of its g-protein-coupled receptor (pth1r)

12	c1z4hA_	Alignment		23.3	11	**PDB header:**protein binding, dna binding protein **Chain:** A: **PDB Molecule:**tor inhibition protein; **PDBTitle:** the response regulator tori belongs to a new family of2 atypical excisionase
13	c3jzaB_	Alignment		23.3	32	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**uncharacterized protein drra; **PDBTitle:** crystal structure of human rab1b in complex with the gef domain of2 drra/sidm from legionella pneumophila
14	c3gyqB_	Alignment		23.3	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna (adenosine-2'-o-)-methyltransferase; **PDBTitle:** structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
15	c2rmiA_	Alignment		22.3	50	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**astressin; **PDBTitle:** 3d nmr structure of astressin
16	d1mw9x_	Alignment		19.0	32	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
17	c3tj6B_	Alignment		18.9	36	**PDB header:**protein binding/toxin **Chain:** B: **PDB Molecule:**protein ps 120; **PDBTitle:** human vinculin head domain (vh1, residues 1-258) in complex with the2 vinculin binding site of the surface cell antigen 4 (sca4-vbs-c;3 residues 812-835) from rickettsia rickettsii
18	d2a07f1	Alignment		17.2	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
19	c3g73A_	Alignment		16.9	23	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**forkhead box protein m1; **PDBTitle:** structure of the foxm1 dna binding
20	c1zwgA_	Alignment		16.5	50	**PDB header:**hormone **Chain:** A: **PDB Molecule:**parathyroid hormone; **PDBTitle:** succinyl human parathyroid hormone 4-37, nmr, 10 structures
21	c2fjlA_	Alignment	not modelled	16.2	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate **PDBTitle:** solution structure of the split ph domain in phospholipase2 c-gamma1
22	c2o59B_	Alignment	not modelled	16.2	43	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase 3; **PDBTitle:** structure of e. coli topoisomerase iii in complex with an 8-2 base single stranded oligonucleotide. frozen in glycerol3 ph 8.0
23	c2ha8A_	Alignment	not modelled	15.5	27	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**tar (hiv-1) rna loop binding protein; **PDBTitle:** methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
24	c1gl9B_	Alignment	not modelled	15.5	25	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
25	c3n6oB_	Alignment	not modelled	15.4	32	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide exchange factor; **PDBTitle:** crystal structure of the gef and p4m domain of drra/sidm from2 legionella pneumophila
26	c3swfA_	Alignment	not modelled	15.3	32	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
27	c1x7pB_	Alignment	not modelled	15.2	60	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna methyltransferase; **PDBTitle:** crystal structure of the spou methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
28	d1gkub3	Alignment	not modelled	14.7	29	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase

						Family: Prokaryotic type I DNA topoisomerase
29	c2pihA_	Alignment	not modelled	14.4	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ymca; **PDBTitle:** crystal structure of protein ymca from bacillus subtilis,2 northeast structural genomics target sr375
30	d2piha1	Alignment	not modelled	14.4	7	**Fold:**YheA-like **Superfamily:**YheA/YmcA-like **Family:**YmcA-like
31	c2l1nA_	Alignment	not modelled	14.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the protein yp_399305.1
32	d2vgna2	Alignment	not modelled	14.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**ERF1/Dom34 middle domain-like
33	c3omdB_	Alignment	not modelled	14.3	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of unknown function protein from leptospirillum2 rubarum
34	d3bpya1	Alignment	not modelled	13.6	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
35	d1ipaa1	Alignment	not modelled	13.3	56	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
36	c1zhcA_	Alignment	not modelled	13.2	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hp1242; **PDBTitle:** solution structure of hp1242 from helicobacter pylori
37	d2c6ya1	Alignment	not modelled	12.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
38	c1e17A_	Alignment	not modelled	11.4	38	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
39	c3co7C_	Alignment	not modelled	10.8	42	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
40	d2hfha_	Alignment	not modelled	10.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
41	c1kq8A_	Alignment	not modelled	10.4	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 3 forkhead homolog 1; **PDBTitle:** solution structure of winged helix protein hfh-1
42	d1kq8a_	Alignment	not modelled	10.4	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
43	d1d5va_	Alignment	not modelled	10.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
44	c1mofA_	Alignment	not modelled	10.1	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**moloney murine leukemia virus p15; **PDBTitle:** coat protein
45	c2eboB_	Alignment	not modelled	10.0	15	**PDB header:**envelope glycoprotein **Chain:** B: **PDB Molecule:**ebola virus envelope glycoprotein; **PDBTitle:** core structure of gp2 from ebola virus
46	d2c4ka2	Alignment	not modelled	9.1	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
47	d2j5ya1	Alignment	not modelled	9.1	33	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**GA module, an albumin-binding domain
48	c2gajA_	Alignment	not modelled	9.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
49	d1i7da_	Alignment	not modelled	8.6	29	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
50	d1whqa_	Alignment	not modelled	8.5	38	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
51	d1jb0b_	Alignment	not modelled	8.4	24	**Fold:**Photosystem I subunits PsaA/PsaB **Superfamily:**Photosystem I subunits PsaA/PsaB **Family:**Photosystem I subunits PsaA/PsaB
52	c1fvyA_	Alignment	not modelled	8.0	50	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**parathyroid hormone; **PDBTitle:** solution structure of the osteogenic 1-31 fragment of the2 human parathyroid hormone
53	d2qi2a2	Alignment	not modelled	7.5	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**ERF1/Dom34 middle domain-like
54	c2kjmA_	Alignment	not modelled	7.3	30	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**histone rna hairpin-binding protein; **PDBTitle:** solution structure of slbp rna binding domain fragment
55	d1v4sa1	Alignment	not modelled	7.3	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase

56	c3he4A_	Alignment	not modelled	7.1	39	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synzip6; **PDBTitle:** heterospecific coiled-coil pair synzip5:synzip6
57	c2wttL_	Alignment	not modelled	7.0	28	**PDB header:**transcription **Chain:** L: **PDB Molecule:**tumor protein p73; **PDBTitle:** structure of the human p73 tetramerization domain (crystal2 form ii)
58	d1gz0a1	Alignment	not modelled	6.9	50	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
59	c1gz0G_	Alignment	not modelled	6.9	50	**PDB header:**transferase **Chain:** G: **PDB Molecule:**hypothetical trna/rrna methyltransferase yjfh; **PDBTitle:** 23s ribosomal rna g2251 2'o-methyltransferase rlmb
60	d1ig8a1	Alignment	not modelled	6.6	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
61	c3bkhA_	Alignment	not modelled	6.5	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
62	d1dkua2	Alignment	not modelled	6.5	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
63	d2eyqa6	Alignment	not modelled	6.5	17	**Fold:**TRCF domain-like **Superfamily:**TRCF domain-like **Family:**TRCF domain
64	d1meka_	Alignment	not modelled	6.3	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
65	c1u0iA_	Alignment	not modelled	6.3	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**iaal-e3; **PDBTitle:** iaal-e3/k3 heterodimer
66	c4a9zD_	Alignment	not modelled	6.1	36	**PDB header:**transcription **Chain:** D: **PDB Molecule:**tumor protein 63; **PDBTitle:** crystal structure of human p63 tetramerization domain
67	c1ipaA_	Alignment	not modelled	5.9	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna 2'-o-ribose methyltransferase; **PDBTitle:** crystal structure of rna 2'-o ribose methyltransferase
68	c3dlaD_	Alignment	not modelled	5.6	21	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
69	c1eboE_	Alignment	not modelled	5.5	15	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**ebola virus envelope protein chimera consisting **PDBTitle:** crystal structure of the ebola virus membrane-fusion2 subunit, gp2, from the envelope glycoprotein ectodomain
70	c2qjvB_	Alignment	not modelled	5.2	33	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**uncharacterized iolb-like protein; **PDBTitle:** crystal structure of an iolb-like protein (stm4420) from salmonella2 typhimurium lt2 at 1.90 a resolution
71	d1z1za1	Alignment	not modelled	5.1	38	**Fold:**Phage tail protein-like **Superfamily:**Phage tail protein-like **Family:**Lambda phage gpU-like