Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8M6
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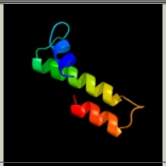
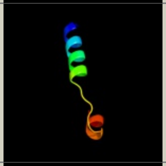
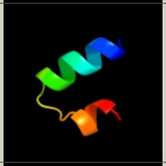
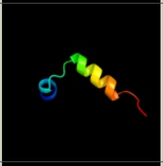
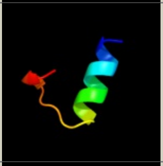
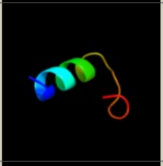
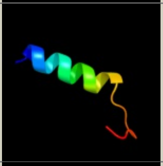
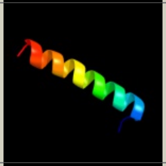
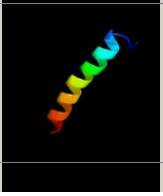
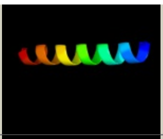
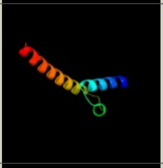
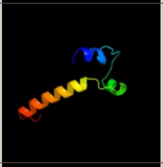
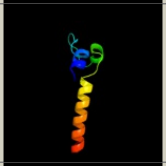
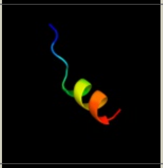
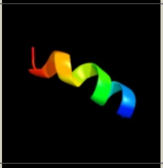
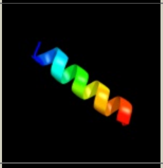
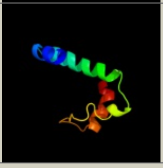
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gsva1	Alignment		52.5	22	**Fold:**Open three-helical up-and-down bundle **Superfamily:**YvfG-like **Family:**YvfG-like
2	c3kheB_	Alignment		21.0	19	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**calmodulin-like domain protein kinase isoform 3; **PDBTitle:** crystal structure of the calcium-loaded calmodulin-like domain of the2 cdpk, 541.m00134 from toxoplasma gondii
3	c2fvhB_	Alignment		20.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**urease gamma subunit; **PDBTitle:** crystal structure of rv1848, a urease gamma subunit urea (urea2 amidohydrolase), from mycobacterium tuberculosis
4	d1e7la2	Alignment		20.2	27	**Fold:**His-Me finger endonucleases **Superfamily:**His-Me finger endonucleases **Family:**Recombination endonuclease VII, N-terminal domain
5	d4ubpa_	Alignment		19.6	11	**Fold:**Urease, gamma-subunit **Superfamily:**Urease, gamma-subunit **Family:**Urease, gamma-subunit
6	d1ejxa_	Alignment		19.0	21	**Fold:**Urease, gamma-subunit **Superfamily:**Urease, gamma-subunit **Family:**Urease, gamma-subunit
7	c1ztaA_	Alignment		16.2	41	**PDB header:**dna-binding motif **Chain:** A: **PDB Molecule:**leucine zipper monomer; **PDBTitle:** the solution structure of a leucine-zipper motif peptide
8	c2f8mB_	Alignment		15.8	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** ribose 5-phosphate isomerase from plasmodium falciparum
9	c1zdbA_	Alignment		15.8	28	**PDB header:**igg binding domain **Chain:** A: **PDB Molecule:**mini protein a domain, z38; **PDBTitle:** phage-selected mini protein a domain, z38, nmr, minimized2 mean structure
10	d1r8ja1	Alignment		14.1	20	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
11	d1sv1a_	Alignment		13.7	20	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain

12	c3l19B_	Alignment		13.1	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calcium/calmodulin dependent protein kinase with a kinase **PDBTitle:** crystal structure of calcium binding domain of cpcdpk3, cgd5_820
13	c2vz4A_	Alignment		12.4	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hth-type transcriptional activator tipa; **PDBTitle:** the n-terminal domain of merr-like protein tipal bound to2 promoter dna
14	c1y2iC_	Alignment		12.0	18	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein s0862; **PDBTitle:** crystal structure of mcsg target apc27401 from shigella2 flexneri
15	d1y2ia_	Alignment		12.0	18	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
16	d1oeyj_	Alignment		11.9	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
17	c1nvpB_	Alignment		11.8	21	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription initiation factor iia alpha chain; **PDBTitle:** human tfiia/tbp/dna complex
18	d1nvpb_	Alignment		11.8	21	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
19	c1ce0B_	Alignment		11.0	29	**PDB header:**hiv-1 envelope protein **Chain:** B: **PDB Molecule:**protein (leucine zipper model h38-p1); **PDBTitle:** trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
20	c3mejA_	Alignment		10.8	18	**PDB header:**transcriptional regulator **Chain:** A: **PDB Molecule:**transcriptional regulator ywtf; **PDBTitle:** crystal structure of putative transcriptional regulator ywtf from2 bacillus subtilis, northeast structural genomics consortium target3 sr736
21	c2oqqB_	Alignment	not modelled	10.7	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor hy5; **PDBTitle:** crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
22	d2gr7a1	Alignment	not modelled	10.6	23	**Fold:**Pili subunits **Superfamily:**Pili subunits **Family:**YadA C-terminal domain-like
23	c2gr7C_	Alignment	not modelled	10.6	23	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**adhesin; **PDBTitle:** hia 992-1098
24	c3hh0C_	Alignment	not modelled	10.5	23	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, merr family; **PDBTitle:** crystal strucure of a transcriptional regulator, merr family2 from bacillus cereus
25	d1v8ga1	Alignment	not modelled	10.5	19	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
26	d1nh2b_	Alignment	not modelled	10.2	14	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
27	c2jd3B_	Alignment	not modelled	10.1	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**stbb protein; **PDBTitle:** parr from plasmid pb171
28	d1edla_	Alignment	not modelled	10.0	33	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
29	c3kltB_	Alignment	not modelled	9.9	13	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**vimentin;

						PDBTitle: crystal structure of a vimentin fragment
30	d1u2ca2	Alignment	not modelled	8.9	17	**Fold:**Dystroglycan, domain 2 **Superfamily:**Dystroglycan, domain 2 **Family:**Dystroglycan, domain 2
31	c2bcxB_	Alignment	not modelled	8.6	63	**PDB header:**calcium binding protein **Chain:** B: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of calmodulin in complex with a ryanodine2 receptor peptide
32	c2o7hF_	Alignment	not modelled	8.5	35	**PDB header:**transcription **Chain:** F: **PDB Molecule:**general control protein gcn4; **PDBTitle:** crystal structure of trimeric coiled coil gcn4 leucine zipper
33	c1ij2C_	Alignment	not modelled	8.4	35	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
34	c3k7zB_	Alignment	not modelled	8.4	35	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
35	c3k7zA_	Alignment	not modelled	8.4	35	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
36	c1rb6C_	Alignment	not modelled	8.4	35	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
37	c1swiA_	Alignment	not modelled	8.4	35	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
38	c1rb1A_	Alignment	not modelled	8.4	35	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
39	c1rb1B_	Alignment	not modelled	8.4	35	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
40	c1ij3B_	Alignment	not modelled	8.4	35	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
41	c1ij3C_	Alignment	not modelled	8.4	35	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
42	c3cvfA_	Alignment	not modelled	8.2	32	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**homer protein homolog 3; **PDBTitle:** crystal structure of the carboxy terminus of homer3
43	c3qfiA_	Alignment	not modelled	8.0	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** x-ray crystal structure of transcriptional regulator (ef0465) from2 enterococcus faecalis, northeast structural genomics consortium3 target efr190
44	d1fc2c_	Alignment	not modelled	7.6	39	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
45	c2pxgA_	Alignment	not modelled	7.5	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein; **PDBTitle:** nmr solution structure of omla
46	c1ij2B_	Alignment	not modelled	7.4	35	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
47	d1vr4a1	Alignment	not modelled	7.3	20	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
48	c1uixA_	Alignment	not modelled	7.3	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rho-associated kinase; **PDBTitle:** coiled-coil structure of the rhoa-binding domain in rho-2 kinase
49	c1xtzA_	Alignment	not modelled	7.2	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
50	d1lp1a_	Alignment	not modelled	7.1	22	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
51	c2a45J_	Alignment	not modelled	7.1	20	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** J: **PDB Molecule:**fibrinogen alpha chain; **PDBTitle:** crystal structure of the complex between thrombin and the central "e"2 region of fibrin
52	c1b6aA_	Alignment	not modelled	6.9	25	**PDB header:**angiogenesis inhibitor **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** human methionine aminopeptidase 2 complexed with tnp-470
53	c1e9zA_	Alignment	not modelled	6.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
54	d1e9ya2	Alignment	not modelled	6.8	11	**Fold:**Urease, gamma-subunit **Superfamily:**Urease, gamma-subunit **Family:**Urease, gamma-subunit
						PDB header:structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein

55	c3okzB_	Alignment	not modelled	6.7	21	gbs0355; **PDBTitle:** crystal structure of protein gbs0355 from streptococcus agalactiae,2 northeast structural genomics consortium target sar127
56	d2etda1	Alignment	not modelled	6.6	27	**Fold:**Bromodomain-like **Superfamily:**LemA-like **Family:**LemA-like
57	d1deeg_	Alignment	not modelled	6.3	33	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
58	c2juiA_	Alignment	not modelled	6.0	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**plne; **PDBTitle:** three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaracin ef
59	d1jfib_	Alignment	not modelled	5.9	24	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
60	c1jfiB_	Alignment	not modelled	5.9	24	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription regulator nc2 beta chain; **PDBTitle:** crystal structure of the nc2-tbp-dna ternary complex
61	d2jwda1	Alignment	not modelled	5.9	39	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
62	d1lp1b_	Alignment	not modelled	5.5	33	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
63	c1m25A_	Alignment	not modelled	5.5	100	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**major prion protein; **PDBTitle:** structure of synthetic 26-mer peptide containing 145-1692 sheep prion protein segment and c-terminal cysteine in tfe3 solution
64	c1r8jB_	Alignment	not modelled	5.5	20	**PDB header:**circadian clock protein **Chain:** B: **PDB Molecule:**kaia; **PDBTitle:** crystal structure of circadian clock protein kaia from2 synechococcus elongatus
65	c3cveC_	Alignment	not modelled	5.4	18	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**homer protein homolog 1; **PDBTitle:** crystal structure of the carboxy terminus of homer1
66	c3qgaD_	Alignment	not modelled	5.4	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**fusion of urease beta and gamma subunits; **PDBTitle:** 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
67	d2a3qa1	Alignment	not modelled	5.2	20	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
68	c2q4pA_	Alignment	not modelled	5.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
69	d1v2za_	Alignment	not modelled	5.2	20	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
70	c3jzaB_	Alignment	not modelled	5.2	37	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**uncharacterized protein drra; **PDBTitle:** crystal structure of human rab1b in complex with the gef domain of2 drra/sidm from legionella pneumophila
71	c1vtpA_	Alignment	not modelled	5.0	40	**PDB header:**targeting peptide **Chain:** A: **PDB Molecule:**vacuolar targeting peptide; **PDBTitle:** vacuolar targeting peptide from na-propi