Phyre2

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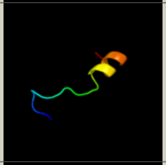
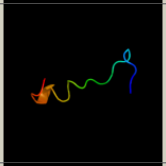
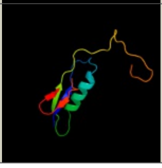
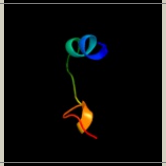
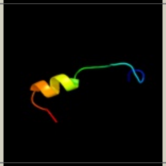
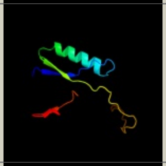
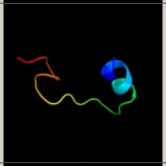
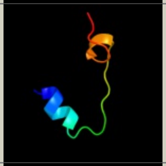
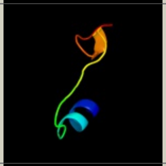
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3e7nB_	Alignment		100.0	86	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**d-ribose high-affinity transport system; **PDBTitle:** crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
2	d1ogda_	Alignment		100.0	46	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
3	d2ob5a1	Alignment		100.0	20	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
4	c3mvkA_	Alignment		100.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein fucu; **PDBTitle:** the crystal structure of fucu from bifidobacterium longum to 1.65a
5	c2wcvl_	Alignment		100.0	19	**PDB header:**isomerase **Chain:** I: **PDB Molecule:**l-fucose mutarotase; **PDBTitle:** crystal structure of bacterial fucu
6	c2wcuB_	Alignment		100.0	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**protein fucu homolog; **PDBTitle:** crystal structure of mammalian fucu
7	c3p13B_	Alignment		100.0	42	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribose pyranase; **PDBTitle:** complex structure of d-ribose pyranase sa240 with d-ribose
8	c2j5dA_	Alignment		26.8	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** nmr structure of bnip3 transmembrane domain in lipid2 bicelles
9	c2dgbA_	Alignment		25.8	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
10	d1t4aa_	Alignment		23.6	14	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
11	c2jerG_	Alignment		21.3	12	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**agmatine deiminase; **PDBTitle:** agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.

12	c3l0zC_	Alignment		21.2	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative nicotinate-nucleotide-dimethylbenzimidazole **PDBTitle:** crystal structure of a putative nicotinate-nucleotide-2 dimethylbenzimidazole phosphoribosyltransferase from3 methanocaldococcus jannaschii dsm 2661
13	d1e3da_	Alignment		21.0	28	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
14	c2yx5A_	Alignment		20.6	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
15	d2jera1	Alignment		18.4	12	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
16	d1cc1s_	Alignment		16.4	32	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
17	d1frfs_	Alignment		16.4	36	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
18	d1gtda_	Alignment		16.4	30	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
19	c3myrE_	Alignment		15.6	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
20	d1wuis1	Alignment		15.4	24	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
21	c1h2aS_	Alignment	not modelled	15.3	24	**PDB header:**oxidoreductase **Chain:** S: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
22	c2xd4A_	Alignment	not modelled	15.0	0	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
23	d1w1we_	Alignment	not modelled	14.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rad21/Rec8-like
24	c1w1wF_	Alignment	not modelled	14.9	18	**PDB header:**cell adhesion **Chain:** F: **PDB Molecule:**sister chromatid cohesion protein 1; **PDBTitle:** sc smc1hd:scc1-c complex, atpgs
25	d1gpma3	Alignment	not modelled	14.0	22	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**GMP synthetase C-terminal dimerisation domain **Family:**GMP synthetase C-terminal dimerisation domain
26	d1guza1	Alignment	not modelled	12.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
27	c2wpnA_	Alignment	not modelled	12.4	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [nifese] hydrogenase, small subunit; **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
28	c3rgwS_	Alignment	not modelled	12.2	28	**PDB header:**oxidoreductase/oxidoreductase **Chain:** S: **PDB Molecule:**membrane-bound hydrogenase (nife) small subunit hoxk; **PDBTitle:** crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel

						iron-sulfur3 cluster
29	d5ldha1	Alignment	not modelled	11.8	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
30	c2qk4A_	Alignment	not modelled	11.0	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trifunctional purine biosynthetic protein adenosine-3; **PDBTitle:** human glycinamide ribonucleotide synthetase
31	d1yq9a1	Alignment	not modelled	10.9	23	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
32	d1y8xb1	Alignment	not modelled	10.1	27	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Ubiquitin activating enzymes (UBA)
33	c3u4gA_	Alignment	not modelled	9.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**namn:dmb phosphoribosyltransferase; **PDBTitle:** the structure of cobt from pyrococcus horikoshii
34	d1qkia1	Alignment	not modelled	9.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
35	d1llda1	Alignment	not modelled	9.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
36	d1ldna1	Alignment	not modelled	9.6	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
37	c2cp8A_	Alignment	not modelled	9.5	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**next to brca1 gene 1 protein; **PDBTitle:** solution structure of the rsgi ruh-046, a uba domain from2 human next to brca1 gene 1 protein (kiaa0049 protein)3 r923h variant
38	d1vq3a_	Alignment	not modelled	9.4	14	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
39	c1okgA_	Alignment	not modelled	9.2	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
40	d1xkna_	Alignment	not modelled	8.3	21	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
41	c2r60A_	Alignment	not modelled	8.3	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
42	d2ldxa1	Alignment	not modelled	8.2	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
43	c2zw2B_	Alignment	not modelled	8.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
44	d1i10a1	Alignment	not modelled	8.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
45	d1jkea_	Alignment	not modelled	8.0	10	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
46	d1ldma1	Alignment	not modelled	8.0	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
47	d1hyha1	Alignment	not modelled	7.8	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
48	d1yjma1	Alignment	not modelled	7.8	23	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
49	d1hyea1	Alignment	not modelled	7.5	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
50	d2cmua1	Alignment	not modelled	7.4	15	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
51	d1llca1	Alignment	not modelled	7.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
52	c3lrxC_	Alignment	not modelled	7.3	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative hydrogenase; **PDBTitle:** crystal structure of the c-terminal domain (residues 78-226)2 of pf1911 hydrogenase from pyrococcus furiosus, northeast3 structural genomics consortium target pfr246a
53	c1yj5C_	Alignment	not modelled	7.3	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
54	d2crna1	Alignment	not modelled	7.2	7	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain

55	c2jy5A_	Alignment	not modelled	7.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
56	d1qx4a2	Alignment	not modelled	7.2	22	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
57	d1vpka2	Alignment	not modelled	7.0	3	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit
58	d176la_	Alignment	not modelled	6.7	18	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
59	c2okvC_	Alignment	not modelled	6.6	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable d-tyrosyl-trna(tyr) deacylase 1; **PDBTitle:** c-myc dna unwinding element binding protein
60	c2cwbA_	Alignment	not modelled	6.4	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**chimera of immunoglobulin g binding protein g **PDBTitle:** solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
61	d1veja1	Alignment	not modelled	6.4	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
62	d2daha1	Alignment	not modelled	6.3	8	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
63	d1zbra1	Alignment	not modelled	6.1	14	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
64	c3kcnA_	Alignment	not modelled	6.1	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase homolog; **PDBTitle:** the crystal structure of adenylate cyclase from2 rhodopirellula baltica
65	d1ez4a1	Alignment	not modelled	6.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
66	c2ys6A_	Alignment	not modelled	6.0	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
67	d1u1ia1	Alignment	not modelled	6.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
68	c2dbfA_	Alignment	not modelled	5.9	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nuclear factor nf-kappa-b p105 subunit; **PDBTitle:** solution structure of the death domain in human nuclear2 factor nf-kappa-b p105 subunit
69	d2dnaa1	Alignment	not modelled	5.8	8	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
70	d1gawa2	Alignment	not modelled	5.6	26	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
71	d189la_	Alignment	not modelled	5.6	18	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
72	c1wr1B_	Alignment	not modelled	5.5	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
73	c2dnaA_	Alignment	not modelled	5.4	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
74	c1umkA_	Alignment	not modelled	5.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-cytochrome b5 reductase; **PDBTitle:** the structure of human erythrocyte nadh-cytochrome b52 reductase
75	d9ldta1	Alignment	not modelled	5.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
76	d1i0za1	Alignment	not modelled	5.2	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
77	c3cioA_	Alignment	not modelled	5.2	18	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase etk; **PDBTitle:** the kinase domain of escherichia coli tyrosine kinase etk