Phyre2

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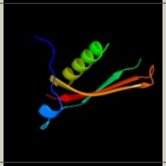
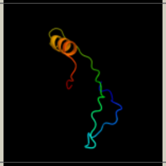
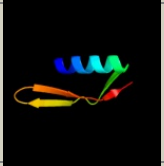
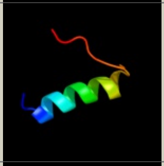
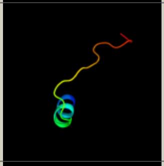
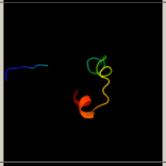
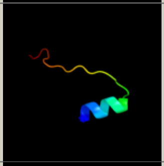
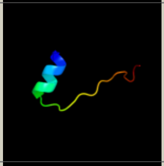
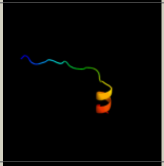
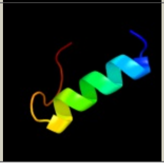
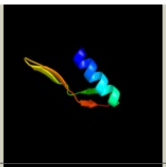
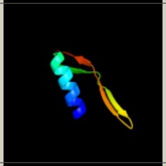
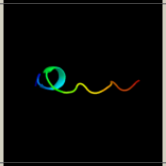
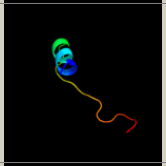
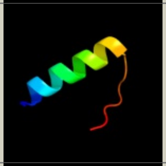
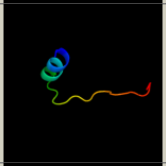
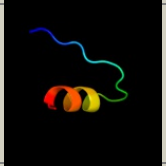
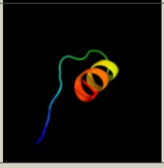
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2noca1	Alignment		99.9	24	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
2	d2jnaa1	Alignment		99.9	22	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
3	c2k4qA_	Alignment		66.1	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major tail protein v; **PDBTitle:** the solution structure of gpv, the major tail protein from2 bacteriophage lambda
4	c3qkbB_	Alignment		38.0	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
5	c3b9nB_	Alignment		30.6	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkane monoxygenase; **PDBTitle:** crystal structure of long-chain alkane monooxygenase (lada)
6	c1hl8B_	Alignment		27.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
7	c2pxgA_	Alignment		20.9	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein; **PDBTitle:** nmr solution structure of omla
8	c3eypB_	Alignment		20.8	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron
9	c3mo4B_	Alignment		19.9	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase; **PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
10	c3ls1A_	Alignment		17.7	33	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
11	c3sdoB_	Alignment		17.5	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei

12	c1y2iC_	Alignment		16.6	26	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein s0862; **PDBTitle:** crystal structure of mcsg target apc27401 from shigella2 flexneri
13	d1y2ia_	Alignment		16.6	26	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
14	c2jpwA_	Alignment		16.1	47	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin i, cardiac muscle; **PDBTitle:** solution structure of the bisphosphorylated cardiac2 specific n-extension of cardiac troponin i
15	d1hl9a2	Alignment		14.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
16	d1luca_	Alignment		14.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
17	c2wvsD_	Alignment		13.4	8	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**alpha-l-fucosidase; **PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
18	d1lucb_	Alignment		13.2	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
19	d1nh2a2	Alignment		11.4	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
20	d1cdwa2	Alignment		10.9	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
21	d2g39a1	Alignment	not modelled	10.7	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
22	c1z69D_	Alignment	not modelled	9.9	30	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**coenzyme f420-dependent n(5),n(10)- **PDBTitle:** crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
23	d1qnaa2	Alignment	not modelled	9.2	10	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
24	c3eikB_	Alignment	not modelled	9.1	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** double stranded dna binding protein
25	d1mp9a1	Alignment	not modelled	8.9	20	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
26	c3gzaB_	Alignment	not modelled	8.6	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
27	d1mp9a2	Alignment	not modelled	8.5	15	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
28	d1aisa2	Alignment	not modelled	8.5	20	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
						Fold:TIM beta/alpha-barrel

29	d1f07a_	Alignment	not modelled	8.4	28	**Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
30	c3ir9A_	Alignment	not modelled	8.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei.
31	d2bsqe1	Alignment	not modelled	8.2	30	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Trafficking protein A-like
32	c1d3uA_	Alignment	not modelled	8.0	20	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**tata-binding protein; **PDBTitle:** tata-binding protein/transcription factor (ii)b/bre+tata-2 box complex from pyrococcus woesei
33	c2jz7A_	Alignment	not modelled	7.9	19	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
34	c1kqfB_	Alignment	not modelled	7.9	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
35	c1mp9B_	Alignment	not modelled	7.7	15	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**tata-binding protein; **PDBTitle:** tbp from a mesothermophilic archaeon, sulfolobus2 acidocaldarius
36	d2hqsa2	Alignment	not modelled	7.4	19	**Fold:**Anticodon-binding domain-like **Superfamily:**TolB, N-terminal domain **Family:**TolB, N-terminal domain
37	c1rm1A_	Alignment	not modelled	7.0	10	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**tata-box binding protein; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
38	c1ngmM_	Alignment	not modelled	7.0	10	**PDB header:**transcription/dna **Chain:** M: **PDB Molecule:**transcription initiation factor tfiid; **PDBTitle:** crystal structure of a yeast brf1-tbp-dna ternary complex
39	d3etja1	Alignment	not modelled	7.0	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
40	c2amlB_	Alignment	not modelled	7.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sis domain protein; **PDBTitle:** crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
41	c2z8uQ_	Alignment	not modelled	6.9	30	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** methanococcus jannaschii tbp
42	c2i7gA_	Alignment	not modelled	6.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monooxygenase; **PDBTitle:** crystal structure of monooxygenase from agrobacterium tumefaciens
43	c3dnfB_	Alignment	not modelled	6.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
44	d1vjpa1	Alignment	not modelled	6.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	d2qrra1	Alignment	not modelled	6.4	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
46	c1tvlA_	Alignment	not modelled	6.4	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein ytnj; **PDBTitle:** structure of ytnj from bacillus subtilis
47	d1tvla_	Alignment	not modelled	6.4	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
48	c1f02T_	Alignment	not modelled	6.2	33	**PDB header:**cell adhesion **Chain:** T: **PDB Molecule:**translocated intimin receptor; **PDBTitle:** crystal structure of c-terminal 282-residue fragment of2 intimin in complex with translocated intimin receptor3 (tir) intimin-binding domain
49	c3hajA_	Alignment	not modelled	6.1	8	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**human pacsin2 f-bar; **PDBTitle:** crystal structure of human pacsin2 f-bar domain (p2121212 lattice)
50	d1ycga1	Alignment	not modelled	6.1	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
51	d1zjca1	Alignment	not modelled	6.1	19	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
52	c2k38A_	Alignment	not modelled	6.0	19	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**cupiennin-1a; **PDBTitle:** cupiennin 1a, nmr, minimized average structure
53	c1k4uP_	Alignment	not modelled	6.0	40	**PDB header:**hormone/growth factor **Chain:** P: **PDB Molecule:**phagocyte nadph oxidase subunit p47phox; **PDBTitle:** solution structure of the c-terminal sh3 domain of p67phox2 complexed with the c-terminal tail region of p47phox
54	c3euaD_	Alignment	not modelled	5.9	11	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase

						(bsu32610) from2 bacillus subtilis at 1.90 a resolution
55	d1nqka_	Alignment	not modelled	5.8	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Ssud-like monoxygenases
56	d2bbaa1	Alignment	not modelled	5.7	16	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Ephrin receptor ligand binding domain
57	d1wu7a1	Alignment	not modelled	5.5	28	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
58	c3fkjA_	Alignment	not modelled	5.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
59	c3mi6A_	Alignment	not modelled	5.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of the alpha-galactosidase from lactobacillus2 brevis, northeast structural genomics consortium target lbr11.
60	d1nh2a1	Alignment	not modelled	5.1	22	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
61	d2ayia1	Alignment	not modelled	5.1	18	**Fold:**Thermophilic metalloprotease-like **Superfamily:**Thermophilic metalloprotease-like **Family:**Thermophilic metalloprotease (M29)
62	c3dfeA_	Alignment	not modelled	5.1	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative pii-like signaling protein; **PDBTitle:** crystal structure of a putative pii-like signaling protein2 (yp_323533.1) from anabaena variabilis atcc 29413 at 2.35 a3 resolution