Phyre^2

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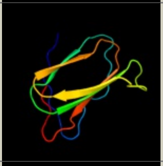
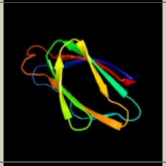
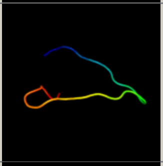
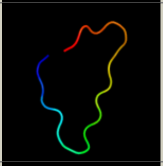
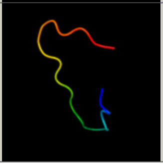
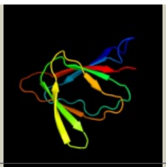
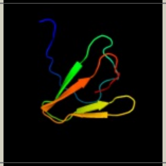
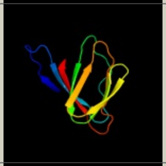
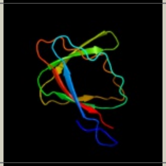
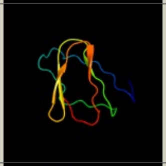
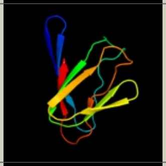
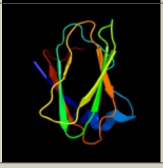
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s4ca1	Alignment		100.0	38	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YhcH-like
2	d1yfua1	Alignment		83.4	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
3	c3cewA_	Alignment		80.2	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cupin protein; **PDBTitle:** crystal structure of a cupin protein (bf4112) from bacteroides2 fragilis. northeast structural genomics consortium target bfr205
4	d1v70a_	Alignment		74.2	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
5	c2i45C_	Alignment		60.1	19	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein nmb1881 from neisseria meningitidis
6	c2oa2A_	Alignment		51.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2720 protein; **PDBTitle:** crystal structure of bh2720 (10175341) from bacillus halodurans at2 1.41 a resolution
7	d1o4ta_	Alignment		47.6	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
8	d2arca_	Alignment		37.8	32	**Fold:**Double-stranded beta-helix **Superfamily:**Regulatory protein AraC **Family:**Regulatory protein AraC
9	d1j3pa_	Alignment		33.6	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
10	c2xxzA_	Alignment		33.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of the human jmjd3 jumonji domain
11	c2xueB_	Alignment		32.3	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of jmjd3

12	c2fqpD_	Alignment		31.3	16	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hypothetical protein bp2299; **PDBTitle:** crystal structure of a cupin domain (bp2299) from bordetella pertussis2 tohama i at 1.80 a resolution
13	c3d82A_	Alignment		31.2	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
14	c3kgzA_	Alignment		30.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2 conserved barrel domain protein; **PDBTitle:** crystal structure of a cupin 2 conserved barrel domain protein from2 rhodopseudomonas palustris
15	d1zvfa1	Alignment		26.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
16	c2oziA_	Alignment		24.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa4178; **PDBTitle:** structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
17	c2ozjB_	Alignment		23.6	29	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel; **PDBTitle:** crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
18	c2gu9B_	Alignment		22.6	12	**PDB header:**immune system **Chain:** B: **PDB Molecule:**tetracenomycin polyketide synthesis protein; **PDBTitle:** crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
19	c2hdlA_	Alignment		20.8	31	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**small inducible cytokine b14; **PDBTitle:** solution structure of brak/cxcl14
20	d2pa7a1	Alignment		19.7	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**dTDP-sugar isomerase
21	d3dl3a1	Alignment	not modelled	19.5	23	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
22	c2w2iC_	Alignment	not modelled	16.6	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate oxygenase; **PDBTitle:** crystal structure of the human 2-oxoglutarate oxygenase2 loc390245
23	d1vj2a_	Alignment	not modelled	16.2	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1459-like
24	c3ht2A_	Alignment	not modelled	16.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**remf protein; **PDBTitle:** zink containing polyketide cyclase remf from streptomyces2 resistomycificus
25	c2pyhB_	Alignment	not modelled	15.9	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**poly(beta-d-mannuronate) c5 epimerase 4; **PDBTitle:** azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide
26	c2r32A_	Alignment	not modelled	15.9	26	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
27	d3bb6a1	Alignment	not modelled	15.7	35	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TehB-like
28	d2bdra1	Alignment	not modelled	15.1	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA
						Fold: Double-stranded beta-helix

29	d1y9qa2	Alignment	not modelled	14.6	22	**Superfamily:**RmlC-like cupins **Family:**Probable transcriptional regulator VC1968, C-terminal domain
30	d1a6qa1	Alignment	not modelled	14.4	19	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
31	c2q8eB_	Alignment	not modelled	14.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**jmjc domain-containing histone demethylation **PDBTitle:** specificity and mechanism of jmjd2a, a trimethyllysine-2 specific histone demethylase
32	c2os2A_	Alignment	not modelled	13.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**jmjc domain-containing histone demethylation protein 3a; **PDBTitle:** crystal structure of jmjd2a complexed with histone h3 peptide2 trimethylated at lys36
33	c3ebrA_	Alignment	not modelled	13.6	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized rmlc-like cupin; **PDBTitle:** crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
34	c3opwA_	Alignment	not modelled	13.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dna damage-responsive transcriptional repressor rph1; **PDBTitle:** crystal structure of the rph1 catalytic core
35	d1j0sa_	Alignment	not modelled	12.2	16	**Fold:**beta-Trefoil **Superfamily:**Cytokine **Family:**Interleukin-1 (IL-1)
36	c3ibmB_	Alignment	not modelled	12.2	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
37	d2es7a1	Alignment	not modelled	12.2	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
38	d2fcta1	Alignment	not modelled	11.3	22	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
39	c3h8uA_	Alignment	not modelled	11.1	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein with double-stranded **PDBTitle:** crystal structure of uncharacterized conserved protein with double-2 stranded beta-helix domain (yp_001338853.1) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.80 a resolution
40	c2bx6A_	Alignment	not modelled	9.7	12	**PDB header:**transduction protein **Chain:** A: **PDB Molecule:**xrp2 protein; **PDBTitle:** crystal structure of the human retinitis pigmentosa2 protein 2 (rp2)
41	c2pfwB_	Alignment	not modelled	9.6	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
42	d1x82a_	Alignment	not modelled	9.4	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Glucose-6-phosphate isomerase, GPI
43	c3jzvA_	Alignment	not modelled	9.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein rru_a2000; **PDBTitle:** crystal structure of rru_a2000 from rhodospirillum rubrum: a cupin-22 domain.
44	d2f4pa1	Alignment	not modelled	8.6	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
45	d1rc6a_	Alignment	not modelled	8.3	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**YlbA-like
46	c3emrA_	Alignment	not modelled	8.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ectd; **PDBTitle:** crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
47	c2q30C_	Alignment	not modelled	8.0	25	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
48	c3l2hD_	Alignment	not modelled	7.7	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative sugar phosphate isomerase; **PDBTitle:** crystal structure of putative sugar phosphate isomerase (afe_0303)2 from acidithiobacillus ferrooxidans atcc 23270 at 1.85 a resolution
49	d1xsqa_	Alignment	not modelled	7.4	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA
50	c3fjsC_	Alignment	not modelled	7.2	17	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**uncharacterized protein with rmlc-like cupin fold; **PDBTitle:** crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
51	c2o8qA_	Alignment	not modelled	6.9	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein with a cupin-like fold and unknown2 function (bxe_c0505) from burkholderia xenovorans lb400 at 1.55 a3 resolution
52	c2opwA_	Alignment	not modelled	6.4	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phyhd1 protein;

52	c2opwA_	Alignment	not modelled	6.4	9	**PDBTitle:** crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
53	d1wzaa1	Alignment	not modelled	6.3	13	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
54	c3jurA_	Alignment	not modelled	6.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-poly-alpha-d-galacturonosidase; **PDBTitle:** the crystal structure of a hyperthermoactive exopolygalacturonase from2 thermotoga maritima
55	c3gjbA_	Alignment	not modelled	6.1	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cytc3; **PDBTitle:** cytc3 with fe(ii) and alpha-ketoglutarate
56	d2f2ha1	Alignment	not modelled	6.0	18	**Fold:**Putative glucosidase YicI, C-terminal domain **Superfamily:**Putative glucosidase YicI, C-terminal domain **Family:**Putative glucosidase YicI, C-terminal domain
57	d1y3ta1	Alignment	not modelled	5.7	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Quercetin 2,3-dioxygenase-like
58	c2yrvA_	Alignment	not modelled	5.7	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**at-rich interactive domain-containing protein 4a; **PDBTitle:** solution structure of the rbb1nt domain of human2 rb(retinoblastoma)-binding protein 1
59	d2a1xa1	Alignment	not modelled	5.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
60	c2vpvA_	Alignment	not modelled	5.2	10	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein mif2; **PDBTitle:** dimerization domain of mif2p