Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q9S4X3
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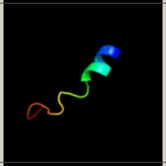
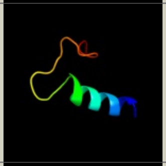
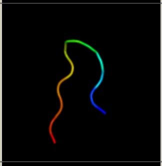
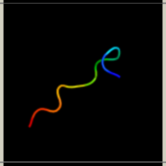
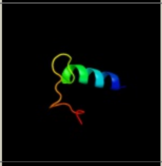
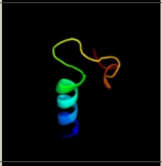
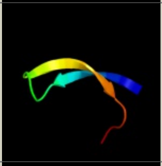
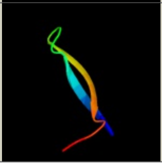
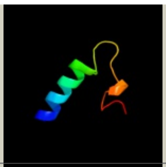
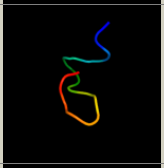
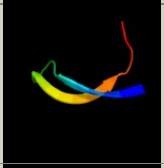
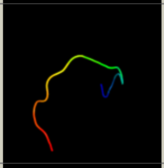
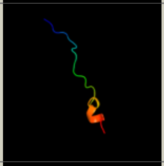
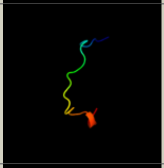
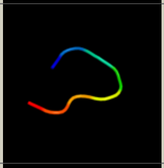
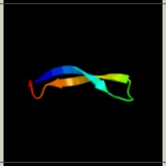
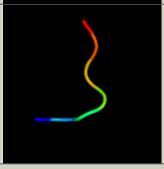
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1keaa_	Alignment		38.2	20	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
2	d1u61a_	Alignment		23.2	42	**Fold:**RNase III domain-like **Superfamily:**RNase III domain-like **Family:**RNase III catalytic domain-like
3	c1rrqA_	Alignment		21.9	23	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
4	c2qvtA_	Alignment		20.9	75	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**avrl567-d; **PDBTitle:** structure of melampsora lini avirulence protein, avrl567-d
5	d1mhna_	Alignment		19.7	25	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
6	d1orna_	Alignment		18.3	17	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
7	c2y8sE_	Alignment		18.1	64	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**rhoptry neck protein 2; **PDBTitle:** co-structure of an ama1 mutant (y230a) with a surface2 exposed region of ron2 from toxoplasma gondii
8	d2abka_	Alignment		17.2	31	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
9	c3n5nX_	Alignment		17.1	22	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**a/g-specific adenine dna glycosylase; **PDBTitle:** crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
10	c4a4fA_	Alignment		14.3	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**survival of motor neuron-related-splicing factor 30; **PDBTitle:** solution structure of spf30 tudor domain in complex with2 symmetrically dimethylated arginine
11	c1g5vA_	Alignment		14.2	30	**PDB header:**translation **Chain:** A: **PDB Molecule:**survival motor neuron protein 1; **PDBTitle:** solution structure of the tudor domain of the human smn2 protein

12	d1kg2a_	Alignment		12.6	17	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
13	c3ushB_	Alignment		12.0	47	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q2s0r5 protein from salinibacter ruber,2 northeast structural genomics consortium target srr207
14	d2d9ta1	Alignment		11.4	22	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
15	c2d9tA_	Alignment		10.6	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tudor domain-containing protein 3; **PDBTitle:** solution structure of the tudor domain of tudor domain2 containing protein 3 from mouse
16	d2aqaa1	Alignment		10.5	33	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
17	d2ey4e1	Alignment		10.4	38	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
18	c2jnvA_	Alignment		10.2	75	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
19	c3qiiA_	Alignment		10.2	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 2 of human phd finger protein 20
20	c2b5lC_	Alignment		9.8	57	**PDB header:**protein binding/viral protein **Chain:** C: **PDB Molecule:**nonstructural protein v; **PDBTitle:** crystal structure of ddb1 in complex with simian virus 5 v2 protein
21	d1xhja_	Alignment	not modelled	9.0	75	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
22	c3pnwX_	Alignment	not modelled	8.9	22	**PDB header:**protein binding/immune system **Chain:** X: **PDB Molecule:**tudor domain-containing protein 3; **PDBTitle:** crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab
23	c2equA_	Alignment	not modelled	8.8	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1
24	d1en2a2	Alignment	not modelled	8.6	48	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant lectins/antimicrobial peptides **Family:**Hevein-like agglutinin (lectin) domain
25	d1ehda2	Alignment	not modelled	8.5	48	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant lectins/antimicrobial peptides **Family:**Hevein-like agglutinin (lectin) domain
26	d1rrqa1	Alignment	not modelled	8.4	24	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
27	d2apob1	Alignment	not modelled	8.4	33	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
28	c2gslE_	Alignment	not modelled	8.1	22	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**hypothetical protein; **PDBTitle:** x-ray crystal structure of protein fn1578 from fusobacterium2 nucleatum. northeast structural genomics consortium target nr1.

29	d1veha_	Alignment	not modelled	8.0	50	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
30	d1khia2	Alignment	not modelled	7.7	39	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
31	c2z51A_	Alignment	not modelled	7.5	75	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 2, chloroplast; **PDBTitle:** crystal structure of arabidopsis cnfu involved in iron-2 sulfur cluster biosynthesis
32	d1eysh2	Alignment	not modelled	7.0	46	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
33	c3p8dB_	Alignment	not modelled	6.8	27	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**medulloblastoma antigen mu-mb-50.72; **PDBTitle:** crystal structure of the second tudor domain of human phf20 (homodimer2 form)
34	c2h2rB_	Alignment	not modelled	6.0	44	**PDB header:**immune system **Chain:** B: **PDB Molecule:**low affinity immunoglobulin epsilon fc receptor **PDBTitle:** crystal structure of the human cd23 lectin domain, apo form
35	d1v7wa2	Alignment	not modelled	5.8	19	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
36	c1xniI_	Alignment	not modelled	5.7	25	**PDB header:**cell cycle **Chain:** I: **PDB Molecule:**tumor suppressor p53-binding protein 1; **PDBTitle:** tandem tudor domain of 53bp1
37	d1vqoi1	Alignment	not modelled	5.6	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
38	d2fug11	Alignment	not modelled	5.4	29	**Fold:**Bromodomain-like **Superfamily:**Nqo1C-terminal domain-like **Family:**Nqo1C-terminal domain-like
39	c3i0uA_	Alignment	not modelled	5.2	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphothreonine lyase ospf; **PDBTitle:** structure of the type iii effector/phosphothreonine lyase ospf from2 shigella flexneri
40	c1vq8I_	Alignment	not modelled	5.1	50	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**50s ribosomal protein l11p; **PDBTitle:** the structure of ccda-phe-cap-bio and the antibiotic sparsomycin bound2 to the large ribosomal subunit of haloarcula marismortui
41	d2p8ta1	Alignment	not modelled	5.1	43	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PH0730 N-terminal domain-like
42	d1twfi1	Alignment	not modelled	5.1	29	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain