Phyre^2

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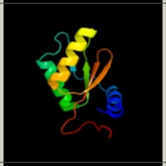
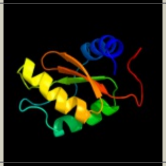
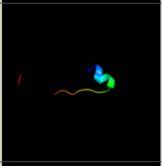
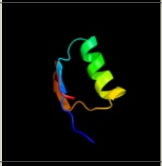
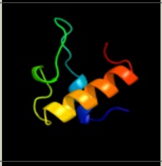
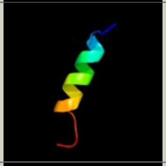
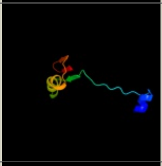
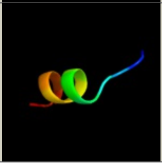
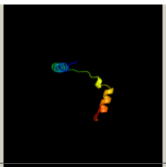
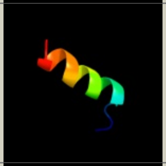
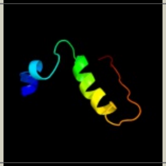
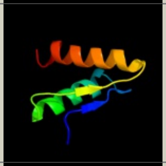
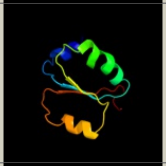
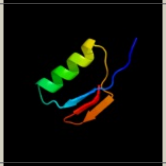
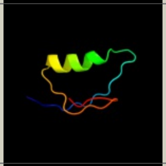
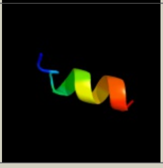
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ln4a_	Alignment		100.0	98	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
2	d1jo0a_	Alignment		100.0	75	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
3	d1rq8a_	Alignment		100.0	38	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
4	c2e6xD_	Alignment		27.4	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ttha1281; **PDBTitle:** x-ray structure of tt1592 from thermus thermophilus hb8
5	d2pc6a1	Alignment		25.8	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
6	d1stza1	Alignment		16.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
7	d1iufa1	Alignment		15.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
8	c2pc6C_	Alignment		15.6	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
9	d1nvpb_	Alignment		13.9	35	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
10	c1nvpB_	Alignment		13.9	35	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription initiation factor iia alpha chain; **PDBTitle:** human tfiia/tbp/dna complex
11	d1wmub_	Alignment		13.1	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins

12	c1lc3A_	Alignment		13.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biliverdin reductase a; **PDBTitle:** crystal structure of a biliverdin reductase enzyme-cofactor2 complex
13	d1nh2b_	Alignment		12.3	18	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
14	d1s16a2	Alignment		11.7	10	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
15	d1nh9a_	Alignment		11.5	17	**Fold:**IF3-like **Superfamily:**AlbA-like **Family:**DNA-binding protein AlbA
16	c1zzgB_	Alignment		11.5	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
17	d2f1fa2	Alignment		11.3	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
18	d1fhjb_	Alignment		10.7	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
19	d2fgca1	Alignment		10.6	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
20	d1cg5b_	Alignment		10.6	38	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
21	d1spgb_	Alignment	not modelled	10.5	8	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
22	c3ka5A_	Alignment	not modelled	10.2	16	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**ribosome-associated protein y (psrp-1); **PDBTitle:** crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
23	c3rbvA_	Alignment	not modelled	9.2	10	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar 3-ketoreductase; **PDBTitle:** crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
24	c3e9mC_	Alignment	not modelled	8.6	8	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
25	d1l3la1	Alignment	not modelled	8.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
26	d1oela2	Alignment	not modelled	8.0	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
27	d3bj1b1	Alignment	not modelled	7.8	0	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
28	c2yu3A_	Alignment	not modelled	7.4	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase iii 39 kda **PDBTitle:** solution structure of the domain swapped wingedhelix in dna-2 directed rna polymerase iii 39 kda polypeptide

29	d2d5xb1	Alignment	not modelled	7.3	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
30	d1srva_	Alignment	not modelled	7.1	17	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
31	c2fgcA_	Alignment	not modelled	7.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
32	d1lc0a1	Alignment	not modelled	7.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
33	d1we3a2	Alignment	not modelled	6.8	17	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
34	c2rrnA_	Alignment	not modelled	6.8	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** solution structure of secdf periplasmic domain p4
35	d1dk7a_	Alignment	not modelled	6.5	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
36	c3k2tA_	Alignment	not modelled	6.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2511 protein; **PDBTitle:** crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
37	c3mvcB_	Alignment	not modelled	6.5	15	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**globin protein 6; **PDBTitle:** high resolution crystal structure of the heme domain of glb-6 from c.2 elegans
38	c1tltB_	Alignment	not modelled	6.4	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase (virulence factor mvim homolog); **PDBTitle:** crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
39	c2nuhA_	Alignment	not modelled	6.4	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**periplasmic divalent cation tolerance protein; **PDBTitle:** crystal structure of cuta from the phytopathgen bacterium xylella2 fastidiosa
40	c2h9uA_	Alignment	not modelled	6.4	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna/rna-binding protein alba 2; **PDBTitle:** crystal structure of the archaea specific dna binding protein
41	d1kida_	Alignment	not modelled	6.3	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
42	d2d0ob1	Alignment	not modelled	6.2	13	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Dehydratase-reactivating factor beta subunit
43	d1nfja_	Alignment	not modelled	6.1	19	**Fold:**IF3-like **Superfamily:**AlbA-like **Family:**DNA-binding protein AlbA
44	d1sjpa2	Alignment	not modelled	6.0	12	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**GroEL-like chaperone, apical domain
45	d1fsla_	Alignment	not modelled	6.0	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
46	d1tw4a_	Alignment	not modelled	5.8	32	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
47	c3em0A_	Alignment	not modelled	5.8	21	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**ileal bile acid-binding protein; **PDBTitle:** crystal structure of zebrafish ileal bile acid-bindin protein2 complexed with cholic acid (crystal form b).
48	d1r6bx3	Alignment	not modelled	5.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
49	d1ofha_	Alignment	not modelled	5.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
50	d1ydha_	Alignment	not modelled	5.6	21	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
51	d2isba1	Alignment	not modelled	5.5	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
52	d1bxni_	Alignment	not modelled	5.4	27	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
53	d1jg5a_	Alignment	not modelled	5.4	22	**Fold:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Superfamily:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Family:**GTP cyclohydrolase I feedback regulatory protein, GFRP
54	d2nrka1	Alignment	not modelled	5.4	25	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**GrpB-like

55	d1owla2	Alignment	not modelled	5.4	17	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
56	d1np7a2	Alignment	not modelled	5.3	17	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
57	d1ub3a_	Alignment	not modelled	5.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
58	d2cvea1	Alignment	not modelled	5.3	25	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
59	d2a4aa1	Alignment	not modelled	5.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
60	d1a04a1	Alignment	not modelled	5.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
61	c1tezB_	Alignment	not modelled	5.2	17	**PDB header:**lyase/dna **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** complex between dna and the dna photolyase from anacystis nidulans