Phyre^2

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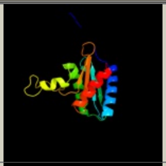
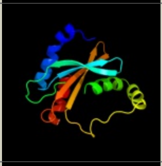
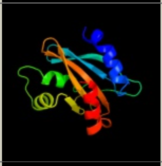
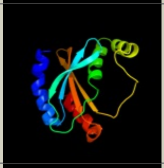
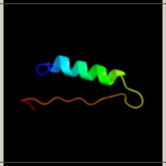
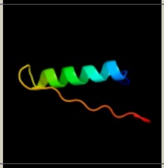
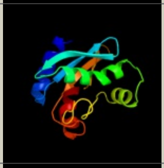
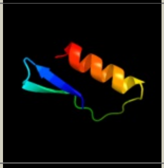
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a2la1	Alignment		100.0	31	**Fold:**Profilin-like **Superfamily:**GlcG-like **Family:**GlcG-like
2	c3fpvC_	Alignment		100.0	31	**PDB header:**heme binding protein **Chain:** C: **PDB Molecule:**extracellular haem-binding protein; **PDBTitle:** crystal structure of hbps
3	c1ysqA_	Alignment		92.3	12	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator yiaj; **PDBTitle:** the crystal structure of transcriptional regulator yaij
4	d2o9aa1	Alignment		88.8	13	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
5	c1yspA_	Alignment		85.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator kdgr; **PDBTitle:** crystal structure of the c-terminal domain of e. coli transcriptional2 regulator kdgr.
6	d1tf1a_	Alignment		83.9	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
7	c2w1rA_	Alignment		78.7	37	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of the c-terminal domain of b. subtilis2 spovt
8	d1mkma2	Alignment		74.0	17	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
9	c1mkmA_	Alignment		71.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
10	c2g7uB_	Alignment		69.8	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
11	c3bjnA_	Alignment		68.3	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, putative; **PDBTitle:** crystal structure of c-terminal domain of putative transcriptional2 regulator from vibrio cholerae, targeted domain 79-240

12	c3r4kD_	Alignment		62.3	22	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**transcriptional regulator, iclr family; **PDBTitle:** crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
13	c3obfA_	Alignment		61.4	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator, iclr family; **PDBTitle:** crystal structure of putative transcriptional regulator, iclr family;2 targeted domain 129...302
14	c3ksiA_	Alignment		60.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
15	d1iruk_	Alignment		57.6	28	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
16	d1irui_	Alignment		55.8	8	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
17	c3mq0A_	Alignment		51.4	11	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**transcriptional repressor of the blcabc operon; **PDBTitle:** crystal structure of agobacterium tumefaciens repressor blcr
18	c2ia2D_	Alignment		49.9	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
19	c2o9bA_	Alignment		48.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
20	c1q5rD_	Alignment		46.5	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**proteasome alpha-type subunit 1; **PDBTitle:** the rhodococcus 20s proteasome with unprocessed pro-peptides
21	d1vhma_	Alignment	not modelled	46.4	36	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
22	c2oolA_	Alignment	not modelled	46.3	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris
23	d1iru2_	Alignment	not modelled	44.5	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
24	d1p0za_	Alignment	not modelled	43.4	23	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
25	d1irul_	Alignment	not modelled	43.1	13	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
26	d1rypi_	Alignment	not modelled	43.0	19	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
27	c3nzwH_	Alignment	not modelled	42.6	19	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** H: **PDB Molecule:**proteasome component pup1; **PDBTitle:** crystal structure of the yeast 20s proteasome in complex with 2b
28	d1iruh_	Alignment	not modelled	39.8	11	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
29	d1ryph	Alignment	not modelled	39.6	17	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn

29	d1ryph_	Alignment	not modelled	39.6	17	hydrolases) **Family:**Proteasome subunits
30	c2o0yB_	Alignment	not modelled	38.4	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
31	d1rypl_	Alignment	not modelled	38.1	18	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
32	d1rypj_	Alignment	not modelled	35.7	11	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
33	d1q5qa_	Alignment	not modelled	35.6	20	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
34	c3bchA_	Alignment	not modelled	34.7	25	**PDB header:**cell adhesion, ribosomal protein **Chain:** A: **PDB Molecule:**40s ribosomal protein sa; **PDBTitle:** crystal structure of the human laminin receptor precursor
35	c1vhmB_	Alignment	not modelled	34.5	36	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein yebr; **PDBTitle:** crystal structure of an hypothetical protein
36	d1iruj_	Alignment	not modelled	34.4	8	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
37	c3dbaB_	Alignment	not modelled	33.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit **PDBTitle:** crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
38	c2w1tB_	Alignment	not modelled	32.0	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
39	d1q5rh_	Alignment	not modelled	31.8	8	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
40	c3ajvA_	Alignment	not modelled	31.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** splicing endonuclease from aeropyrum pernix
41	d1iru1_	Alignment	not modelled	29.6	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
42	c2zyzA_	Alignment	not modelled	29.4	10	**PDB header:**splicing **Chain:** A: **PDB Molecule:**putative uncharacterized protein pae0789; **PDBTitle:** pyrobaculum aerophilum splicing endonuclease
43	d1ryp1_	Alignment	not modelled	29.0	11	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
44	c2gx5B_	Alignment	not modelled	28.2	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**gtp-sensing transcriptional pleiotropic repressor cody; **PDBTitle:** n-terminal gaf domain of transcriptional pleiotropic repressor cody
45	c3nzxK_	Alignment	not modelled	28.0	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** K: **PDB Molecule:**proteasome component pre2; **PDBTitle:** crystal structure of the yeast 20s proteasome in complex with ligand2 2c
46	c3d3oA_	Alignment	not modelled	27.7	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator, icir family; **PDBTitle:** crystal structure of the effector domain of the putative2 transcriptional regulator iclr from acinetobacter sp. adp1
47	c2k31A_	Alignment	not modelled	27.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase 5a, cgmp-specific; **PDBTitle:** solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5
48	d1k3sa_	Alignment	not modelled	25.5	30	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
49	c1h4uA_	Alignment	not modelled	24.9	26	**PDB header:**extracellular matrix protein **Chain:** A: **PDB Molecule:**nidogen-1; **PDBTitle:** domain g2 of mouse nidogen-1
50	d2veaa1	Alignment	not modelled	24.7	19	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
51	d2o9ca1	Alignment	not modelled	24.6	44	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
52	c3p01C_	Alignment	not modelled	24.1	11	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
53	d2uubb1	Alignment	not modelled	23.5	36	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
54	d1rypk_	Alignment	not modelled	23.4	14	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
						PDB header:structural genomics, unknown function

55	c3eeaB_	Alignment	not modelled	23.3	28	**Chain:** B: **PDB Molecule:**gaf domain/hd domain protein; **PDBTitle:** the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
56	d1b28a_	Alignment	not modelled	22.8	17	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
57	d3c2wa1	Alignment	not modelled	22.3	27	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
58	d1r5ta_	Alignment	not modelled	21.1	6	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
59	c3mmhA_	Alignment	not modelled	20.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
60	c3bbnB_	Alignment	not modelled	20.3	14	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
61	c2fhgC_	Alignment	not modelled	19.4	8	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome, beta subunit; **PDBTitle:** crystal structure of mycobacterial tuberculosis proteasome
62	c3izbA_	Alignment	not modelled	18.6	29	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein rps0 (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
63	d2oola1	Alignment	not modelled	17.5	19	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
64	d1mq0a_	Alignment	not modelled	17.4	13	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
65	c2zkqb_	Alignment	not modelled	17.1	25	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
66	c3h4pj_	Alignment	not modelled	16.4	17	**PDB header:**hydrolase **Chain:** J: **PDB Molecule:**proteasome subunit alpha; **PDBTitle:** proteasome 20s core particle from methanocaldococcus2 jannaschii
67	d1bdta_	Alignment	not modelled	16.3	17	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
68	d1xmta_	Alignment	not modelled	16.2	29	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
69	d1iruc_	Alignment	not modelled	16.1	12	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
70	d1ktea_	Alignment	not modelled	16.0	38	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
71	d2gy9b1	Alignment	not modelled	15.9	23	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
72	c3c1sA_	Alignment	not modelled	15.6	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structure of grx1 in glutathionylated form
73	d1irub_	Alignment	not modelled	15.6	11	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
74	c3d5jB_	Alignment	not modelled	15.5	46	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-2, mitochondrial; **PDBTitle:** structure of yeast grx2-c30s mutant with glutathionyl mixed2 disulfide
75	d1wosa1	Alignment	not modelled	15.2	21	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
76	c2jacA_	Alignment	not modelled	15.1	38	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** glutaredoxin grx1p c30s mutant from yeast
77	d1egoa_	Alignment	not modelled	14.8	54	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
78	c3ipzA_	Alignment	not modelled	14.7	25	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-s14, chloroplastic; **PDBTitle:** crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
79	d1q5qh_	Alignment	not modelled	14.5	8	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
80	c2h6jI_	Alignment	not modelled	14.5	8	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**proteasome beta-type subunit 1; **PDBTitle:** crystal structure of the beta f145a rhodococcus proteasome (casp2 target)
						PDB header:hydrolase/rna binding protein

81	c3ieyB_	Alignment	not modelled	14.3	13	**Chain:** B: **PDB Molecule:**neq261; **PDBTitle:** crystal structure of the functional nanoarchaeum equitans trna2 splicing endonuclease
82	c2hzfA_	Alignment	not modelled	14.0	31	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes
83	c2ht9A_	Alignment	not modelled	13.8	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
84	c3ef5A_	Alignment	not modelled	13.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase; **PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
85	c1s1hB_	Alignment	not modelled	13.2	33	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
86	c3r2nC_	Alignment	not modelled	13.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytidine deaminase; **PDBTitle:** crystal structure of cytidine deaminase from mycobacterium leprae
87	d1jhba_	Alignment	not modelled	12.9	38	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
88	c2e7pC_	Alignment	not modelled	12.8	46	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
89	c2wulB_	Alignment	not modelled	12.5	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin related protein 5; **PDBTitle:** crystal structure of the human glutaredoxin 5 with bound2 glutathione in an fes cluster
90	d1pj5a1	Alignment	not modelled	12.5	21	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
91	c3p01A_	Alignment	not modelled	12.4	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
92	c2c5sA_	Alignment	not modelled	12.4	47	**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
93	c3o5yA_	Alignment	not modelled	12.1	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a
94	d1j2qh_	Alignment	not modelled	12.1	8	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
95	c1mc0A_	Alignment	not modelled	12.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3',5'-cyclic nucleotide phosphodiesterase 2a; **PDBTitle:** regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains
96	c2xznB_	Alignment	not modelled	11.7	33	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rps0e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
97	d1yarh1	Alignment	not modelled	11.5	8	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
98	c3h8qB_	Alignment	not modelled	11.0	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
99	c3l4nA_	Alignment	not modelled	11.0	42	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monothiol glutaredoxin-6; **PDBTitle:** crystal structure of yeast monothiol glutaredoxin grx6