Phyre^2

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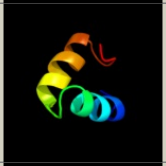
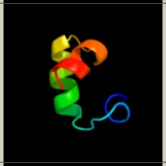
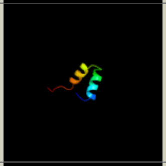
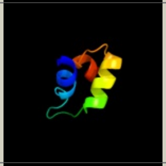
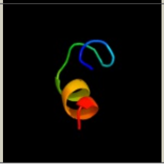
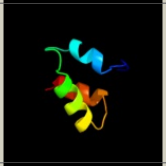
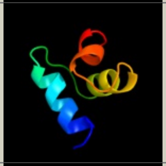
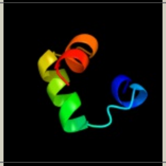
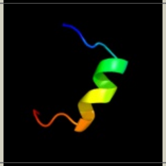
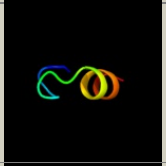
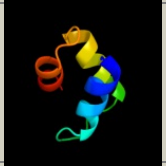
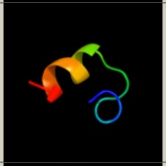
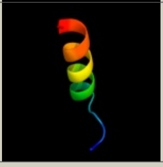
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tr8A_	Alignment		64.9	39	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**conserved protein (mth177); **PDBTitle:** crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
2	d1vega_	Alignment		40.9	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
3	d1veja1	Alignment		36.6	31	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
4	d2bwba1	Alignment		36.6	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
5	c2cwbA_	Alignment		36.2	34	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**chimera of immunoglobulin g binding protein g **PDBTitle:** solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
6	c2dahA_	Alignment		35.8	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquilin-3; **PDBTitle:** solution structure of the c-terminal uba domain in the2 human ubiquilin 3
7	d1vdla_	Alignment		35.8	29	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
8	c1wr1B_	Alignment		31.1	25	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
9	c2jy5A_	Alignment		30.2	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
10	d1ifya_	Alignment		28.3	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
11	d1aipc1	Alignment		28.1	47	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain

12	c2dnaA_	Alignment		27.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
13	c2d9sA_	Alignment		27.4	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cbl e3 ubiquitin protein ligase; **PDBTitle:** solution structure of rsgi ruh-049, a uba domain from mouse2 cdna
14	d1oqya1	Alignment		27.3	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
15	d2dnaa1	Alignment		25.0	25	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
16	c2dchX_	Alignment		25.0	50	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**putative homing endonuclease; **PDBTitle:** crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i
17	d1xb2b1	Alignment		24.1	35	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
18	d1z96a1	Alignment		24.0	38	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
19	d2cp9a1	Alignment		23.0	35	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
20	d1ir1s_	Alignment		22.8	26	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
21	d2daha1	Alignment	not modelled	21.9	28	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
22	d1efub3	Alignment	not modelled	21.1	47	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
23	c2do6A_	Alignment	not modelled	20.7	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of rsgi ruh-065, a uba domain from human2 cdna
24	d1rbli_	Alignment	not modelled	18.6	37	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
25	c1umqA_	Alignment	not modelled	16.5	17	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
26	d1umqa_	Alignment	not modelled	16.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
27	d1etxa_	Alignment	not modelled	15.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
28	d1uzhc1	Alignment	not modelled	15.4	37	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit

29	d1fipa_	Alignment	not modelled	15.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
30	c3lwfD_	Alignment	not modelled	15.1	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
31	d1ngka_	Alignment	not modelled	14.5	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
32	c3d19E_	Alignment	not modelled	14.1	25	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**conserved metalloprotein; **PDBTitle:** crystal structure of a conserved metalloprotein from bacillus cereus
33	d1bwvs_	Alignment	not modelled	14.0	32	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
34	d1bxni_	Alignment	not modelled	13.6	42	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
35	d1svdm1	Alignment	not modelled	13.1	26	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
36	d1ylfa1	Alignment	not modelled	12.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
37	c2jnhA_	Alignment	not modelled	12.9	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase cbl-b; **PDBTitle:** solution structure of the uba domain from cbl-b
38	d1x38a2	Alignment	not modelled	12.6	31	**Fold:**Flavodoxin-like **Superfamily:**Beta-D-glucan exohydrolase, C-terminal domain **Family:**Beta-D-glucan exohydrolase, C-terminal domain
39	d1wiva_	Alignment	not modelled	12.1	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
40	c3zv0A_	Alignment	not modelled	12.0	24	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein shq1; **PDBTitle:** structure of the shq1p-cbf5p complex
41	d1etob_	Alignment	not modelled	11.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
42	c3iv1F_	Alignment	not modelled	11.0	47	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**tumor susceptibility gene 101 protein; **PDBTitle:** coiled-coil domain of tumor susceptibility gene 101
43	d1ejxc2	Alignment	not modelled	10.6	34	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
44	c2y75F_	Alignment	not modelled	10.1	24	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
45	c2cosA_	Alignment	not modelled	10.0	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine protein kinase lats2; **PDBTitle:** solution structure of rsgi ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
46	d1id3c_	Alignment	not modelled	10.0	27	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
47	c3ju8B_	Alignment	not modelled	9.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinylglutamic semialdehyde dehydrogenase; **PDBTitle:** crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
48	c2bmmA_	Alignment	not modelled	9.5	15	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**thermostable hemoglobin from thermobifida fusca; **PDBTitle:** x-ray structure of a novel thermostable hemoglobin from the2 actinobacterium thermobifida fusca
49	d1v92a_	Alignment	not modelled	9.4	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
50	d1bdfa1	Alignment	not modelled	9.4	24	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RNA polymerase alpha subunit dimerisation domain
51	d8ruci_	Alignment	not modelled	9.1	26	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
52	d2ezia_	Alignment	not modelled	8.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
53	d1k3ra1	Alignment	not modelled	8.4	42	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
54	c2dakA_	Alignment	not modelled	8.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
55	d1wdds_	Alignment	not modelled	8.1	26	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit

56	d1e9yb2	Alignment	not modelled	8.1	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**alpha-subunit of urease, catalytic domain
57	d1q8ba_	Alignment	not modelled	8.1	27	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YjcS
58	d2ezha_	Alignment	not modelled	8.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
59	d1gk8i_	Alignment	not modelled	8.0	37	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
60	c1zvaA_	Alignment	not modelled	8.0	64	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** a structure-based mechanism of sars virus membrane fusion
61	d2v6ai1	Alignment	not modelled	7.9	37	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
62	d2f2ga1	Alignment	not modelled	7.8	43	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**TENA/THI-4
63	c3f44A_	Alignment	not modelled	7.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative monooxygenase; **PDBTitle:** crystal structure of putative monooxygenase (yp_193413.1) from2 lactobacillus acidophilus ncfm at 1.55 a resolution
64	c3iukB_	Alignment	not modelled	7.2	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative bacterial protein of unknown function2 (duf885, pf05960.1,) from arthrobacter aurescens tc1, reveals fold3 similar to that of m32 carboxypeptidases
65	d1ej7s_	Alignment	not modelled	7.1	26	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
66	d2jssa1	Alignment	not modelled	7.0	27	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
67	d1uzdc1	Alignment	not modelled	7.0	37	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
68	c1ygmA_	Alignment	not modelled	7.0	47	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein bsu31320; **PDBTitle:** nmr structure of mistic
69	d2hkja2	Alignment	not modelled	6.9	36	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
70	d2f5va2	Alignment	not modelled	6.9	20	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GMC oxidoreductases
71	c2f8nK_	Alignment	not modelled	6.8	33	**PDB header:**structural protein/dna **Chain:** K: **PDB Molecule:**histone h2a type 1; **PDBTitle:** 2.9 angstrom x-ray structure of hybrid macroh2a nucleosomes
72	c3lk6A_	Alignment	not modelled	6.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
73	d1ntca_	Alignment	not modelled	6.7	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
74	c3e7lD_	Alignment	not modelled	6.6	10	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
75	d1tzya_	Alignment	not modelled	6.6	33	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
76	c2kzhA_	Alignment	not modelled	6.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tryptophan biosynthesis protein trpcf; **PDBTitle:** three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
77	d1kx3c_	Alignment	not modelled	6.5	33	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
78	d1u35c1	Alignment	not modelled	6.4	20	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
79	c3cxjB_	Alignment	not modelled	6.4	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
80	d2g3qa1	Alignment	not modelled	6.3	34	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
81	c2rdxG_	Alignment	not modelled	6.2	21	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme, putative; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from roseovarius nubinhibens ism

82	c2o4wA_	Alignment	not modelled	6.1	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** t4 lysozyme circular permutant
83	c3exqA_	Alignment	not modelled	6.1	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
84	d1f66c_	Alignment	not modelled	6.0	27	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
85	c1f66C_	Alignment	not modelled	6.0	27	**PDB header:**structural protein/dna **Chain:** C: **PDB Molecule:**histone h2a.z; **PDBTitle:** 2.6 a crystal structure of a nucleosome core particle2 containing the variant histone h2a.z
86	d2cosa1	Alignment	not modelled	5.9	41	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
87	d1cuka1	Alignment	not modelled	5.9	50	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
88	c1xb2B_	Alignment	not modelled	5.8	35	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor ts, mitochondrial; **PDBTitle:** crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex
89	c2jssA_	Alignment	not modelled	5.8	27	**PDB header:**chaperone/nuclear protein **Chain:** A: **PDB Molecule:**chimera of histone h2b.1 and histone h2a.z; **PDBTitle:** nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
90	c3osyA_	Alignment	not modelled	5.8	41	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3c protease; **PDBTitle:** human enterovirus 71 3c protease
91	d1hioa_	Alignment	not modelled	5.7	33	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
92	d1mxaa1	Alignment	not modelled	5.7	23	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
93	d1eqza_	Alignment	not modelled	5.6	33	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
94	d2p02a1	Alignment	not modelled	5.5	31	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
95	d1qm4a1	Alignment	not modelled	5.5	23	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
96	d1euha_	Alignment	not modelled	5.5	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
97	c3kn1A_	Alignment	not modelled	5.4	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**golgi phosphoprotein 3; **PDBTitle:** crystal structure of golgi phosphoprotein 3 n-term2 truncation variant
98	c3c38A_	Alignment	not modelled	5.4	11	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**autoinducer 2 sensor kinase/phosphatase luxq; **PDBTitle:** crystal structure of the periplasmic domain of vibrio2 cholerae luxq
99	c3bmxB_	Alignment	not modelled	5.4	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase (ybbd) from bacillus subtilis