Phyre^2

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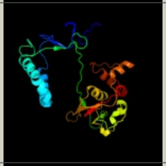
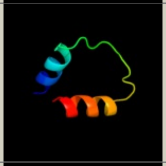
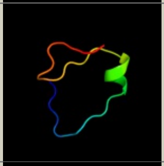
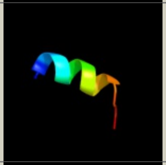
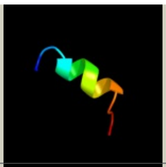
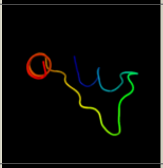
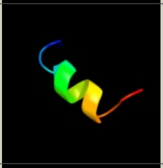
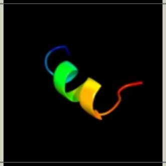
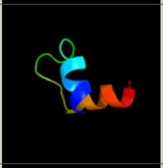
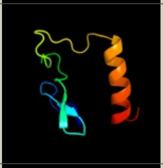
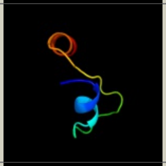
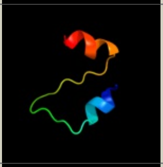
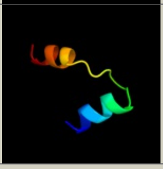
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2g5da1	Alignment		100.0	30	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
2	d2ae0x1	Alignment		100.0	99	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
3	d2pnwa1	Alignment		100.0	31	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
4	c3czbA_	Alignment		100.0	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transglycosylase; **PDBTitle:** crystal structure of putative transglycosylase from caulobacter2 crescentus
5	d2pi8a1	Alignment		100.0	96	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
6	c1vbkA_	Alignment		39.5	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
7	c2kvsA_	Alignment		37.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mw0776; **PDBTitle:** nmr solution structure of q7a1e8 protein from staphylococcus2 aureus: northeast structural genomics consortium target:3 zr215
8	c2opkC_	Alignment		29.9	20	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
9	d2v0ea1	Alignment		27.5	14	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
10	d1usua_	Alignment		26.2	17	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Hsp90 middle domain
11	d2ckca1	Alignment		25.2	14	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like

12	c2ckcA_	Alignment		25.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 7; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
13	c1hk7A_	Alignment		25.1	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp82; **PDBTitle:** middle domain of hsp90
14	c2ckaA_	Alignment		24.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 8; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
15	d2ckaa1	Alignment		24.9	21	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
16	d1ussa_	Alignment		24.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
17	d1dw0a_	Alignment		23.7	21	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
18	c1y6zA_	Alignment		21.8	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**heat shock protein, putative; **PDBTitle:** middle domain of plasmodium falciparum putative heat shock protein2 pf14_0417
19	c2gq0B_	Alignment		21.7	20	**PDB header:**chaperone, hydrolase **Chain:** B: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of the middle domain of htpg, the e. coli2 hsp90
20	c2dd4H_	Alignment		21.5	16	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**thiocyanate hydrolase beta subunit; **PDBTitle:** thiocyanate hydrolase (scnase) from thiobacillus thioparus2 recombinant apo-enzyme
21	d1ef5a_	Alignment	not modelled	21.4	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
22	d2ga1a1	Alignment	not modelled	21.3	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Alr1493-like
23	c3mayE_	Alignment	not modelled	21.0	12	**PDB header:**heme-binding protein **Chain:** E: **PDB Molecule:**possible exported protein; **PDBTitle:** crystal structure of a secreted mycobacterium tuberculosis heme-2 binding protein
24	c3pryA_	Alignment	not modelled	19.3	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp 90-beta; **PDBTitle:** crystal structure of the middle domain of human hsp90-beta refined at2 2.3 a resolution
25	c3g6iA_	Alignment	not modelled	19.0	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative outer membrane protein, part of carbohydrate **PDBTitle:** crystal structure of an outer membrane protein, part of a putative2 carbohydrate binding complex (bt_1022) from bacteroides3 thetaiotaomicron vpi-5482 at 1.93 a resolution
26	c2jroA_	Alignment	not modelled	18.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of so0334 from shewanella oneidensis. northeast2 structural genomics target sor75
27	c1wnfA_	Alignment	not modelled	18.2	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of ph0066 from pyrococcus horikoshii
28	d1yqaa1	Alignment	not modelled	18.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5

29	c2h9aA_	Alignment	not modelled	17.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron- **PDBTitle:** corrinoid iron-sulfur protein
30	d2ocda1	Alignment	not modelled	17.1	26	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
31	c3qmlC_	Alignment	not modelled	17.0	15	**PDB header:**chaperone/protein transport **Chain:** C: **PDB Molecule:**nucleotide exchange factor sil1; **PDBTitle:** the structural analysis of sil1-bip complex reveals the mechanism for2 sil1 to function as a novel nucleotide exchange factor
32	d1zvfa1	Alignment	not modelled	15.9	16	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
33	d2dl6a1	Alignment	not modelled	15.8	30	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
34	d2e9xd2	Alignment	not modelled	15.7	50	**Fold:**GINS/PriA/YqbF domain **Superfamily:**PriA/YqbF domain **Family:**SLD5 C-terminal domain-like
35	c2yxlA_	Alignment	not modelled	15.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein; **PDBTitle:** crystal structure of ph0851
36	c1zq1B_	Alignment	not modelled	15.2	33	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
37	d1ei5a2	Alignment	not modelled	15.1	20	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
38	c3l6gA_	Alignment	not modelled	15.1	28	**PDB header:**glycine betaine-binding protein **Chain:** A: **PDB Molecule:**betaine abc transporter permease and substrate binding **PDBTitle:** crystal structure of lactococcal opuac in its open conformation
39	d1v29b_	Alignment	not modelled	15.0	16	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
40	d2cnaa_	Alignment	not modelled	14.9	29	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Legume lectins
41	d1h8ca_	Alignment	not modelled	14.9	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
42	c2o1wB_	Alignment	not modelled	14.7	27	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
43	c2rqpA_	Alignment	not modelled	14.6	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**heterochromatin protein 1-binding protein 3; **PDBTitle:** the solution structure of heterochromatin protein 1-binding2 protein 74 histone h1 like domain
44	c3pvpA_	Alignment	not modelled	14.1	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
45	d2b9ea1	Alignment	not modelled	13.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
46	c3h4wA_	Alignment	not modelled	13.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatidylinositol-specific phospholipase c1; **PDBTitle:** structure of a ca+2 dependent phosphatidylinositol-specific2 phospholipase c (pi-plc) enzyme from streptomyces antibioticus
47	c1vzyA_	Alignment	not modelled	13.2	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of the bacillus subtilis hsp33
48	d1hsta_	Alignment	not modelled	12.7	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
49	d1vrba1	Alignment	not modelled	12.7	22	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
50	c1f3mB_	Alignment	not modelled	12.7	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** crystal structure of human serine/threonine kinase pak1
51	c1ynmA_	Alignment	not modelled	12.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**r.hinp1i restriction endonuclease; **PDBTitle:** crystal structure of restriction endonuclease hinp1i
52	d2b3aa1	Alignment	not modelled	12.4	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
53	c2dzkA_	Alignment	not modelled	12.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubx domain-containing protein 2; **PDBTitle:** structure of the ubx domain in mouse ubx domain-containing2 protein 2

54	d1uhma_	Alignment	not modelled	12.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
55	c3gasA_	Alignment	not modelled	12.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**heme oxygenase; **PDBTitle:** crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
56	d1yfua1	Alignment	not modelled	12.3	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**3-hydroxyanthranilic acid dioxygenase-like
57	c2xdvA_	Alignment	not modelled	12.1	17	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
58	c1y4sA_	Alignment	not modelled	12.1	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
59	d1i42a_	Alignment	not modelled	11.9	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
60	d2cr5a1	Alignment	not modelled	11.9	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
61	c1x3lA_	Alignment	not modelled	11.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph0495; **PDBTitle:** crystal structure of the ph0495 protein from pyrococcus horikoshii2 ot3
62	d2d28c1	Alignment	not modelled	11.7	31	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**EspE N-terminal domain-like **Family:**GSPII protein E N-terminal domain-like
63	d1hw7a_	Alignment	not modelled	11.7	20	**Fold:**Hsp33 domain **Superfamily:**Hsp33 domain **Family:**Hsp33 domain
64	c1hw7A_	Alignment	not modelled	11.7	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp33; **PDBTitle:** hsp33, heat shock protein with redox-regulated chaperone activity
65	c3o7kA_	Alignment	not modelled	11.6	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline2 decarboxylase from klebsiella pneumoniae
66	c3a52A_	Alignment	not modelled	11.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
67	d1s3sg_	Alignment	not modelled	11.3	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
68	d2b8na1	Alignment	not modelled	11.2	14	**Fold:**GckA/TtuD-like **Superfamily:**GckA/TtuD-like **Family:**GckA/TtuD-like
69	c3al6A_	Alignment	not modelled	11.2	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
70	d1usta_	Alignment	not modelled	11.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
71	c2d6fA_	Alignment	not modelled	10.8	26	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
72	d1vzya1	Alignment	not modelled	10.7	17	**Fold:**Hsp33 domain **Superfamily:**Hsp33 domain **Family:**Hsp33 domain
73	d1ixka_	Alignment	not modelled	10.7	12	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
74	c3bcwB_	Alignment	not modelled	10.5	9	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
75	d1prya_	Alignment	not modelled	10.2	16	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
76	d1bg6a1	Alignment	not modelled	10.1	23	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**N-(1-D-carboxylethyl)-L-norvaline dehydrogenase
77	d1ugpb_	Alignment	not modelled	9.8	10	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
78	d1gu2a_	Alignment	not modelled	9.8	13	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
79	d2bxxa1	Alignment	not modelled	9.7	41	**Fold:**Coronavirus RNA-binding domain **Superfamily:**Coronavirus RNA-binding domain **Family:**Coronavirus RNA-binding domain
						Fold:GYF/BRK domain-like

80	d2v0fa1	Alignment	not modelled	9.4	23	**Superfamily:**BRK domain-like **Family:**BRK domain-like
81	c3q6nF_	Alignment	not modelled	9.3	10	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock protein hsp 90-alpha; **PDBTitle:** crystal structure of human mc-hsp90 in p21 space group
82	d1o5ua_	Alignment	not modelled	9.1	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
83	c2c5sA_	Alignment	not modelled	9.0	13	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
84	d1wj4a_	Alignment	not modelled	9.0	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
85	d2f9zc1	Alignment	not modelled	8.8	23	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**CheD-like
86	c1a79B_	Alignment	not modelled	8.7	25	**PDB header:**endonuclease **Chain:** B: **PDB Molecule:**trna endonuclease; **PDBTitle:** crystal structure of the trna splicing endonuclease from2 methanococcus jannaschii
87	d1lfda_	Alignment	not modelled	8.6	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
88	d2qdyb1	Alignment	not modelled	8.4	6	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
89	c2kxjA_	Alignment	not modelled	8.3	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubx domain-containing protein 4; **PDBTitle:** solution structure of ubx domain of human ubxd2 protein
90	d1vq0a1	Alignment	not modelled	8.1	21	**Fold:**Hsp33 domain **Superfamily:**Hsp33 domain **Family:**Hsp33 domain
91	c3d6zA_	Alignment	not modelled	7.9	8	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**multidrug-efflux transporter 1 regulator; **PDBTitle:** crystal structure of r275e mutant of bmrr bound to dna and rhodamine
92	d1vl7a_	Alignment	not modelled	7.6	20	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
93	c2kngA_	Alignment	not modelled	7.5	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** solution structure of c-domain of lsr2
94	c1vq0A_	Alignment	not modelled	7.4	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of 33 kda chaperonin (heat shock protein 33 homolog)2 (hsp33) (tm1394) from thermotoga maritima at 2.20 a resolution
95	d2d6fa2	Alignment	not modelled	7.3	24	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
96	c3hefB_	Alignment	not modelled	7.2	17	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
97	c3kh0A_	Alignment	not modelled	7.2	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ral guanine nucleotide dissociation stimulator; **PDBTitle:** crystal structure of the ras-association (ra) domain of2 ralgds
98	d1xhna1	Alignment	not modelled	7.1	24	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
99	d1h2ka_	Alignment	not modelled	7.0	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)