Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AAX6
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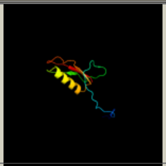
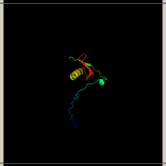
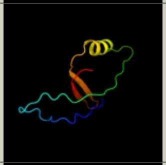
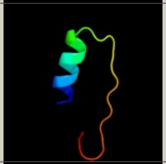
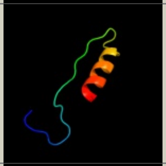
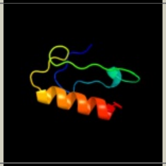
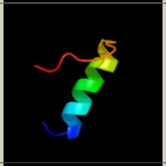
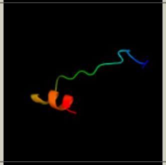
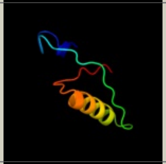
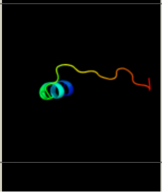
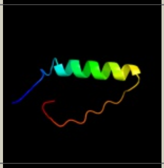
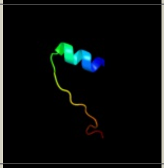
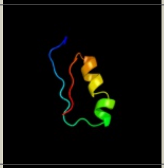
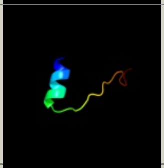
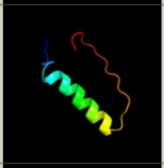
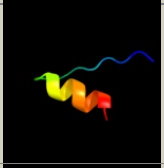
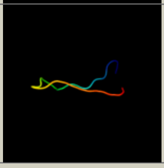
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2noca1	Alignment		100.0	34	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
2	d2jnaa1	Alignment		100.0	31	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like
3	c2k4qA_	Alignment		54.2	12	**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	c3dfeA_	Alignment		31.8	38	**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
5	c3dnfB_	Alignment		26.1	16	**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
6	d1kjqa1	Alignment		25.7	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
7	c3ke8A_	Alignment		22.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
8	c3b9nB_	Alignment		20.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkane monoxygenase; **PDBTitle:** crystal structure of long-chain alkane monooxygenase (lada)
9	d3etja1	Alignment		20.0	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
10	c2y1bA_	Alignment		20.0	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative outer membrane protein, signal; **PDBTitle:** crystal structure of the e. coli outer membrane lipoprotein2 rcsf
11	c1hl8B_	Alignment		19.4	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase

12	c3lubE_	Alignment		19.3	13	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
13	c3no4A_	Alignment		18.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**creatinine amidohydrolase; **PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
14	c3eypB_	Alignment		14.6	4	**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
15	c2v82A_	Alignment		13.5	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
16	c3qkbB_	Alignment		13.2	24	**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
17	c3mo4B_	Alignment		13.2	13	**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
18	d1v7za_	Alignment		11.9	18	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
19	d1cdwa2	Alignment		11.7	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
20	c2w1sB_	Alignment		11.5	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** unique ligand binding specificity of a family 322 carbohydrate-binding module from the mu toxin produced by3 clostridium perfringens
21	c2jz7A_	Alignment	not modelled	10.9	23	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
22	c3eikB_	Alignment	not modelled	10.5	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** double stranded dna binding protein
23	c1f02T_	Alignment	not modelled	10.5	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
24	d1hl9a2	Alignment	not modelled	10.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
25	d1aisa2	Alignment	not modelled	10.4	20	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
26	c3sdoB_	Alignment	not modelled	10.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
27	c2wvsD_	Alignment	not modelled	9.5	29	**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
28	d1mp9a2	Alignment	not modelled	9.3	20	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
						PDB header:dna binding protein

29	c1mp9B_	Alignment	not modelled	9.0	20	**Chain:** B: **PDB Molecule:**tata-binding protein; **PDBTitle:** tbp from a mesothermophilic archaeon, sulfolobus2 acidocaldarius
30	c1d3uA_	Alignment	not modelled	8.8	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
31	d1nh2a2	Alignment	not modelled	8.7	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
32	d1txka2	Alignment	not modelled	8.7	29	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
33	d1mp9a1	Alignment	not modelled	8.6	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
34	c2z8uQ_	Alignment	not modelled	8.4	30	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**tata-box-binding protein; **PDBTitle:** methanococcus jannaschii tbp
35	c1txkA_	Alignment	not modelled	8.3	29	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg
36	d1luca_	Alignment	not modelled	8.2	4	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
37	c1ngmM_	Alignment	not modelled	7.9	20	**PDB header:**transcription/dna **Chain:** M: **PDB Molecule:**transcription initiation factor tfiid; **PDBTitle:** crystal structure of a yeast brf1-tbp-dna ternary complex
38	c1rm1A_	Alignment	not modelled	7.9	20	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**tata-box binding protein; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
39	d2g39a1	Alignment	not modelled	7.9	29	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
40	d1qnaa2	Alignment	not modelled	7.6	17	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
41	d1ycga1	Alignment	not modelled	7.5	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
42	d1lucb_	Alignment	not modelled	7.5	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Bacterial luciferase (alkanal monooxygenase)
43	d1f07a_	Alignment	not modelled	7.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**F420 dependent oxidoreductases
44	c3ir9A_	Alignment	not modelled	7.0	22	**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.
45	c1oy8A_	Alignment	not modelled	6.6	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein b; **PDBTitle:** structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
46	d1nh2a1	Alignment	not modelled	6.4	30	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
47	c2k38A_	Alignment	not modelled	6.2	38	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**cupiennin-1a; **PDBTitle:** cupiennin 1a, nmr, minimized average structure
48	d1uqra_	Alignment	not modelled	6.0	45	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
49	d1gqoa_	Alignment	not modelled	6.0	30	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
50	c2zfdB_	Alignment	not modelled	5.9	12	**PDB header:**signaling protein/transferase **Chain:** B: **PDB Molecule:**putative uncharacterized protein t20l15_90; **PDBTitle:** the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcipk14
51	d1aisa1	Alignment	not modelled	5.7	35	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
52	c3gzaB_	Alignment	not modelled	5.7	21	**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
53	c3n8kG_	Alignment	not modelled	5.3	25	**PDB header:**lyase **Chain:** G: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
54	c2uygF_	Alignment	not modelled	5.3	27	**PDB header:**lyase **Chain:** F: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystallogaphic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
55	c2cokA_	Alignment	not modelled	5.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of brct domain of poly(adp-ribose)2


polymerase-1